



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 117210

TO: Robert Landsman  
Location: rem/4d83/4c70  
Art Unit: 1647  
Wednesday, March 24, 2004

Case Serial Number: 09/646224

From: Peggy Ruppel  
Location: Biotech-Chem Library  
Phone: 571-272-2557  
REM E01b65  
peggy.ruppel@uspto.gov

### Search Notes

Dear Examiner Landsman:

The results for your search request are attached.

Feel free to contact me if you have any questions.

Thank you for using STIC services.

Peggy Ruppel  
2-2557

**BEST AVAILABLE COPY**



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STIC-Biotech/ChemLib

CRFE

117210

From: Landsman, Robert  
Sent: Thursday, March 18, 2004 1:18 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/646,224

my.

commercial and patent databases only and on disk:

SEQ ID NO:11-17

thanks

Robert Landsman, Ph.D  
Patent Examiner  
Remsen, Rm 4D83, AU 1647  
571.272.0888  
U.S. Patent and Trademark Office  
robert.landsman@uspto.gov

seq 11 - 215  
12 - 346  
13 - 223  
14 - 244  
15 - 409  
16 - 585  
17 - 223

MASS ael

RECEIVED  
MAR 18 2004  
STIC

Searcher: T. Ryzael  
Phone: 2-2857  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:36:49 ; Search time 29.3051 Seconds

(without alignments)  
4071.453 Million cell updates/sec

Title:	US-09-646-224A-11
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Sequence: 1 cagacaatgagaactcgcgt.....caacggttacgccttcgaag 215

Scoring table: IDENTITY\_NUC

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

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**Pred1.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90.2	42.0	3701	4	US-09-354-147C-6	Sequence 6, Appl1
2	90.2	42.0	5860	4	US-09-354-147C-41	Sequence 41, Appl
3	47.4	22.0	5822	4	US-09-354-147C-4	Sequence 4, Appl1
4	45.8	21.3	5875	4	US-09-354-147C-1	Sequence 1, Appl1
5	31.4	14.6	4062	4	US-09-620-312D-348	Sequence 348, Appl
6	30.2	14.0	780	4	US-08-956-171E-736	Sequence 736, Appl
7	30	14.0	1451	1	US-08-161-286-2	Sequence 2, Appl1
8	29.8	13.9	5544	3	US-08-851-843A-68	Sequence 68, Appl
9	29.8	13.9	5544	3	US-08-974-549A-111	Sequence 111, Appl
10	29.8	13.9	5544	3	US-08-854-050-68	Sequence 68, Appl
11	29.8	13.9	5544	4	US-09-430-323-68	GENERAL INFORMA
12	29.8	13.9	5544	4	US-08-912-951-111	Sequence 111, Appl
13	29.8	13.9	5544	4	US-09-402-181B-111	GENERAL INFORMA
14	29.8	13.9	5544	4	US-09-721-456-111	GENERAL INFORMA
15	28.6	13.3	1656	4	US-09-540-236-516	Sequence 516, Appl
16	28.6	13.3	2091	4	US-09-144-001C-1459	Sequence 1459, Appl
17	28.6	13.3	3105	4	US-08-956-171E-529	Sequence 529, Appl
18	28.6	13.3	65792	4	US-09-596-002-31	Sequence 31, Appl
19	28.2	13.1	4675	4	US-09-556-921-97	Sequence 97, Appl
20	27.8	12.9	308	4	US-08-985-171E-863	Sequence 863, Appl
21	27.8	12.9	2368	4	US-09-559-804-2	Sequence 2, Appl1
22	27.8	12.9	14602	1	US-08-597-236-1	Sequence 1, Appl1
23	27.8	12.9	14602	1	US-08-746-682A-1	Sequence 1, Appl1
24	27.6	12.8	1581	4	US-09-333-195A-16	Sequence 16, Appl
25	27.6	12.8	1596	4	US-09-333-195A-19	Sequence 19, Appl
26	27.6	12.8	3002	4	US-09-359-264A-1	Sequence 1, Appl1
27	27.2	12.7	526	1	US-08-666-878A-35	Sequence 35, Appl

C 28	27.2	12.7	526	4	US-09-175-928-35	Sequence 35, Appl
C 29	27	12.6	447	4	US-09-621-976-1068	Sequence 1068, A
C 30	27	12.6	474	4	US-09-621-976-1803	Sequence 1803, A
C 31	27	12.6	2103	4	US-09-107-532A-1440	Sequence 1440, A
C 32	26.8	12.5	1191	4	US-09-134-000C-1065	Sequence 1065, A
C 33	26.8	12.5	1299	4	US-09-350-985-33	Sequence 33, Appl
C 34	26.8	12.5	2636	4	US-09-370-807-5	Sequence 5, Appl
C 35	26.8	12.5	2636	4	US-09-921-255-5	Sequence 5, Appl
C 36	26.8	12.5	6156	4	US-08-891-640-1	Sequence 1, Appl
C 37	26.8	12.5	6156	4	US-09-723-535-3	Sequence 3, Appl
C 38	26.8	12.5	12173	4	US-09-723-535-3	Sequence 310, Appl
C 39	26.6	12.4	1351	4	US-09-205-258-114	Sequence 114, App
C 40	26.6	12.4	45175	4	US-09-455-702B-10	Sequence 106, App
C 41	26.4	12.3	509	4	US-09-221-017B-526	Sequence 526, App
C 42	26.4	12.3	426	4	US-09-621-976-9157	Sequence 9157, A
C 43	26.2	12.2	3981	4	US-08-259-164-1	Sequence 1, Appl
C 44	26.2	12.2	3981	4	US-08-403-663-1	Sequence 1, Appl
C 45	26.2	12.2	3981	4	US-08-473-204-1	Sequence 1, Appl

## ALIGNMENTS

```

RESULT 1
US-09-354-147C-6
; Sequence 6, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3699)
; OTHER INFORMATION: partial human NAN CDNA sequence
; NAME/KEY: unsure
; LOCATION: (922)
; OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is
; OTHER INFORMATION: Leu.
US-09-354-147C-6
Query Match          42.0%; Score 90.2; DB 4; Length 3701;
Best Local Similarity 96.8%; Pred. No. 2.8e-21;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY      81 AGAAGTCGTGATGGTACCGAGTACTATCATCAGAATGTAGCAACATTGATCTTCAGATGGCT   140
       |||||
DB      2351 AGAAGTCGTGATGGTACCAGTACTATCATCAGAATGTAGCACCACTGATCTTCAGATGGCT   2410
QY      141 TTGGATGGTTACCTGAGATGGTGTCCCAAGAAAA    175
       |||||
DB      2411 TTGGATGGTTACCTGAGATGGTGTCCCAAAAGCAA    2445

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	Query Match	Similarity	Score	DB	Length
Best Local	96.8%	42.0%	90.2	DB 4	5860
Matches	92	Conservative	0	Mismatches	3
				Indels	0
				Gaps	0

  

	Query	DB	Score	DB	Length
01	AGAAGTCGATGTTACACGATATCATCATGAGATGAGACCATGATTTGAGATGCT	140			
2978	AGAAGTCGATGTTACCGATATCATCATGAGATGAGACCATGATTTGAGATGCT	3037			
141	TTGATGCTTACCTGAGATGTTCCCAAGAAAA	175			
3038	TTGATGCTTACCTGAGATGTTCCCAAGAAAA	3072			

Query Match	22.0%;	Score	47.4;	DB	4;	Length	5822;
Best Local Similarity	60.5%;	Pred. No.	2.2e-06;				
Matches	78;	Conservative	0;	Mismatches	51;	Indels	0;
						Gaps	0

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/ RESULT 4
/ US-09-354-147C-1
/ Sequence 1, Application US/09354147C
/ Patent No. 6573067
/ GENERAL INFORMATION:
/ APPLICANT: Dib-Hajj, Sulayman
/ APPLICANT: Waxman, Stephen G.
/ TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
/ FILE REFERENCE: 44574-5004-01-US
/ CURRENT APPLICATION NUMBER: US/09/354,147C
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US 60/072,990
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: US 60/109,402
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: PCT/US99/02008
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1

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1 type: DNA
2 ORGANISM: Rattus norvegicus
3 FEATURE:
4 NAME/KEY: CDS
5 LOCATION: (41)..(5335)
6 OTHER INFORMATION: cDNA sequence for rat Nan
7 NAME/KEY: unsure
8 LOCATION: (1996)..(4042)
9 OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
10 OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
11 OTHER INFORMATION: or Lys.
12
13 US-09-354-147C-1

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Query Match	21.3%	Score 45.8	DB 4	Length 5875
Best Local Similarity	61.2%	Pred. No. 7.7e-06		
Matches 74	Conservative 0	Mismatches 47	Indels 0	Gaps 0

QY	81	AGAAGTCGAGTGTACCAACGATTA	CTACGAGATATAGACCACTGATCTT	CGAGATGCT	140
Db	2919	AGAAGTCGAGCGAGTGGAGCATGCT	CTCTCGGAATCAGACCAATTA	CACTTGAGATGATATCT	2978
QY	141	TTGATGCTPAACCGAGATGGTTCCCA	AAAAATTCCAGCGATTTT	TGTAACAACG	200
Db	2979	TTAGAAATTTACAGAAACAGTTTCC	CCCCAAAAGCAGCGATATGATGCTT	CCCCAAG	3033
QY	201	G	201		
Db	3039	G	3039		

RESULT 5  
US-09-620-312D-348/c  
Sequence 348, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyun  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aiding J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yungqing  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Dmanac, Radote T.  
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and  
FILE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pt\_fl\_genes Version 1.0  
SEQ ID NO 348  
LENGTH: 4062  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (25)..(2976)  
US-09-620-312D-348

Query Match 14.6%; Score 31.4; DB 4; Length 4062;  
Best Local Similarity 56.2%; Pred. No. 0.63;  
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CAGCAATGAGAACTCCGTACTACTGTGGAAGAAGCTTTAGTAAAGCACCCTTCTT 60

Db 507 CAGATAATTGGAACTGGGTAAACATCAAGTTGAACAAGTTCATTAGGAAGGCATGAG 448

Qy 61 TTCTTTTGTCTGATGTGAGAGTGTGATGATACCGATACCT 105  
Db 447 CGCTTTAGGAATAGCCACAGATGTAAATGTACCAAGTTGATT 403

RESULT 6  
US-08-956-171E-736/C  
Sequence 736, Application US/08956171E  
Patent No. 6593114

GENERAL INFORMATION:  
APPLICANT: Charles Kunach

Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 736:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 736:  
US-08-956-171E-736

Query Match 14.0%; Score 30.2; DB 4; Length 780;  
Best Local Similarity 49.1%; Pred. No. 0.8;  
Matches 80; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 7 ATGAGAACTCCGTACTACTATGTGGAAGAAGCTTTAGTAAAGCACCCTTCTT 66

Db 563 ATATACTGCCCGTATCGTATAAATGATCGGTTCTAAGTTAATGCACTGAACGCTT 504

Qy 67 TTGTTGATGTGAGAGTGTATGTTACCAAGTATCAAGTATCAAGTATGACACATGTA 126

Db 503 TAACTCTGTAATGAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 444

Qy 127 TCTTCAGATGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 169

Db 443 TGCTAAGCTTGAAGAACTAAGATGCCACCATTTGATTCGATA 401

RESULT 7  
US-08-161-286-2  
Sequence 2, Application US/08161286  
Patent No. 5674703

GENERAL INFORMATION:  
APPLICANT: WOO, SAVIO L. C.

APPLICANT: NORDLOH, PETER W.

APPLICANT: STENLUND, ARNE

TITLE OF INVENTION: PRISMAL VECTORS FOR GENE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.4mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/161,286  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 07/984,400  
FILING DATE: 02 DECEMBER 1992  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1451  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-161-286-2

Query Match 14.0%; Score 30; DB 1; Length 1451;  
Best Local Similarity 57.4%; Pred. No. 1.2;  
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Db 103 ACTATCAGATGTACGACATTCCTTCAGATGGCTTGATGGTTACCTGAGATGCT 162  
1244 ACTATCAGATGTACGACATTCCTTCAGATGGCTTGATGGTTACCTGAGATGCT 1303

Qy 163 TCCCAAGAAATTTCCAGCATTTTGTAC 196  
1304 TTCAAAAAAAACTGTTAGCATTTATGGCC 1337

Db

RESULT 8  
US-08-851-843A-68  
Sequence 68, Application US/08851843A  
Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Hartley, Calvin H.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(959..1216, 1273..1353, 1425..1543,  
LOCATION: 1595..1857, 1894..2286, 2326..2396, 2436..2705,  
LOCATION: 2746..2862, 2914..3083, 3125..3309, 3356..3504,  
LOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..4392,  
LOCATION: 4435..4597)  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRR)"  
US-08-851-843A-68

Query Match 13.9%; Score 29.8; DB 3; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 64 CTTTGTCTGATGCGAGAGCTGATGTTACGATTAACGATTAATCAGATGACACAT 123  
4364 GCTTCTGCTCTGCGAGAGTCAATGATGATGCTGCTGCGATTCAGACATTAAT 4423

Db 124 TGATCTCAGATGCGCTTGGATGTTACTGATGTTCCCA 168  
4424 TGACACATCAGGCTTTTGTCTTGATGATGAGATGTTGAA 4468

Qy

Db

RESULT 9  
US-08-974-549A-111  
Sequence 111, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Hartley, Calvin H.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997  
PRIOR APPLICATION DATA: US 08/851,843  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA: US 08/854,050  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA: US 08/911,312  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA: US 08/912,951  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA: US 08/915,503  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA: WO PCT/US97/17618  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA: WO PCT/US97/17885  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION: NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS: LENGTH: 5544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(959..1216, 1273..1353, 1425..1543,  
LOCATION: 1595..1857, 1894..2286, 2326..2396, 2436..2705,  
LOCATION: 2746..2862, 2914..3083, 3125..3309, 3356..3504,  
LOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..4392,  
LOCATION: 4435..4597)  
OTHER INFORMATION: /note= "Schizosaccharomyces pombe  
OTHER INFORMATION: telomerase catalytic subunit (TRT)"  
US-08-974-549A-111

Query Match 13.9%; Score 29.8; DB 3; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 64 CTTTGTCTGATGTGAGAGTCTGATGTATACCACTATACAGATGTACACCAT 123  
Db 4364 CGTTCTGTCTCTGAGAGTCAATGTATACGTCGCTCGAGACTTCACCAATAT 4423

Qy 124 TGATCTTCAGAGTGGCTTTGGATGTTACCTGAGATGGTTCCCA 168  
Db 4424 TGACACATCAGGCTTTTGTCTGGAATGAGAGATGGTTGAAA 4468

RESULT 10  
US-08-854-050-68  
Sequence 68, Application US/08854050  
Patent No. 6261836  
GENERAL INFORMATION:  
APPLICANT: Cecch, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: NO. 6261836el Telomerase

NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS: LENGTH: 5544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(959..1216, 1273..1353, 1425..1543,  
LOCATION: 1595..1857, 1894..2286, 2326..2396, 2436..2705,  
LOCATION: 2746..2862, 2914..3083, 3125..3309, 3356..3504,  
LOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..4392,  
LOCATION: 4435..4597)  
OTHER INFORMATION: /note= "Schizosaccharomyces pombe  
OTHER INFORMATION: telomerase catalytic subunit (TRT)"  
US-08-854-050-68

Query Match 13.9%; Score 29.8; DB 3; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 64 CTTTGTCTGATGTGAGAGTCTGATGTATACCACTATACAGATGTACACCAT 123  
Db 4364 CGTTCTGTCTCTGAGAGTCAATGTATACGTCGCTCGAGACTTCACCAATAT 4423

Qy 124 TGATCTTCAGAGTGGCTTTGGATGTTACCTGAGATGGTTCCCA 168  
Db 4424 TGACACATCAGGCTTTTGTCTGGAATGAGAGATGGTTGAAA 4468

RESULT 11  
US-09-430-323-68

GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"  
SEQUENCE DESCRIPTION: SEQ ID NO: 68  
US-09-430-323-68  
Query Match 13.9%; Score 29.8; DB 4; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
DB 4423  
4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468  
DB 4364 CTTTGTCTGATGTCAGAGTCTGATGTTACCAATATATACAGATGTAACCAT 123  
124 TGAATCTTCAGATGCTTTGAGTGTACCTGAGATGTTCCCA 168  
DB 4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468  
RESULT 12  
US-08-912-951-111  
Sequence 111, Application US/08912951  
Patent No. 6475789  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,951  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1959..1216, 1273..1353, 1425..1543,  
1595..1857, 1894..2286, 2326..2396, 2436..2705,  
2746..2862, 2914..3083, 3125..3309, 3356..3504,  
3546..3759, 3797..4046, 4086..4252, 4296..4392,  
4435..4597)  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"  
US-08-912-951-111  
Query Match 13.9%; Score 29.8; DB 4; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
DB 4423  
4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468  
DB 4364 CTTTGTCTGATGTCAGAGTCTGATGTTACCAATATATACAGATGTAACCAT 123  
124 TGAATCTTCAGATGCTTTGAGTGTACCTGAGATGTTCCCA 168  
DB 4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468

APPLICANT: Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,951  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1959..1216, 1273..1353, 1425..1543,  
1595..1857, 1894..2286, 2326..2396, 2436..2705,  
2746..2862, 2914..3083, 3125..3309, 3356..3504,  
3546..3759, 3797..4046, 4086..4252, 4296..4392,  
4435..4597)  
OTHER INFORMATION: /note="Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"  
US-08-912-951-111  
Query Match 13.9%; Score 29.8; DB 4; Length 5544;  
Best Local Similarity 55.2%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
DB 4423  
4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468  
DB 4364 CTTTGTCTGATGTCAGAGTCTGATGTTACCAATATATACAGATGTAACCAT 123  
124 TGAATCTTCAGATGCTTTGAGTGTACCTGAGATGTTCCCA 168  
DB 4424 TCACACATCAGCGCTTTTGTCTTGGAAGAGATGTTGAAA 4468



Oy 124 TGATCTTCAGATGCGTTTGATGATTACCTGATGATGTTCCAA 168  
Db 4424 TGACACATCAGCGTTTCTTTCTTGGAATGAGATGTTGAAA 4468

## RESULT 13

US-09-402-181B-111

## GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

OTHER INFORMATION: /note="Schizosaccharomyces pombe

telomerase catalytic subunit (TRT)"

SEQUENCE DESCRIPTION: SEQ ID NO: 111:

US-09-402-181B-111

Query Match

Best Local Similarity 13.9%; Score 29.8; DB 4; Length 5544;

Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 64 CTTTGTTCGATGCGAAGTCTGATGTTACAGATATACAGATGACCAT 123

Db 4364 CGTTCTTGTCCTGCGAAGTCAATGATGATGCTGCGAGACTTCAGCAATAT 4423

Oy 124 TGATCTTCAGATGCGTTTGATGATTACCTGATGATGTTCCAA 168

Db 4424 TGACACATCAGCGTTTCTTTCTTGGAATGAGATGTTGAAA 4468

## RESULT 14

US-09-721-456-111

## GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-No. 6617110-2000

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

OTHER INFORMATION: /note="Schizosaccharomyces pombe

telomerase catalytic subunit (TRT)"

SEQUENCE DESCRIPTION: SEQ ID NO: 111:

US-09-721-456-111

Query Match

Best Local Similarity 13.9%; Score 29.8; DB 4; Length 5544;

Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 64 CTTTGTTCGATGCGAAGTCTGATGTTACAGATATACAGATGACCAT 123

Db 4364 CGTTTCTTGCTCTGCAGAAATCAATGTAGTCGTGCTCGAGACTTCAGCAATAT 4423  
QY 124 TGATCTTACGATGCTTGTGATGTCTACCTGAGATGTTCCCA 168  
Db 4424 TGACACATCAGCTTTTGTCTTGAAATGAGAGATGTTGAAA 4468

## RESULT 15

US-09-540-236-516  
; Sequence 516, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 516  
; LENGTH: 1656  
; TYPE: DNA  
; ORGANISM: M.catarrhalis  
US-09-540-236-516

Query Match 13.3%; Score 28.6; DB 4; Length 1656;  
Best Local Similarity 64.2%; Pred.No.3.9;  
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 192 GTACCA 198  
Db 1423 TTAATAA 1429

Search completed: March 22, 2004, 23:17:31  
Job time : 35.3051 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:36:49 ; Search time 47.1608 Seconds  
(without alignments)  
4071.453 Million cell updates/sec

Title: US-09-646-224A-12

Perfect score: 346  
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Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents: NA.\*  
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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
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5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	35.8	10.3	5822	4	US-09-354-147C-4 Sequence 4, Appli
4	35.8	10.3	5875	4	US-09-354-147C-1 Sequence 1, Appli
5	34.8	10.1	1830121	4	US-09-557-884-1 Sequence 1, Appli
6	34.8	10.1	1830121	4	US-09-643-990A-1 Sequence 1, Appli
7	31.8	9.2	1632	4	US-09-540-236-1710 Sequence 1710, Ap
8	31.8	9.2	119211	4	US-09-598-002-40 Sequence 40, Appli
9	31.6	9.1	1095	4	US-09-543-681A-3259 Sequence 3259, Ap
10	31.6	9.0	3090	4	US-09-762-724-5 Sequence 5, Appli
11	31	9.0	1664976	4	US-08-916-421B-1 Sequence 1, Appli
12	30.6	8.8	1835	3	US-09-338-671-3 Sequence 3, Appli
13	30.4	8.8	1764	3	US-08-481-190-14 Sequence 14, Appli
14	30.4	8.8	1764	5	PCT-US93-00869-14 Sequence 14, Appli
15	29.8	8.6	514	4	US-09-621-976-3851 Sequence 3851, Ap
16	29.6	8.6	11887	4	US-08-961-527-146 Sequence 146, App
17	29.4	8.5	264	4	US-09-134-001C-2149 Sequence 2149, Ap
18	29.4	8.5	4692	4	US-08-961-527-220 Sequence 220, App
19	29.4	8.5	8797	2	US-08-723-306-6 Sequence 6, Appli
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27	28.6	8.3	514	4	US-09-621-976-3850 Sequence 3850, Ap

28	28.6	8.3	515	4	US-09-621-976-3849 Sequence 3849, Ap
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31	28.6	8.3	519	4	US-09-621-976-3854 Sequence 3854, Ap
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33	28.6	8.3	1717	1	US-08-645-865-12 Sequence 12, Appli
34	28.6	8.3	1956	4	US-09-715-858-1 Sequence 1, Appli
35	28.6	8.3	2191	3	US-09-039-555B-12 Sequence 12, Appli
36	28.6	8.3	2236	3	US-09-234-163-11 Sequence 11, Appli
37	28.6	8.3	2236	3	US-08-901-379-11 Sequence 11, Appli
38	28.6	8.3	2612	4	US-09-484-970B-142 Sequence 142, App
39	28.6	8.3	176373	3	US-09-128-155-17 Sequence 17, Appli
40	28.6	8.3	640681	4	US-09-790-988-1 Sequence 1, Appli
41	28.4	8.2	2050	4	US-09-026-001A-5 Sequence 5, Appli
42	28.4	8.2	2901	4	US-09-606-312-1 Sequence 1, Appli
43	28.4	8.2	5549	4	US-08-956-171E-188 Sequence 188, App
44	28.2	8.2	428	4	US-09-621-976-3856 Sequence 3856, Ap
45	28.2	8.2	174493	4	US-09-804-471A-3 Sequence 3, Appli

#### ALIGNMENTS

```
RESULT 1
US-09-354-147C-6
; Sequence 6, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Maxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US/09/354,147C
; CURRENT APPLICATION NUMBER: US/09-072,990
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3699)
; OTHER INFORMATION: partial human Nan cDNA sequence
; NAME/KEY: unsure
; LOCATION: (922)
; OTHER INFORMATION: Y = c or t. Xaa at amino acid position 308 is
; OTHER INFORMATION: Leu.
US-09-354-147C-6
Query Match 13.5%; Score 46.8; DB 4; Length 3701;
Best Local Similarity 88.1%; Pred. No. 6.8e-06;
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
QY 46 TAACTTAATGAAAT-AGAACTTCCGATCTCTGAGCACTGAGGCTC-TCTGGCGCT 102
Db 2817 TAACTTAATGAAATGAAATGAACTTCCGACTCTGAGCACTGAGGCTCTCTGGCGCT 2876
QY 103 GTCCCAATTGAAGATGAAGGT 126
Db 2877 GTCCCAATTGAAGATGAAGGT 2900
RESULT 2
US-09-354-147C-41
; Sequence 41, Application US/09354147C
; Patent No. 6573067
```

GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: full length cDNA sequence for human Nan  
US-09-354-147C-41

Query Match 13.5%; Score 46.8; DB 4; Length 5860;  
Best Local Similarity 88.1%; Pred. No. 8 6e-06;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACCTTAATGAAAT-AGAACCTTCGGATCTAGACGACTGAGGCTTC-TGTCGCGCT 102  
DB 3444 TAACCTTAATGAAATGAACTCCTCCGACTCTAGACGACTGAGGCTTCGTCGCGCT 3503  
QY 103 GTCCAGTTGAAGATGAAGT 126  
DB 3504 GTCCAGTTGAAGATGAAGT 3527

RESULT 3  
US-09-354-147C-4  
Sequence 4, Application US/09354147C  
Patent No. 6573067  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 5822  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (19)..(5313)  
NAME/KEY: unsure  
LOCATION: (5804)  
OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t  
US-09-354-147C-4

Query Match 10.3%; Score 35.8; DB 4; Length 5822;  
Best Local Similarity 80.6%; Pred. No. 0.053;  
Matches 54; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 61 AGAACCTTCGGATCTAGACGACTGAGGCTCT-CGTCGCTGTCCAGTTGAAGAA 119  
DB 3386 AGTCCTTCGGAACTGTGAGCGCTGAGACTCTGCGGCGACTGTCTCAGTTGAAGAA 3445  
QY 120 TGAAGT 126  
DB 3446 TGAAGT 3452

RESULT 4  
US-09-354-147C-1  
Sequence 1, Application US/09354147C  
Patent No. 6573067  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 5875  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (41)..(5335)  
NAME/KEY: unsure  
LOCATION: (1996)..(4042)  
OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position  
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn  
US-09-354-147C-1

Query Match 10.3%; Score 35.8; DB 4; Length 5875;  
Best Local Similarity 80.6%; Pred. No. 0.053;  
Matches 54; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 61 AGAACCTTCGGATCTAGACGACTGAGGCTCT-CGTCGCTGTCCAGTTGAAGAA 119  
DB 3405 AGTCCTTCGGACTGTGCGGCGCTGAGACTCTGCGGCGCTGTCCAGTTGAAGAA 3464  
QY 120 TGAAGT 126  
DB 3465 TGAAGT 3471

RESULT 5  
US-09-557-884-1  
Sequence 1, Application US/09557884  
Patent No. 6506581  
GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1

Query Match 10.1%; Score 34.8; DB 4; Length 1830121;  
Best Local Similarity 54.8%; Pred. No. 2;  
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 64511 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 7 TTCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
Db 64571 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 67 TTCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
Db 64571 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 127 ACATTC 132  
Db 64631 TCTTGC 64636

RESULT 6  
US-09-643-990A-1  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

Query Match 10.1%; Score 34.8; DB 4; Length 1830121;  
Best Local Similarity 54.8%; Pred. No. 2;  
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 64511 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 7 TTCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
Db 64571 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 67 TTCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
Db 64571 TGCCGATCTAACCGCTGTACGAGATCTCGAATCTCTAATCTTAATGAATTAGAACC 66  
QY 127 ACATTC 132  
Db 64631 TCTTGC 64636

RESULT 7  
US-09-540-236-1710/C  
Sequence 1710, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI  
FILE REFERENCE: 2709,2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 1710  
LENGTH: 1632  
TYPE: DNA  
ORGANISM: M.cathartalis  
US-09-540-236-1710

Query Match 9.2%; Score 31.8; DB 4; Length 1632;  
Best Local Similarity 52.7%; Pred. No. 0.68;  
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 74 TCTAGAGCACTGAGGCTCTCTGCGCTGCTCCAGTTGAAGGATGAAGTACATCTT 133  
Db 1540 TTTGTGCTATGATTAATCTTCAATGCTGTGAGCATTAATGATGATATAGCTTTT 1481  
QY 134 GCAGAGAAATGGGTAGAGTTCAGTTACAGAGAAAGTGAAGACACAGTCTTTT 193  
Db 1480 TTAGCATTCGCTGGAGTGTGAATTAATCAACTTTGTAATGGCGAGAGTCTTTT 1421  
QY 194 TGGGCTGAGAT 204  
Db 1420 TTAGTTAGAT 1410

RESULT 8  
US-09-596-002-40  
; Sequence 40, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:  
; APPLICANT: Lagace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Beeg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US  
; CURRENT APPLICATION NUMBER: US/09/596,002  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/140,121  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 40  
; LENGTH: 119211  
; TYPE: DNA  
; ORGANISM: M. catarrhalis  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte template ID No. 6632636 40  
; PUBLICATION INFORMATION:  
US-09-596-002-40

Query Match 9.2%; Score 31.8; DB 4; Length 119211;  
Best Local Similarity 52.7%; Pred. No. 5.6;  
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 74 TCTAGACACGACGAGCCCTGCTGCGCTGCCAGTTTGAAGAAATGAAGTACATTCT 133  
DB 109316 TTTTGCTGCTAATGAACTTCTTATGCTGTGAGCAATGAGTGTATAGCCCTTTT 109375  
QY 134 GCAGAAAGATGGGTGAAGTTCACTTAACAGAGAAAGTGAAGAACCAAGTCTTTT 193  
DB 109376 TTAGCAATTCGGCTTGCTGATGCTGAATTAATCAACTTTGTAATGCGACAGTCTTTT 109435

QY 194 TGGGCTGAGAT 204  
DB 109436 TTAGTTAGAT 109446

RESULT 9  
US-09-543-681A-3259  
; Sequence 3259, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 3259  
; LENGTH: 1095  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-3259

Query Match 9.1%; Score 31.6; DB 4; Length 1095;  
Best Local Similarity 52.2%; Pred. No. 0.65;  
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 98 GCGCTGTCCCAAGTTGAAGAAATGAAGTACATTCTGCAAGAAAGATGGTGAAGTTGAG 157  
DB 847 GAGCTGACCTTCTTTAAATATATGCTTAAGAAATTAACGAGGATGAAGCGGTATTTGTTGGG 906

QY 158 TTAACAGAAAGGTGAAGAAAGCAACAGTCTTTTGGCTGAGATTCTCTTAATGTC 217  
DB 907 CATACCATATATGTTGTGCAAGATACCGTTATGCTGCAATCTTGCGGAGTCTC 966  
QY 218 CAAGCTTTCTCTG 231  
DB 967 CCACTTATATATAG 980

RESULT 10  
US-09-762-724-5  
; Sequence 5, Application US/09762724  
; Patent No. 6664053  
; GENERAL INFORMATION:  
; APPLICANT: Kovacs, et al.  
; TITLE OF INVENTION: Identification of a region of the major surface  
; FILE REFERENCE: 4239-58054  
; CURRENT APPLICATION NUMBER: US/09/762,724  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: PCT/US99/18750  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 60/096,805  
; PRIOR FILING DATE: 1998-08-17  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3090  
; TYPE: DNA  
; ORGANISM: Pneumocystis carinii sp. f. hominis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3090)  
US-09-762-724-5

Query Match 9.0%; Score 31; DB 4; Length 3090;  
Best Local Similarity 49.7%; Pred. No. 1.8;  
Matches 79; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 148 AGAAGTTAGTTACAGAGAAAGGTGGAAGAACCAACAGTCTTTTGGGCTGAGATTTC 207  
DB 1795 AGAAATGCCATTAATGCTCTAAGAGGGGTATGATCTTTTCTTTGATGCTTTTC 1854  
QY 208 CTTAATTGCCAAGCTTTCTCGGTTACTTACAGCCCTGCCAGTCTTGAATTGAG 267  
DB 1855 CAAAACGTACATGTGAGCTATGTATAAAGACGTGCAAGTAGTGCAAAATATTCGA 1914  
QY 268 GGGTAGAGAAAGCCTAAGATATCTTTCTACCTTAAA 306  
DB 1915 GAAATATGCAAGCATCATATTAATGATTCCTTAAA 1953

RESULT 11  
US-08-916-421B-1/c  
; Sequence 1, Application US/08916421B  
; Patent No. 6503729  
; GENERAL INFORMATION:  
; APPLICANT: Bult et al.  
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ-  
; PATENT NO. 6503729  
; FILE REFERENCE: P8275  
; CURRENT APPLICATION NUMBER: US/08/916,421B  
; CURRENT FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/024,428  
; PRIOR FILING DATE: 1996-08-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1664976  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii  
; FEATURE:

NAME/KEY: misc\_feature  
LOCATION: (28222)..(28222)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (28257)..(28258)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84773)..(84773)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84808)..(84808)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84812)..(84812)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98120)..(98120)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98159)..(98159)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98239)..(98239)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98266)..(98266)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98343)..(98343)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (103998)..(103998)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (148948)..(148948)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (163385)..(163385)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (191989)..(191989)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (191995)..(191995)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (231980)..(231980)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (234187)..(234187)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (234220)..(234220)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (234814)..(234814)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (309398)..(309398)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (309418)..(309418)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (312837)..(312837)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (312993)..(312993)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (319226)..(319226)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature

LOCATION: (559167)..(559167).  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (559241)..(559241)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (600992)..(600992)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (622708)..(622708)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (657081)..(657081)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (657203)..(657203)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (674435)..(674435)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (682442)..(682442)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (713652)..(713652)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (741684)..(741684)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (779455)..(779455)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (779676)..(779676)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (85539)..(85539)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (871619)..(871619)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1084830)..(1084830)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1096846)..(1096846)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1119881)..(1119881)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1130881)..(1130881)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1310988)..(1310988)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1313224)..(1313224)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1349473)..(1349473)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1349491)..(1349491)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1470091)..(1470091)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1569020)..(1569020)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1602912)..(1602912)

OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1603734)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1637998)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1664854)..  
OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

Query Match 9.0%; Score 31; DB 4; Length 1664976;  
Best Local Similarity 48.1%; Pred. No. 36;  
Matches 88; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 31 AATCTGGAATCTCTTAATTATGGAATTAGAACCTTCGGATCTTACAGACATGAGGC 90  
DB 1437358 AATATAGATTAATGTCAGAAATTAATGGAATTAATGACTTGAATTTGAAA 1437299  
QY 91 CTCTGTCGCTGCTCCAGTTGAAGATGAAGTACTTCTGAGAAAGATGGGTGA 150  
DB 1437298 AACATGTTGTTGCTTAAGTTGTTACAAATCTGCTTAATGAAAGAGAGTGA 1437239  
QY 151 AGTCAGTTAACAAGAAAGTGAAGACCAACAGTTCTTTTGGCTGAGATTTCCTT 210  
DB 1437238 GAGACACTTATAGGAGAGACTTCCAGAAACAAAGAGTGAAGATTAATT 1437179  
QY 211 AAA 213  
DB 1437178 ATA 1437176

RESULT 12  
US-09-338-671-3  
Sequence 3, Application US/09338671  
Patent No. 6194638  
GENERAL INFORMATION:  
APPLICANT: Dhugga, Kanwarpal  
APPLICANT: Fallis, Patricia Lynne  
TITLE OF INVENTION: Alteration of Hemichloase  
FILE REFERENCE: 0782  
CURRENT APPLICATION NUMBER: US/09/338,671  
EARLIER FILING DATE: 1999-06-22  
EARLIER APPLICATION NUMBER: 60/090,416  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 1827  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (567)..  
US-09-338-671-3

Query Match 8.8%; Score 30.6; DB 3; Length 1835;  
Best Local Similarity 62.3%; Pred. No. 1.9;  
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 160 AACAGAGAAAGGTGAGAAACCAACAGTTCTTTTGGCTGAGATTCTTAATTGCA 219  
DB 1706 AACTCATGAGGTGAATTAACAACAGTCTTTATGCCGTGAATTTGGATGAGATG 1765  
QY 220 AGCTTTCTGGGTTC 236  
DB 1766 AGCATCTCATTTATTC 1782

RESULT 13

US-08-481-190-14  
Sequence 14, Application US/08481190  
Patent No. 6160204  
GENERAL INFORMATION:  
APPLICANT: John C. Steffens  
TITLE OF INVENTION: Polyphehol Oxidase cDNA  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,190  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 203,533  
FILING DATE: 02-24-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: UA 816 CIP  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1764 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-481-190-14

Query Match 8.8%; Score 30.4; DB 3; Length 1764;  
Best Local Similarity 53.3%; Pred. No. 2.1;  
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 98 GGCCTGCCAGTTGAAGATGAGTACATTCTGCAAGAAAGTGGTGAAGTTG 157  
DB 117 GCGTATCAAGTTTCAAGTTTCATGCAAGCCCAACATATGTTGGCGAGCATGACA 176  
QY 158 TTAACAGAGAAAGGTGAGAAACCAACAGTTCTTTTGGGCTGAGATTCTTAATTGC 217  
DB 177 AAACCTGACACTGTGATGAGCGCAATGTTCTTTTGAAGGTTAGAGGTCTTTATGTC 236

RESULT 14  
PCT-US93-00869-14  
Sequence 14, Application PC/TUS9300869  
GENERAL INFORMATION:  
APPLICANT: John C. Steffens  
TITLE OF INVENTION: Polyphehol Oxidase cDNAs: Cloning  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh



OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00869  
FILING DATE: 19930129  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: CRF D-1057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1764 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US93-00869-14

Query Match 8.8%; Score 30.4; DB 5; Length 1764;  
Best Local Similarity 53.3%; Pred. No. 2.1;  
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 98 GCGCTGCCAGTTGAGGATGAGTACATTCTGCAGAGAGATGGTAGAGTTGAG 157  
DB 117 GCGTAATCAAGTTTCAAGTTTCATGCAACGCAACATATATGTGGCGAGATGACAA 176  
QY 158 TTAACAGAGAAAGGTGAGAAAGCCACACATTTCTTTTGGGCTGAGATTTCTTAATTGC 217  
DB 177 AAACCTTGACACTGTTGATAGCGCAATGTTCTTTAGGGTTAGAGAGTCTTTATGTGTGC 236

## RESULT 15

US-09-621-976-3851  
Sequence 3851, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 3851  
LENGTH: 514  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..401  
US-09-621-976-3851

Query Match 8.6%; Score 29.8; DB 4; Length 514;  
Best Local Similarity 64.2%; Pred. No. 1.9;  
Matches 43; Conservative 1; Mismatches 23; Indels 0; Gaps 0;

QY 129 ATTCTGACAGAGATGGTAGAGTTCACTTAACAGAGAAAGTGGAAGACCAACAGTT 188  
DB 322 ATTGACGACGACGAGTGCACATGCAGATACAGAAAACCATCAAGAAGACAGTT 381  
QY 189 CTTTTTG 195  
DB 382 TCTTTGG 388

Search completed: March 22, 2004, 23:17:46  
Job time : 62.1608 secs

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:36:49 ; Search time 30.3955 Seconds  
(without alignments)  
4071.453 Million cell updates/sec

Title: US-09-646-224a-13

Perfect score: 223  
Sequence: 1 ggcgcacccaccaccatc.....aggaattccagcattcct 223

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	107.8	48.3	3701 4 US-09-354-147C-6	Sequence 6, Appli
2	107.8	48.3	5860 4 US-09-354-147C-41	Sequence 41, Appli
3	83.6	37.5	5822 4 US-09-354-147C-4	Sequence 4, Appli
4	72.8	32.6	5875 4 US-09-354-147C-1	Sequence 1, Appli
5	56	25.1	6048 4 US-09-634-920-3	Sequence 3, Appli
6	56	25.1	6048 4 US-09-514-907A-1	Sequence 1, Appli
7	56	25.1	6048 4 US-09-896-994-1	Sequence 1, Appli
8	52.2	23.4	6348 4 US-09-976-594-756	Sequence 756, App
9	52.2	23.4	6371 3 US-08-836-325-13	Sequence 13, Appli
10	52.2	23.4	6404 3 US-08-836-325-14	Sequence 14, Appli
11	50.6	22.7	3033 3 US-08-836-325-1	Sequence 1, Appli
12	50.6	22.7	6452 3 US-08-836-325-9	Sequence 9, Appli
13	50.4	22.6	5874 3 US-08-843-417-9	Sequence 9, Appli
14	50.4	22.6	5874 4 US-09-527-013-9	Sequence 9, Appli
15	50.2	22.5	6344 3 US-08-843-417-1	Sequence 1, Appli
16	50.2	22.5	6344 4 US-09-527-013-1	Sequence 1, Appli
17	50.2	22.5	6524 4 US-08-669-656A-1	Sequence 1, Appli
18	50.2	22.5	6527 4 US-08-669-656A-7	Sequence 7, Appli
19	50.2	22.5	7052 4 US-08-669-656A-5	Sequence 5, Appli
20	49	22.0	6826 3 US-09-024-020B-8	Sequence 8, Appli
21	49	22.0	6826 4 US-09-425-043-8	Sequence 8, Appli
22	47.4	21.3	5977 3 US-09-024-020B-1	Sequence 1, Appli
23	47.4	21.3	5977 4 US-09-425-043-1	Sequence 1, Appli
24	47.4	21.3	6007 3 US-09-024-020B-2	Sequence 2, Appli
25	47.4	21.3	6007 4 US-09-425-043-2	Sequence 2, Appli
26	47.4	21.3	6556 3 US-09-024-020B-7	Sequence 7, Appli
27	47.4	21.3	6556 4 US-09-425-043-7	Sequence 7, Appli

28	47.4	21.3	6586 3 US-09-024-020B-43	Sequence 43, Appli
29	47.4	21.3	6586 4 US-09-425-043-43	Sequence 43, Appli
30	45	20.2	5106 4 US-09-976-594-1104	Sequence 1104, Ap
31	43.8	19.6	7218 1 US-08-232-463-14	Sequence 14, Appli
32	39.6	17.8	568 3 US-07-998-289B-10	Sequence 10, Appli
33	39.6	17.8	2279 3 US-07-998-289B-3	Sequence 3, Appli
34	38.6	17.3	6315 2 US-08-808-793-2	Sequence 2, Appli
35	38.6	17.3	6315 3 US-08-772-512A-2	Sequence 2, Appli
36	38.6	17.3	6318 2 US-08-808-793-1	Sequence 1, Appli
37	38.6	17.3	6318 3 US-08-772-512A-1	Sequence 1, Appli
38	37.2	16.7	5461 3 US-07-998-289B-7	Sequence 7, Appli
39	37.2	16.7	6513 1 US-08-338-702-7	Sequence 7, Appli
40	37.2	16.7	6513 1 US-08-337-339-7	Sequence 7, Appli
41	37.2	16.7	6513 1 US-08-724-095-7	Sequence 7, Appli
42	37.2	16.7	6513 5 PCT-US95-14262-7	Sequence 7, Appli
43	37.2	16.7	6513 5 PCT-US95-14378-7	Sequence 7, Appli
44	37.2	16.7	6519 2 US-08-808-793-24	Sequence 24, Appli
45	32.4	14.5	1104 4 US-09-134-001C-841	Sequence 841, App

#### ALIGNMENTS

RESULT 1  
US-09-354-147C-6  
Sequence 6, Application US/09354147C  
Patent No. 6573067  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: Y = c or t. Xaa at amino acid position 308 is  
OTHER INFORMATION: Leu.  
US-09-354-147C-6

Query Match 48.3%; Score 107.8; DB 4; Length 3701;  
Best Local Similarity 96.0%; Pred. No. 1.4e-23;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY	52	AAGGTGGTGCATATGCTTCATAGTGCCTACTCTCCATCTCGAATGTTTGCTGT	111
DB	2896	AAGGTGGTGCATATGCTTCATAGTGCCTACTCTCCATCTCGAATGTTTGCTGT	2954
QY	112	CTGCCTCATTTTCTGCTCGATATTTTGAATCTGGAGTACTCTTTTCTGGAATA	171
DB	2955	CTGCCTCATTTTCTGCTCGATATTTTGAATCTGGAGTACTCTTTTCTGGAATA	3012
QY	172	TTTGGAAATGATTCATTCAGTGAACACT	200
DB	3013	TTTGGAAATGATTCATTCAGTGAACACT	3040

```
RESULT 2
US-09-354-147C-41
; Sequence 41, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human Nan
US-09-354-147C-41

Query Match          48.3%; Score 107.8; DB 4; Length 5860;
Best Local Similarity 96.0%; Pred. No. 1,6e-23;
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 111
    |||||
DB 3523 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 3581
    |||||

QY 112 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAANA 171
    |||||
DB 3582 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAANA 3639
    |||||

QY 172 TTGGGAATGCATTCATGGAACAGACT 200
    |||||
DB 3640 TTGGGAATGCATTCATGGAACAGACT 3667
    |||||

RESULT 3
US-09-354-147C-4
; Sequence 4, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; NAME/KEY: unsure
```

```
LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-09-354-147C-4

Query Match          37.5%; Score 83.6; DB 4; Length 5822;
Best Local Similarity 82.5%; Pred. No. 4,3e-16;
Matches 132; Conservative 0; Mismatches 24; Indels 4; Gaps 3;

QY 52 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 111
    |||||
DB 3448 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 3506
    |||||

QY 112 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAANA 171
    |||||
DB 3507 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAAG 3564
    |||||

QY 172 TTGGGAATGCATTCATGGAACAGACTTTAGGAATTT 211
    |||||
DB 3565 TTGGGAATGCATTCATGGAACAGACTTAATATAT 3603
    |||||

RESULT 4
US-09-354-147C-1
; Sequence 1, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; NAME/KEY: unsure
; LOCATION: (196)..(4042)
; OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
; OTHER INFORMATION: or Lys.
US-09-354-147C-1

Query Match          32.6%; Score 72.8; DB 4; Length 5875;
Best Local Similarity 78.9%; Pred. No. 9e-13;
Matches 112; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 52 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 111
    |||||
DB 3467 AAGGTGGTGTCAATGCTCTCATAGTGGCCATACCTCCCATTCCTGAATGTTTGGCTGT 3525
    |||||

QY 112 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAANA 171
    |||||
DB 3526 CTGCGCTCATTTCTGGCTGCTGATTTTGTATTCGGGAGATATCTTCCTTCCTGGAAG 3583
    |||||

QY 172 TTGGGAATGCATTCATGGAACAGACT 193
    |||||
DB 3584 TTGGGAATGCATTCATGGAACAGACT 3605
    |||||

RESULT 5
```

US-09-634-920-3  
Sequence 3, Application US/09634920  
Patent No. 6342357  
GENERAL INFORMATION:  
APPLICANT: Spiawski, Igor  
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND  
TITLE OF INVENTION: SCNA AND METHODS FOR DETECTING SAME  
FILE REFERENCE: 2323-155  
CURRENT APPLICATION NUMBER: US/09/634,920  
PRIOR FILING DATE: 2000-08-09  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/190,057  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 3  
LENGTH: 6048  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(6048)  
US-09-634-920-3

Query Match 25.1%; Score 56; DB 4; Length 6048;  
Best Local Similarity 68.8%; Pred. No. 1.3e-07;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

Qy 40 TTTGTTTCCATAGAGTGTGTCATGCTCTCATAGTGCATACCTCCATCTCTGAA 99  
Db 3949 TTTAGGGGCGATGAGGGTGTGTCTCATAGCCCTGGGGCGCCATCCCTCA-TCATGAA 4007  
Qy 100 TGTTCCTGCTGTGCTCCTCATTTTCTGCTGCTGATTTTGTATTCGGAGATATCTTCT 159  
Db 4008 CGTCTCTCTGCTGTGCTCCTCATTTTCTGCTGCTGATTTTGTATTCGGAGATATCTTCT 4065  
Qy 160 TTTCTGGAATAATTTGGGAATGATTCATGGA 193  
Db 4066 TTTGCGGGGAAGTTGGAGGTGATCAACGAGA 4099

RESULT 6  
US-09-514-907A-1  
Sequence 1, Application US/09514907A  
Patent No. 6567705  
GENERAL INFORMATION:  
APPLICANT: Kenneth B. Stokes  
TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL  
SENSING BY CARDIAC PACEMAKERS THROUGH  
GENETIC TREATMENT  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705tris LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/514,907A  
FILING DATE: 08-Feb-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6048 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-514-907A-1

Query Match 25.1%; Score 56; DB 4; Length 6048;  
Best Local Similarity 68.8%; Pred. No. 1.3e-07;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

Qy 40 TTTGTTTCCATAGAGTGTGTCATGCTCTCATAGTGCATACCTCCATCTCTGAA 99  
Db 3949 TTTAGGGGCGATGAGGGTGTGTCTCATAGCCCTGGGGCGCCATCCCTCA-TCATGAA 4007  
Qy 100 TGTTCCTGCTGTGCTCCTCATTTTCTGCTGCTGATTTTGTATTCGGAGATATCTTCT 159  
Db 4008 CGTCTCTCTGCTGTGCTCCTCATTTTCTGCTGCTGATTTTGTATTCGGAGATATCTTCT 4065  
Qy 160 TTTCTGGAATAATTTGGGAATGATTCATGGA 193  
Db 4066 TTTGCGGGGAAGTTGGAGGTGATCAACGAGA 4099

RESULT 7  
US-09-896-994-1  
Sequence 1, Application US/09896994  
Patent No. 6665563  
GENERAL INFORMATION:  
APPLICANT: Ken Stokes  
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATME  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563tris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/896,994  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION NUMBER: 09/514,907  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6048 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-896-994-1

Query Match 25.1%; Score 56; DB 4; Length 6048;  
Best Local Similarity 68.8%; Pred. No. 1.3e-07;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

40 TTTGTTTTCATTAAGTGTGTCATGCTCATAGGTCATACCTCCATTCCTGAA 99  
|||||

DB 3949 TTTGAGGCATGAGGTGTGTGTCAATGCCCTGTGGGCGCATCCCTCCA-TCATGAA 4007  
|||||

QY 100 TGTGTTGCTGTCTGCTCATTTTCTGCTGCTGATTTGTAATTCGGAGATACCTCT 159  
|||||

DB 4008 CGTCTCTCGTCTGCTCATCTTCTGGCTCATCTTCAGCATCATGAGGCGTAACCTC- 4065  
|||||

QY 160 TTTCTCGAATAATTGGGAAATGCAATTCATGGA 193  
|||||

DB 4066 TTTGGGGGAAGTTGGAGGATGATCAACGAGA 4099  
|||||

RESULT 8

US-09-976-594-756  
Sequence 756, Application US/09976594  
Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO 756

LENGTH: 6348

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME: misc. feature

OTHER INFORMATION: Incyte ID No. 6673549 1719478CBI

US-09-976-594-756

Query Match 23.4%; Score 52.2; DB 4; Length 6348;  
Best Local Similarity 73.4%; Pred. No. 1.9e-06;  
Matches 80; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 52 AAGGTGTCATGTCATGCTCTCATAGTGCATACCTCCCATTCGTGATGTTGCTTGT 111  
|||||

DB 3937 AGGTCGTGTGATGATGCACTCATAGAGCAATTCCTTCCA-TCATGATGCTACTTGT 3995  
|||||

QY 112 CTGCTCATTTTCTGGCTCGATTTTGTATTCTGGAGATACCTTCTT 160  
|||||

DB 3996 GTGCTTATATTCTGGCTGATATTTCAGCATTCATGAGGAGTAATTGTTT 4044  
|||||

RESULT 9

US-08-836-325-13  
Sequence 13, Application US/08836325  
Patent No. 6110672

GENERAL INFORMATION:

APPLICANT: Mandel, Gail

APPLICANT: Halegoua, Simon

APPLICANT: Borden, Laurence A.

TITLE OF INVENTION: Peripheral Nervous System Specific

TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,

TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Ave., N. W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,325

FILING DATE: 2-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14251

FILING DATE: 02-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/482,401

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/334,029

FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917, 0240002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 6371 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: DNA (genomic)

US-08-836-325-13

Query Match 23.4%; Score 52.2; DB 3; Length 6371;  
Best Local Similarity 73.4%; Pred. No. 1.9e-06;  
Matches 80; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 52 AAGGTGTCATGTCATGCTCTCATAGTGCATACCTCCCATTCGTGATGTTGCTTGT 111  
|||||

DB 3937 AGGTCGTGTGATGATGCACTCATAGAGCAATTCCTTCCA-TCATGATGCTACTTGT 3995  
|||||

QY 112 CTGCTCATTTTCTGGCTCGATTTTGTATTCTGGAGATACCTTCTT 160  
|||||

DB 3996 GTGCTTATATTCTGGCTGATATTTCAGCATTCATGAGGAGTAATTGTTT 4044  
|||||

RESULT 10

US-08-836-325-14  
Sequence 14, Application US/08836325  
Patent No. 6110672

GENERAL INFORMATION:

APPLICANT: Mandel, Gail

APPLICANT: Halegoua, Simon

APPLICANT: Borden, Laurence A.

TITLE OF INVENTION: Peripheral Nervous System Specific

TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,

TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN &amp; FOX P.L.L.C.

STREET: 1100 New York Ave., N. W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836.325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482.401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334.029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6404 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-836-325-14

Query Match 23.4%; Score 52.2; DB 3; Length 6404;  
Best Local Similarity 73.4%; Pred. No. 2e-06;  
Matches 80; Conservative 0; Mismatches 28; Indels 1; Gaps 1;  
QY 52 AGGTGGTGCATAGCTCTCATAGAGTGCACATCTCCCATCTCGAATGTTTGTCTGT 111  
DB 3970 AGGTCGCTGTGATGACATCATATGAGCAATTCCTTCCA-TCAATGATGTCTACTGT 4028  
QY 112 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGATACCTTCTT 160  
DB 4029 GTGCTTATATTTCTGCTGATATTCAGCATCATGGAGATATTTGTTT 4077

RESULT 11  
US-08-836-325-1  
Sequence 1, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halesoua, Simon  
APPLICANT: Borden, Laurence A.  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836.325  
FILING DATE: 2-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482.401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334.029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3033 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3033  
US-08-836-325-1

Query Match 22.7%; Score 50.6; DB 3; Length 3033;  
Best Local Similarity 72.5%; Pred. No. 4.5e-06;  
Matches 79; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
QY 52 AGGTGGTGCATAGCTCTCATAGAGTGCACATCTCCCATCTCGAATGTTTGTCTGT 111  
DB 1057 AGGTAGTGCATAGCTCATATGAGCAATTCCTTCCA-TCAATGATGTCTACTGT 1115  
QY 112 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGATACCTTCTT 160  
DB 1116 GTGCTTATATTTCTGCTGATATTTACATCATGGAGTCAATGTGTTT 1164

RESULT 12  
US-08-836-325-9  
Sequence 9, Application US/08836325  
Patent No. 6110672  
GENERAL INFORMATION:  
APPLICANT: Mandel, Gail  
APPLICANT: Halesoua, Simon  
APPLICANT: Borden, Laurence A.  
TITLE OF INVENTION: Peripheral Nervous System Specific  
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,  
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C  
STREET: 1100 New York Ave., N. W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836.325  
FILING DATE: 2-MAY-1997

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14251  
FILING DATE: 02-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/482,401  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/334,029  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0917.0240002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6452 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 326..6277  
US-08-843-325-9

Query Match 22.7%; Score 50.6; DB 3; Length 6452;  
Best Local Similarity 72.5%; Pred. No. 6.1e-06;  
Matches 79; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 52 AAGGTGCTGCTCAATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGTCT 111  
DB 4241 AAGGTGCTGCTCAATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGTCT 4299  
QY 112 CTGACCTATTTCTGAGCTCGTATTTGTATTCGGAGATATCTTCTT 160  
DB 4300 GTGCTTATTTCTGCTATTTTTCATGCTATGAGATGATCTGTTT 4348

RESULT 13  
US-08-843-417-9  
Sequence 9, Application US/08843417  
Patent No. 6184349  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
APPLICANT: Delgado, Stephen G  
APPLICANT: Fish, Linda M  
APPLICANT: Sangameswaran, Lakshmi  
APPLICANT: Rabert, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 525 University Ave  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/843,417  
FILING DATE: April 15, 1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796  
REFERENCE/DOCKET NUMBER: 28340-P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-324-7041  
TELEFAX: (415)-324-0638  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5874 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-843-417-9

Query Match 22.6%; Score 50.4; DB 3; Length 5874;  
Best Local Similarity 69.0%; Pred. No. 6.7e-06;  
Matches 98; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 54 GGTGTGCTCAATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGTCT 113  
DB 3804 GGTGTGCTCAATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGTCT 3862  
QY 114 GCTTCATTTCTGAGCTCGTATTTGTATTCGGAGATATCTTCTTCTTCTGAAAAT 173  
DB 3863 GCTTCATTTCTGAGCTCGTATTTGTATTCGGAGATATCTTCTTCTTCTGAAAAT 3920  
QY 174 TGGGAATGCTATTCATGGAAC 195  
DB 3921 TTGGAGGTGCTATTCATGGAAC 3942

RESULT 14  
US-09-527-013-9  
Sequence 9, Application US/09527013  
Patent No. 6479259  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
APPLICANT: Delgado, Stephen G  
APPLICANT: Fish, Linda M  
APPLICANT: Sangameswaran, Lakshmi  
APPLICANT: Rabert, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 525 University Ave  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/527,013  
FILING DATE: 16-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/843,417  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William  
REGISTRATION NUMBER: 31,796  
REFERENCE/DOCKET NUMBER: 28340-P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-324-7041  
TELEFAX: (415)-324-0638  
INFORMATION FOR SEQ ID NO: 9:



## SEQUENCE CHARACTERISTICS:

LENGTH: 5874 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 9

US-09-527-013-9

Query Match 22.6%; Score 50.4; DB 4; Length 5874;

Best Local Similarity 69.0%; Pred. No. 6.7e-06;

Matches 99; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 54 GGTGGTGTCAATGCTCTCATAGGTGCAATCCCATTCCTGAATGTTTGGCTGTCT 113

Db 3804 GGTGGTGTGAGATCCCTGGTGGGCGCATCCCATCCA-TCATGAATGTCTCTCTGTCT 3862

QY 114 GCTTCATTTTCTGGCTGTCTATTTTGTATTTCTGGAGATATCTTCTTTCTGGAATTT 173

Db 3863 GCTTCATTTTCTGGCTGTCTATTTTGTATTTCTGGAGATATCTTCTTTCTGGAATTT 173

QY 174 TGGGAATGCATTCATGGAAC 195

Db 3921 TTGGAGGTGCTCACTATATAC 3942

## RESULT 15

US-08-843-417-1

Sequence 1, Application US/08843417

Patent No. 6184349

GENERAL INFORMATION:

APPLICANT: Herman, Ronald C

APPLICANT: Delgado, Stephen G

APPLICANT: Fish, Linda M

APPLICANT: Sangameswaran, Lakshmi

APPLICANT: Rabert, Douglas K

TITLE OF INVENTION: CLONED PERIPHERAL NERVE

TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White &amp; McNuliffe

STREET: 525 University Ave

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.A.

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/843,417

FILING DATE: April 15, 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 28340-P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)-324-7041

TELEFAX: (415)-324-0638

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6344 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

## ORIGINAL SOURCE:

ORGANISM: rat

TISSUE TYPE: Dorsal root ganglia

CELL TYPE: Peripheral nerve

US-08-843-417-1

Query Match 22.5%; Score 50.2; DB 3; Length 6344;

Best Local Similarity 60.7%; Pred. No. 8e-06;

Matches 99; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 13 CCCCATCTGTATAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 72

Db 3788 CTCGACCGCTGCGGCTGTCTGTCTGATTCGAAGGATGAGGATGATGATGATGATGATGAT 3847

QY 73 ATAGTCCATTAATCTCCATTCCTGAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 132

Db 3848 GTGGGCGCCATCCCTTCCA-TCATGAACGTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3906

QY 133 ATTTGTATTCTGGAGATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 175

Db 3907 CTTCAGCATCATGAGGCTGAACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3949

Search completed: March 22, 2004, 23:17:49

Job time: 33.3955 secs

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APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

```

? FILE REFERENCE: 44574-5004-01-US
? CURRENT APPLICATION NUMBER: US/09/354,147C
? CURRENT FILING DATE: 1999-07-16
? PRIOR APPLICATION NUMBER: US 60/072,990
? PRIOR FILING DATE: 1998-01-29
? PRIOR APPLICATION NUMBER: US 60/109,402
? PRIOR FILING DATE: 1998-11-20
? PRIOR APPLICATION NUMBER: PCT/US99/02008
? PRIOR FILING DATE: 1999-01-29
? NUMBER OF SEQ ID NOS: 44
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 41
? LENGTH: 5860
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (31)..(5403)
? OTHER INFORMATION: full length cDNA sequence for human NAN
US-09-354-147C-41

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Query Match 19.3%; Score 47; Length 5860;  
 Query Local Similarity 90.9%;  
 Predicted Local Similarity 90.9%;  
 Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DY 36 GGCACAAATTTAAGGGCTGGATGGATATCGTTTATGACGCTGTGATTCCACAG 90  
| | | | |  
Db 3789 GGCACAAATTTAAGGGCTGGATGGATATGATATGACGCTGTGATTCCACAG 3843

### RESULT 3

US-08-843-41/-9  
; Sequence 9, Application US/08843417  
; Patent No. 6184349

GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
APPLICANT: Delgado, Stephen G  
APPLICANT: Fish, Linda M  
APPLICANT: Sangameswaran, Lakshmi  
APPLICANT: Rabert, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/843,417
? FILING DATE: April 15, 1997

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ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William  
REGISTRATION NUMBER: 31,796  
REFERENCE/DOCKET NUMBER: 26340-P1  
TELECOMMUNICATION INFORMATION:

```

? INFORMATION FOR SEQ ID NO: 9
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5874 base pairs
? TYPE: nucleic acid
? STRANDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: cDNA
?

```

;  
; ANTI-SENSE: NO  
US-08-843-417-9

Query Match	17.0%;	Score	41.4;	DB 3;	Length	5874;			
Best Local Similarity	72.0%;	Score	No. 0.00025;						
Matches	54;	Conservative	0;	Mismatches	21;	Indels	0;	Gaps	0

```

Qy      20 TTCTGCTTTTGTGCAGGCACATTTAAAGGGCTGATTCGTTATGACGCTGTG   79
          ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4073 TTGCACCTTGCAAGTGGACAATTAAAGCTGGATGACATTAATGATGACGCTGTG   41

```

QY 80 ATTCACAGAGTGA 94  
||| |  
Db 4133 ATTCCTGGGAGGTCA 4147

#### RESULT 4

US-09-527-013-9  
; Sequence 9, Application US/09527013  
; Patent No. 6479259  
AGENCY: AUTOMATRON

GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
Delgado, Stephen G  
Fish, Linda M  
Sangameswaran, Lakshmi  
Rabert, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 525 University Ave  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Parentin Release #1.0, Version #1.30
6
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/527, 013
9  FILING DATE: 16-Mar-2000
10 CLASSIFICATION: <Unknown>

```

```

? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 5874 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: unknown
?     TOPOLOGY: unknown
?     MOLECULE TYPE: cDNA
?     HYPOTHETICAL: NO
?
?

```

SEQUENCE DESCRIPTION:	SEQ ID NO:
US-09-527-013-9	9:

Query Match	17.0%;	Score 41.4;	DB 4;	Length 5874;
Best Local Similarity	72.0%;	Pred. NO. 0.00025;		
Matches 54;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0.

20 TTCTGCTTTTTCAGGCACAACTTAAGGCTGATGATATCGTTATGCAGCTGTG 79

Db 4073 TTGCAGCTTCGACAGTGCACCTTTAAAGCTGAGATGACATATATGATGACCTGTTG 4132  
QY 80 ATTCCAGAGGTGA 94  
Db 4133 ATTCCGGAGGTGA 4147

RESULT 5  
US-08-843-417-1  
; Sequence 1, Application US/08843417  
; Patent No. 6184349  
; GENERAL INFORMATION:  
; APPLICANT: Herman, Ronald C  
; APPLICANT: Delgado, Stephen G  
; APPLICANT: Fish, Linda M  
; APPLICANT: Sangameswaran, Lakshmi  
; APPLICANT: Rabert, Douglas K  
; TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
; TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McCauliffe  
; STREET: 525 University Ave  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/843,417  
; FILING DATE: April 15, 1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schmonees, William  
; REGISTRATION NUMBER: 31,796  
; REFERENCE/DOCKET NUMBER: 28340-P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)-324-7041  
; TELEFAX: (415)-324-0638  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6344 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: rat  
; TISSUE TYPE: Dorsal root ganglia  
; CELL TYPE: Peripheral nerve  
; CELL TYPE: Peripheral nerve  
; US-08-843-417-1

Query Match 16.9%; Score 41.2; DB 3; Length 6344;  
Best Local Similarity 74.3%; Pred. No. 0.00031;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGCAGCATTTAAGGCTGATGATATCGTTATGACAGCTGTGATTC 84  
Db 4103 CTTTCAGGTGGACACTTCAAGGCTGATGACATATATGATGACGCTGTGATTC 4162

QY 85 ACAGAGGTGA 94  
Db 4163 GGAGAGATCA 4172

RESULT 6

US-09-527-013-1

; Sequence 1, Application US/09527013  
; Patent No. 6479259  
; GENERAL INFORMATION:  
; APPLICANT: Herman, Ronald C  
; APPLICANT: Delgado, Stephen G  
; APPLICANT: Fish, Linda M  
; APPLICANT: Sangameswaran, Lakshmi  
; APPLICANT: Rabert, Douglas K  
; TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
; TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McCauliffe  
; STREET: 525 University Ave  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/527,013  
; FILING DATE: 16-Mar-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/843,417  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schmonees, William  
; REGISTRATION NUMBER: 31,796  
; REFERENCE/DOCKET NUMBER: 28340-P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)-324-7041  
; TELEFAX: (415)-324-0638  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6344 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: rat  
; TISSUE TYPE: Dorsal root ganglia  
; CELL TYPE: Peripheral nerve  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
; US-09-527-013-1

Query Match 16.9%; Score 41.2; DB 4; Length 6344;  
Best Local Similarity 74.3%; Pred. No. 0.00031;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGCAGCATTTAAGGCTGATGATATCGTTATGACAGCTGTGATTC 84  
Db 4103 CTTTCAGGTGGACACTTCAAGGCTGATGACATATATGATGACGCTGTGATTC 4162

QY 85 ACAGAGGTGA 94  
Db 4163 GGAGAGATCA 4172

RESULT 7  
US-08-669-656A-1  
; Sequence 1, Application US/08669656A  
; Patent No. 6451554  
; GENERAL INFORMATION:  
; APPLICANT: Wood, John N.

APPLICANT: Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656A  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6524 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
US-08-669-656A-1

Query Match 16.9%; Score 41.2; DB 4; Length 6524;  
Best Local Similarity 74.3%; Pred. No. 0.00031;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 25 CTTTTCGACGACCAATTTAAGGCTGATGATATCGTTTATGACGCTGTGATTCC 84  
DB 4287 CTTCTTCAGGTGGCACTTCAAGGCTGGATGACATATATGATGACGCTGTGATTCC 4346

OY 85 ACAGAGGTGA 94  
DB 4347 GGAGAGATCA 4356

RESULT 8  
US-08-669-656A-7  
Sequence 7, Application US/08669656A  
Patent No. 6451554  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
APPLICANT: Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656A

FILING DATE: 24-JUN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6527 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
US-08-669-656A-7

Query Match 16.9%; Score 41.2; DB 4; Length 6527;  
Best Local Similarity 74.3%; Pred. No. 0.00031;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 25 CTTTTCGACGACCAATTTAAGGCTGATGATATCGTTTATGACGCTGTGATTCC 84  
DB 4287 CTTCTTCAGGTGGCACTTCAAGGCTGGATGACATATATGATGACGCTGTGATTCC 4346

OY 85 ACAGAGGTGA 94  
DB 4347 GGAGAGATCA 4356

RESULT 9  
US-08-669-656A-5  
Sequence 5, Application US/08669656A  
Patent No. 6451554  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
APPLICANT: Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656A  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7052 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS

LOCATION: 204..6602  
US-08-669-656A-5

Query Match 16.9%; Score 41.2; DB 4; Length 7052;  
Best Local Similarity 74.3%; Pred. No. 0.00033;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGCACAATTAAAGGCTGATGATATCGTTATGAGCTGTGATTC 84  
DB 4812 CTTCTGAGGTGGACACCTTCAAGGCTGATGACATAATGATGACGCTGTGATTC 4871  
QY 85 ACAGAGGTGA 94  
DB 4872 GGAGAGATCA 4881

## RESULT 10

US-09-976-594-1104  
Sequence 1104, Application US/09976594  
Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO 1104

LENGTH: 5106

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 347316.1

US-09-976-594-1104

Query Match 16.5%; Score 40.2; DB 4; Length 5106;  
Best Local Similarity 70.1%; Pred. No. 0.00063;  
Matches 54; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 18 TTTTCGCTTTTTCGAGCACAATTAAAGGCTGATGATATCGTTATGAGCTGT 77  
DB 4224 TCTTGACGTCTTCAAGTGGCACAATTAAAGGCTGATGATATGATGAGCTGT 4283  
QY 78 TGATTCCACAGAGGTGA 94  
DB 4284 TGATTCCACAGAGGTGA 4300

## RESULT 11

US-09-634-920-3  
Sequence 3, Application US/09634920  
Patent No. 6342357

GENERAL INFORMATION:

APPLICANT: Splawski, Igor

APPLICANT: Keating, Mark T.

TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND

FILE REFERENCE: 2323-155

CURRENT APPLICATION NUMBER: US/09/634,920

PRIOR FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: 60/190,057

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/147,488

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 6048

TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(6048)

US-09-634-920-3

Query Match 15.2%; Score 37.2; DB 4; Length 6048;  
Best Local Similarity 72.7%; Pred. No. 0.0079;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGCACAATTAAAGGCTGATGATATCGTTATGAGCTGTGATTC 84  
DB 4234 CTTCTGAGGTGGACACATTAAAGGCTGATGACATAATGATGACGCTGTGATTC 4293  
QY 85 ACAGAG 90  
DB 4294 AGGGGG 4299

## RESULT 12

US-09-514-907A-1  
Sequence 1, Application US/09514907A  
Patent No. 6567705

GENERAL INFORMATION:

APPLICANT: Kenneth B. Stokes

APPLICANT: Joe Morrisette

TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL

SENSING BY CARDIAC PACEMAKERS THROUGH

GENETIC TREATMENT

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705rls LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/514,907A

FILING DATE: 08-Feb-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6048 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-514-907A-1

Query Match 15.2%; Score 37.2; DB 4; Length 6048;  
Best Local Similarity 72.7%; Pred. No. 0.0079;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGCACAATTAAAGGCTGATGATATCGTTATGAGCTGTGATTC 84  
DB 4234 CTTCTGAGGTGGACACATTAAAGGCTGATGACATAATGATGACGCTGTGATTC 4293  
QY 85 ACAGAG 90

Db 4294 AGGGGG 4299

## RESULT 13

US-09-896-994-1  
Sequence 1, Application US/09896994  
Patent No. 6665563

## GENERAL INFORMATION:

APPLICANT: Ken Stokes  
JOS e Morissette

TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/896,994

FILING DATE: 02-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/514,907

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6048 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-896-994-1

Query Match 15.2%; Score 37.2; DB 4; Length 6048;

Best Local Similarity 72.7%; Pred. No. 0.0079; Mismatches 18; Indels 0; Gaps 0;

Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGGCAATTAAAGGCTGGATGATGCTTTATGACGCTGTGATTCC 84

DB 4224 CTTTCGAGGCTGGCAATTAAAGGCTGGATGATGCTTTATGACGCTGTGACCTCC 4293

QY 85 ACAGAG 90

DB 4294 AGGGGG 4299

## RESULT 14

US-09-354-147C-1

Sequence 1, Application US/09354147C

Patent No. 6573067

GENERAL INFORMATION:

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Maxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/09/354,147C

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1

LENGTH: 5875

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (41)..(5335)

OTHER INFORMATION: cDNA sequence for rat Nan

NAME/KEY: unsure

LOCATION: (1996)..(4042)

OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position

OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn

OTHER INFORMATION: or Lys.

US-09-354-147C-1

Query Match 14.7%; Score 35.8; DB 4; Length 5875;

Best Local Similarity 78.2%; Pred. No. 0.025;

Matches 43; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 36 GGCACATTTTAAGGCTGGATGATGCTTTATGACGCTGTGATCCACAGAG 90

DB 3739 GGCACCTATTAAGGCTGGCTGGAAATCATGATGCTGTGATTCACAGAG 3793

## RESULT 15

US-09-024-020B-1

Sequence 1, Application US/09024020B

Patent No. 6030810

GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.

APPLICANT: FISH, LINDA M.

APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI

TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSER: JANET PAULINE CLARK

STREET: 3401 HILLVIEW AVENUE, MS A2-250

CITY: PALO ALTO

STATE: CA

COUNTRY: U.S.A.

ZIP: 94304-1197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/024,020B

FILING DATE: 16-FEB-1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,447

FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R0020B-REG

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-3097

TELEFAX: (650) 852-3097

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5977 base pairs



```

:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: DNA (genomic)
US-09-024-020B-1

```

```

Query Match      14.6% Score 35.6; DB 3; Length 5977;
Best Local Similarity 71.2%; Pred. No. 0.029;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 25 CTTTCTTGGAGGACACATTTAAGGCTGGATGATATCGTTTATGAGCTGTGATTCC 84
      |||||
Db 4231 CTTCTTCAAGTGGACACTTCAAGGCTGGATGACATCATGTATGCGGCTGTGATTCC 4290
      |||||
QY 85 ACAGAG 90
      |||||
Db 4291 CGAAG 4296

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Search completed: March 22, 2004, 23:17:50
Job time : 34.2579 secs

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RESULT 2
US-09-354-147C-41
; Sequence 41, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human Nan
US-09-354-147C-41

Query Match      32.9%; Score 134.4; DB 4; Length 5860;
Best Local Similarity 90.1%; Pred. No. 7.4e-27;
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY      202 ATTTTAAACAGAAAGAACACGCGGAGTTTGAGGCAATTCCTGGTTACATTT-CT 260
      |||
DB      3833 ATTCACAGAGAAAGAACACGCGGAGTTTGAGGCAATTCCTGGTTACATTTACT 3892
      |||
QY      261 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATCA 320
      |||
DB      3893 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATCA 3952
      |||
QY      321 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 372
      |||
DB      3953 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 4004
      |||

RESULT 3
US-09-354-147C-4
; Sequence 4, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; NAME/KEY: unsure
```

```
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-09-354-147C-4

Query Match      21.5%; Score 88; DB 4; Length 5822;
Best Local Similarity 73.3%; Pred. No. 2.6e-14;
Matches 126; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY      202 ATTTTAAACAGAAAGAACACGCGGAGTTTGAGGCAATTCCTGGTTACATTT-CT 260
      |||
DB      3764 ATTCACAGAGAAAGAACACGCGGAGTTTGAGGCAATTCATACCATTCCTTTACT 3823
      |||
QY      261 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATCA 320
      |||
DB      3824 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATTA 3883
      |||
QY      321 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 372
      |||
DB      3884 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 3935
      |||

RESULT 4
US-09-354-147C-1
; Sequence 1, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; NAME/KEY: unsure
; LOCATION: (1996)..(4042)
; OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
; OTHER INFORMATION: or Lys.
US-09-354-147C-1

Query Match      20.0%; Score 81.6; DB 4; Length 5875;
Best Local Similarity 70.9%; Pred. No. 1.4e-12;
Matches 122; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY      202 ATTTTAAACAGAAAGAACACGCGGAGTTTGA-GAGCAATTCCTGGTTACATTTCT 260
      |||
DB      3783 ATTCACAGAGAAAGAACACGCGGAGCTTTGAGGCAACCTTACCGGATCTCTACT 3842
      |||
QY      261 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATCA 320
      |||
DB      3843 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGTAATCTCTTCAATTGGCGTTATTA 3902
      |||
QY      321 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 372
      |||
DB      3903 TTGACAACTTCAACCAACAGCAGAAAAGATAGTATCTGGTGTCTTGAT 3954
      |||

RESULT 5
```

US-09-024-020B-1  
Sequence 1, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERRMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-1  
Query Match 18.9%; Score 77.2; DB 3; Length 5977;  
Best Local Similarity 69.0%; Pred. No. 2.2e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 200 AAATTTCTAACAAGAACAGCAAGCCAGATTGAGAGCAATTCACCTGGTTACAT-TT 258  
DB 4284 AGATTCCGAAGACGACAGAGCCTGACTACGAGGCAACATCTACATGTACATCTA 4343  
QY 259 CTTGTAGCTTTATCATCTTTGGCTCATCTTCACTCTGAATCTCTTCATTTGGCGTTAT 318  
DB 4344 CTTGTATCTTATCATCTTGGCTCTCTCTTCACTCACTGTTCACTGGTGTCAAT 4403  
QY 319 CATTGACAACCTTCAACGACGAGAAAGATATAGTATCTGGGTGTCTTGAT 372  
DB 4404 CATTGACAACCTTCAACGACGAGAAAGATTTGGAGGTCAAGACATCTTCAAT 4457  
RESULT 6  
US-09-425-043-1  
Sequence 1, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERRMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-1  
Query Match 18.9%; Score 77.2; DB 4; Length 5977;  
Best Local Similarity 69.0%; Pred. No. 2.2e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 200 AAATTTCTAACAAGAACAGCAAGCCAGATTGAGAGCAATTCACCTGGTTACAT-TT 258  
DB 4284 AGATTCCGAAGACGACAGAGCCTGACTACGAGGCAACATCTACATGTACATCTA 4343  
QY 259 CTTGTAGCTTTATCATCTTTGGCTCATCTTCACTCTGAATCTCTTCATTTGGCGTTAT 318  
DB 4344 CTTGTATCTTATCATCTTGGCTCTCTCTTCACTCACTGTTCACTGGTGTCAAT 4403  
QY 319 CATTGACAACCTTCAACGACGAGAAAGATATAGTATCTGGGTGTCTTGAT 372  
DB 4404 CATTGACAACCTTCAACGACGAGAAAGATTTGGAGGTCAAGACATCTTCAAT 4457  
RESULT 7  
US-09-024-020B-2  
Sequence 2, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERRMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK

STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6007 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
us-09-024-020B-2

Query Match 18.9%; Score 77.2; DB 3; Length 6007;  
Best Local Similarity 69.0%; Pred. No. 2.2e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 200 AATTCTTCAAGAAAGCAACAGCAGAGTTGAGAGCAATTCACGCGTTACAT-TT 258  
DB 4314 AGATTCGGAAGCAAGCAGAGCAGCCTGACTACGAGGCAACATCTACATGTA 4373  
QY 259 CTTGCTAGCTTTATCATCTTTGGCTCATCTTCTCACTCTGATCTCTTCATTTGCGCTTAT 318  
DB 4374 CTTGCTCATCTTCATCATCTTGGCTCTCTCTTCTTCAACCTGTTTCATCGGTGTCAT 4433  
QY 319 CATTGACAACTTCAACGACGAGCAAGAAAGTAAATGATCTGGTTCCTTCAT 372  
DB 4434 CATGACAACTTCAACGACGAGCAAGAAAGTTGGAGGTCAAGACATCTTCAT 4487

RESULT 8  
US-09-425-043-2  
Sequence 2, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6007 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
us-09-425-043-2

Query Match 18.9%; Score 77.2; DB 4; Length 6007;  
Best Local Similarity 69.0%; Pred. No. 2.2e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 200 AATTCTTCAAGAAAGCAACAGCAGAGTTGAGAGCAATTCACGCGTTACAT-TT 258  
DB 4314 AGATTCGGAAGCAAGCAGAGCAGCCTGACTACGAGGCAACATCTACATGTA 4373  
QY 259 CTTGCTAGCTTTATCATCTTTGGCTCATCTTCTCACTCTGATCTCTTCATTTGCGCTTAT 318  
DB 4374 CTTGCTCATCTTCATCATCTTGGCTCTCTCTTCTTCAACCTGTTTCATCGGTGTCAT 4433  
QY 319 CATTGACAACTTCAACGACGAGCAAGAAAGTAAATGATCTGGTTCCTTCAT 372  
DB 4434 CATGACAACTTCAACGACGAGCAAGAAAGTTGGAGGTCAAGACATCTTCAT 4487

RESULT 9  
US-09-024-020B-7  
Sequence 7, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-7

Query Match 18.9%; Score 77.2; DB 3; Length 6556;  
Best Local Similarity 69.0%; Pred. No. 2.3e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Db 200 AAATTCTACAGAAAGCAAGCAGAGTTGAGAGCAATTCACGCTTACAT-TT 258  
4431 AGATTCCCGAAGCAGACGAGCCTGACTACGAGGCAACATCTACATGATCTA 4490

Qy 259 CTTCGATCTTATCATCTTTGGCTCATCTTCACTCTGAATCTTCAATGGCGTTAT 318  
4491 CTTCGATCTTATCATCTTTGGCTCATCTTCACTCTGAATCTTCAATGGCGTTAT 4550

Db 319 CATTGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 372  
4551 CATGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 4604

Qy 319 CATTGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 372  
4551 CATGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 4604

RESULT 10  
US-09-425-043-7  
Sequence 7, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid

REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-7

Query Match 18.9%; Score 77.2; DB 4; Length 6556;  
Best Local Similarity 69.0%; Pred. No. 2.3e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Db 200 AAATTCTACAGAAAGCAAGCAGAGTTGAGAGCAATTCACGCTTACAT-TT 258  
4431 AGATTCCCGAAGCAGACGAGCCTGACTACGAGGCAACATCTACATGATCTA 4490

Qy 259 CTTCGATCTTATCATCTTTGGCTCATCTTCACTCTGAATCTTCAATGGCGTTAT 318  
4491 CTTCGATCTTATCATCTTTGGCTCATCTTCACTCTGAATCTTCAATGGCGTTAT 4550

Db 319 CATTGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 372  
4551 CATGACACTTCAACCAACAGCAAGAAAGATAGATCTGGGTTCGTTGAT 4604

RESULT 11  
US-09-024-020B-43  
Sequence 43, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-43

Query Match 18.9%; Score 77.2; DB 3; Length 6586;  
Best Local Similarity 69.0%; Pred. No. 2.3e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 200 AAATTCTTAACGAAAGAACACAGCCGAGAGTTGAGCAATTCATCGGTTACAT-TT 258  
DB 4461 AGATTCCGGAAGCCAGACGAGCTGACTACGAGGCAACATCTACATGATCATCTA 4520  
QY 259 CTGCTAGCTTTATCATCTTTGGCTCATCTTCTCACTGATCTCTTCAATTTGGCTTAT 318  
DB 4521 CTTCGTACCTTTCATCATCTTGGCTCTCTTCTTCACTCTTCACTGATCGGTGTCAT 4580  
QY 319 CATTGACAACCTTCAACCAACAGCAAGAAAAGATTAATGATCTGGGTGTTGAT 372  
DB 4581 CATGACAACCTTCAACCAACAGCAAGAAAAGTTTGAGGTGACGACATCTTCAT 4634

RESULT 12  
US-09-425-043-43  
Sequence 43, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6586 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-43  
Query Match 18.9%; Score 77.2; DB 4; Length 6586;

Best Local Similarity 69.0%; Pred. No. 2.3e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 200 AAATTCTTAACGAAAGAACACAGCCGAGAGTTGAGCAATTCATCGGTTACAT-TT 258  
DB 4461 AGATTCCGGAAGCCAGACGAGCTGACTACGAGGCAACATCTACATGATCATCTA 4520  
QY 259 CTGCTAGCTTTATCATCTTTGGCTCATCTTCTCACTGATCTCTTCAATTTGGCTTAT 318  
DB 4521 CTTCGTACCTTTCATCATCTTGGCTCTCTTCTTCACTCTTCACTGATCGGTGTCAT 4580  
QY 319 CATTGACAACCTTCAACCAACAGCAAGAAAAGATTAATGATCTGGGTGTTGAT 372  
DB 4581 CATGACAACCTTCAACCAACAGCAAGAAAAGTTTGAGGTGACGACATCTTCAT 4634

RESULT 13  
US-09-024-020B-8  
Sequence 8, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6826 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-8  
Query Match 18.9%; Score 77.2; DB 3; Length 6826;  
Best Local Similarity 69.0%; Pred. No. 2.3e-11;  
Matches 120; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 200 AAATTCTTAACGAAAGAACACAGCCGAGAGTTGAGCAATTCATCGGTTACAT-TT 258  
DB 4257 AGATTCCGGAAGCCAGACGAGCTGACTACGAGGCAACATCTACATGATCATCTA 4316  
QY 259 CTGCTAGCTTTATCATCTTTGGCTCATCTTCTCACTGATCTGATCTCTTCAATTTGGCTTAT 318





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## RESULT 2

US-09-354-147C-6

Sequence 6, Application US/09354147C

Patent No. 6573067

GENERAL INFORMATION:

APPLICANT: Dlb-Hajj, Sulayman

APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/09/354,147C

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 3701

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (3699)

OTHER INFORMATION: partial human Nan cDNA sequence

LOCATION: (922)

OTHER INFORMATION: Y = c or t. Xaa at amino acid position 308 is

OTHER INFORMATION: Leu.

US-09-354-147C-6

Query Match

Best Local Similarity 22.5%; Score 131.4; DB 4; Length 3701;

Matches 160; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

## FEATURE:

NAME/KEY: CDS

LOCATION: (19) .. (5313)

NAME/KEY: unsure

LOCATION: (5804)

TITLE OF INVENTION: CDNA sequence of mouse Nan, n = a or c or g or t

US-09-354-147C-4

Query Match

Best Local Similarity 19.3%; Score 113; DB 4; Length 5822;

Matches 152; Conservative 0; Mismatches 45; Indels 2; Gaps 1;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

## RESULT 4

US-09-354-147C-1

Sequence 1, Application US/09354147C

Patent No. 6573067

GENERAL INFORMATION:

APPLICANT: Dlb-Hajj, Sulayman

APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/09/354,147C

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 5875

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (41) .. (5335)

OTHER INFORMATION: cDNA sequence for rat Nan

LOCATION: (1996) .. (4042)

OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position

OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn

OTHER INFORMATION: or Lys.

US-09-354-147C-1

Query Match

Best Local Similarity 19.3%; Score 112.8; DB 4; Length 5875;

Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Db 4169 ACCTTGATATACCTCAACATAGCCTTGCTGTCATCTTACATAGAGTGTCTACAA 4228  
Qy 193 ATCTTGCTTTGAGGCAATCTACTCAACATGGCTGGAAATTTATTTGACTGTGTGTC 252  
Db 4229 GTCTTGCTTTGAGGCAACACTACTCAACATGGCTGGAAATTTATTTGATGTGTGTC 4288  
Qy 253 GTGCTTCTTCCATGTTAGTA 274  
Db 4289 GTGCTTCTTCTATCATTTAGTA 4310

RESULT 5  
US-08-843-417-9

Sequence 9, Application US/08843417  
Patent No. 6184349  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
APPLICANT: Delgado, Stephen G  
APPLICANT: Fish, Linda M  
APPLICANT: Sangameswaran, Lakshmi  
APPLICANT: Rabeit, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Heller Ehrman White & Mcauliffe  
STREET: 525 University Ave  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/843,417  
FILING DATE: April 15, 1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William  
REGISTRATION NUMBER: 31,796  
REFERENCE/DOCKET NUMBER: 28340-P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-324-7041  
TELEFAX: (415)-324-0638  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5874 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-843-417-9

Query Match 13.9%; Score 81.6; DB 3; Length 5874;  
Best Local Similarity 75.0%; Pred. No. 1.5e-14;  
Matches 102; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
Qy 137 TGACCATCTCCAACTGGGCTTTTGTGTCATCTTTAGCTTAGAAATGTCATCAAAATCT 196  
Db 4223 TGGCAAAATCAACAGATTCTTTGTGGCCGTCTTCAACAGCGAATGTGTCAAGAATGT 4582  
Qy 197 TTGCTTTGAGGCAATCTTACCAATGCGTGAATTTATTTGACTGTGTGTGTCGTC 256  
Db 4583 TCGCTTTGAGGCAATCTTACCAATGCGTGAATGTGTGACTTCAATGTGTGTG 4642  
Qy 257 TTCTTTCATTTAG 272  
Db 4643 TTCTTTCATTTAG 4658

RESULT 6  
US-09-527-013-9

Sequence 9, Application US/09527013  
Patent No. 6479259  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
APPLICANT: Delgado, Stephen G  
APPLICANT: Fish, Linda M  
APPLICANT: Sangameswaran, Lakshmi  
APPLICANT: Rabeit, Douglas K  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Heller Ehrman White & Mcauliffe  
STREET: 525 University Ave  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/527,013  
FILING DATE: 16-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/843,417  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William  
REGISTRATION NUMBER: 31,796  
REFERENCE/DOCKET NUMBER: 28340-P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-324-7041  
TELEFAX: (415)-324-0638  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5874 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-527-013-9

Query Match 13.9%; Score 81.6; DB 4; Length 5874;  
Best Local Similarity 75.0%; Pred. No. 1.5e-14;  
Matches 102; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
Qy 137 TGACCATCTCCAACTGGGCTTTTGTGTCATCTTTAGCTTAGAAATGTCATCAAAATCT 196  
Db 4523 TGGCAAAATCAACAGATTCTTTGTGGCCGTCTTCAACAGCGAATGTGTCAAGAATGT 4582  
Qy 197 TTGCTTTGAGGCAATCTTACCAATGCGTGAATTTATTTGACTGTGTGTGTCGTC 256  
Db 4583 TCGCTTTGAGGCAATCTTACCAATGCGTGAATGTGTGACTTCAATGTGTGTG 4642  
Qy 257 TTCTTTCATTTAG 272  
Db 4643 TTCTTTCATTTAG 4658  
-RESULT 7  
US-09-024-020B-8  
Sequence 8, Application US/09024020B

Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6826 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-8

Query Match 13.5%; Score 78.8; DB 3; Length 6826;  
Best Local Similarity 75.4%; Pred. No. 1.1e-13;  
Matches 98; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 148 AACTGGGCTTTGGTGCATCTTTAGTAGATGTCATCAAAATCTTTGCTTGAGG 207  
DB 4660 AATCTGGCTTTGTCATCTTTCTTACCTCGAGTGCTCAAAATCTTTGCTTGAGA 4719

QY 208 CAATPACTTCCCAATGCTGGAATTATTGACTGTGTGCTGCTTCTTCATT 267  
DB 4720 CACTACTACTTCCACCATTTGCTGGAACATCTTGACTTTGTGTGTCATCTTCATT 4779

QY 268 GTTAGTAGT 277  
DB 4780 GTGGGAATGT 4789

RESULT 8  
US-09-425-043-8  
Sequence 8, Application US/09425043  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6826 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-8

Query Match 13.5%; Score 78.8; DB 4; Length 6826;  
Best Local Similarity 75.4%; Pred. No. 1.1e-13;  
Matches 98; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 148 AACTGGGCTTTGGTGCATCTTTAGTAGATGTCATCAAAATCTTTGCTTGAGG 207  
DB 4660 AATCTGGCTTTGTCATCTTTCTTACCTCGAGTGCTCAAAATCTTTGCTTGAGA 4719

QY 208 CAATPACTTCCCAATGCTGGAATTATTGACTGTGTGCTGCTTCTTCATT 267  
DB 4720 CACTACTACTTCCACCATTTGCTGGAACATCTTGACTTTGTGTGTCATCTTCATT 4779

QY 268 GTTAGTAGT 277  
DB 4780 GTGGGAATGT 4789

RESULT 9  
US-09-024-020B-5  
Sequence 5, Application US/09024020B  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO

STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-5

Query Match 13.2%; Score 77.2; DB 3; Length 696;  
Best Local Similarity 74.6%; Pred. No. 1.2e-13;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACTGGCTTTGGTCATCTTACCTTAGAAGTCGCAAAATCTTGGCTTGGAG 207  
DB 73 AATCTGCTTTGTGATCTTCTTACCTGCGAGTGTGCTCAAAATGTTGCTTAGA 132  
QY 208 CAATACCTACTTCAACCAATGCTGGAATTATTGACTGTGTGCTGCTCTTTCATT 267  
DB 133 CACTACTATTTCACCATTTGCTGGAACATCTTTGACTTTGTGTGCTCCTCCATT 192  
QY 268 GTTAGTAAGT 277  
DB 193 GTGGGAATGT 202

RESULT 10  
US-09-425-043-5  
Sequence 5, Application US/09425043  
Patent No. 6335172  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-5

Query Match 13.2%; Score 77.2; DB 4; Length 696;  
Best Local Similarity 74.6%; Pred. No. 1.2e-13;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACTGGCTTTGGTCATCTTACCTTAGAAGTCGCAAAATCTTGGCTTGGAG 207  
DB 73 AATCTGCTTTGTGATCTTCTTACCTGCGAGTGTGCTCAAAATGTTGCTTAGA 132  
QY 208 CAATACCTACTTCAACCAATGCTGGAATTATTGACTGTGTGCTGCTCTTTCATT 267  
DB 133 CACTACTATTTCACCATTTGCTGGAACATCTTTGACTTTGTGTGCTCCTCCATT 192  
QY 268 GTTAGTAAGT 277  
DB 193 GTGGGAATGT 202

RESULT 11  
US-09-024-020B-1  
Sequence 1, Application US/09024020B  
Patent No. 6030810  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447

```

      FILING DATE: 26-FEB-1997
      ATTORNEY/AGENT INFORMATION:
        NAME: CLARK, JANET P.
        REGISTRATION NUMBER: 34,799
        REFERENCE/DOCKET NUMBER: R0020B-REG
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (650) 852-3097
        TELEFAX: (650) 852-5322
        INFORMATION FOR SEQ ID NO: 1:
          SEQUENCE CHARACTERISTICS:
            LENGTH: 5977 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
          MOLECULE TYPE: DNA (genomic)
    US-09-024-020B-1

Query Match      13.2%, Score 77.2; DB 3; Length 5977;
Best Local Similarity 74.6%; Pred. No. 3,2e-13;
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY      148 AACTGGGCTTTGTGGTCATCTTACGTTAGAAATGCTCATCAAAATCTTGCTTAGG 207
Db      4687 AATCGGCTTTGCATCTTCACTCTTCAACCCTGCAGATGTGCTCAAATGTGGCCTGAGA 4746
QY      208 CAATACACTTCCACCAATGGCTGAATTATTGACTGTGTGTCGTCCTCTTCCATT 267
Db      4747 CACTACACTTTCACCATTCGCTGGAACAATCTTTGACTTGTGTCATCTCTCCATT 4806
QY      268 GTTAGTAAGT 277
Db      4807 GTGGGAATGT 4816

RESULT 12
US-09-425-043-1
Sequence 1, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:

```

```

/ TELEPHONE: (650) 852-3097
/ TELEFAX: (650) 855-5322
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5977 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-09-425-043-1

Query Match      13.2%; Score 77.2; DB 4; Length 5977;
Best Local Similarity 74.6%; Pred. No. 3.2e-13;
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy      148  AACTGGGCTCTTTGGTGCATCTTTAGCTTGAATGTCTCAACAAATCTTTGCTTGAAG 207
           |||
Db      4687  AATGTGCTCTTTGCATCTTCTTCACCTGGAGGTGTGCTCAAAAGTTTGCTTGA 4746
           |||

Oy      208  CAATACACTCTCAACCATGGCTGGAAATTATTTGACTGTGNGGCGTCTCTTTCATT 267
           |||
Db      4747  CACTACATTTTCACCATTTGGCTGGACATCTTTGACTTTGTGTGTGATCACTTCATT 4806
           |||

Oy      268  GTTAGTAGT 277
           |||
Db      4807  GTGGGATGT 4816

RESULT 13
US-09-024-0208-2
/ Sequence 2, Application US/090240208
/ Patent No. 6030810
/ GENERAL INFORMATION:
/ APPLICANT: DELGADO, STEPHEN G.
/ APPLICANT: DIETRICH, PAUL S.
/ APPLICANT: FISH, LINDA M.
/ APPLICANT: HERMAN, RONALD C.
/ APPLICANT: SANGAMESWARAN, LAKSHMI
/ TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
/ TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: JANET PAULINE CLARK
/ STREET: 3401 HILLVIEW AVENUE, MS A2-250
/ CITY: PALO ALTO
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94304-1397
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/024,020B
/ FILING DATE: 16-FEB-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/039,447
/ FILING DATE: 26-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CLARK, JANET P.
/ REGISTRATION NUMBER: 34,799
/ REFERENCE/DOCKET NUMBER: R0020B-REG
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 852-3097
/ TELEFAX: (650) 855-5322
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6007 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/

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MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-2

Query Match 13.2%; Score 77.2; DB 3; Length 6007;  
Best Local Similarity 74.6%; Pred. No. 3.2e-13;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACGGGCTTTGGGCACTTACCTTAGAATGCTCATCAAAATCTTGCTTGAAG 207  
DB 4717 AACCTGGCTTTGTCATCTTCTTACCTGCGAGTGCTCAAAAGTTTGCTTGAGA 4776

QY 208 CAATACACTTCCCAATGCGTGAATTTATTTAGCTGTGCTGCTTCTTCCATT 267  
DB 4777 CACTACTATTTCACCATTTGGCTGGAACATCTTTGCTTGATTCCTTCATT 4836

QY 268 GTTAGTAAGT 277  
DB 4837 GTGGGAATGT 4846

RESULT 14  
US-09-425-043-2  
Sequence 2, Application US/09425043  
Patent No. 6335172

GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6007 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-2

Query Match 13.2%; Score 77.2; DB 4; Length 6007;  
Best Local Similarity 74.6%; Pred. No. 3.2e-13;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACGGGCTTTGGGCACTTACCTTAGAATGCTCATCAAAATCTTGCTTGAAG 207

DB 4717 AACCTGGCTTTGTCATCTTCTTACCTGCGAGTGCTCAAAAGTTTGCTTGAGA 4776

QY 208 CAATACACTTCCCAATGCGTGAATTTATTTAGCTGTGCTGCTTCTTCCATT 267

DB 4777 CACTACTATTTCACCATTTGGCTGGAACATCTTTGCTTGATTCCTTCATT 4836

QY 268 GTTAGTAAGT 277  
DB 4837 GTGGGAATGT 4846

RESULT 15  
US-09-024-020B-7  
Sequence 7, Application US/09024020B  
Patent No. 6030810

GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.  
APPLICANT: HERMAN, RONALD C.  
APPLICANT: SANGAMESWARAN, LAKSHMI  
TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JANET PAULINE CLARK  
STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94304-1397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,020B  
FILING DATE: 16-FEB-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6556 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-024-020B-7

Query Match 13.2%; Score 77.2; DB 3; Length 6556;  
Best Local Similarity 74.6%; Pred. No. 3.3e-13;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACGGGCTTTGGGCACTTACCTTAGAATGCTCATCAAAATCTTGCTTGAAG 207

DB 4834 AACCTGGCTTTGTCATCTTCTTACCTGCGAGTGCTCAAAAGTTTGCTTGAGA 4893

QY 208 CAATACACTTCCCAATGCGTGAATTTATTTAGCTGTGCTGCTTCTTCCATT 267

DB 4894 CACTACTATTTCACCATTTGGCTGGAACATCTTTGCTTGATTCCTTCATT 4953

OY 268 GTTACTAAGT 277  
Db 4954 GTGGGAATGT 4963

Search completed: March 22, 2004, 23:17:53  
Job time : 80.7372 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:36:49 ; Search time 30.3955 Seconds  
(without alignments)  
4071.453 Million cell updates/sec

Title: US-09-646-224A-17  
Perfect score: 223  
Sequence: 1 tgaaccaagtcgacccaatt.....gagagtcgacccaatt 223

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*
  - 2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*
  - 3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq:\*
  - 4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq:\*
  - 5: /cgn2\_6/prodata/2/ina/PTUS\_COMB.seq:\*
  - 6: /cgn2\_6/prodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200.6	90.0	5860	4 US-09-354-147C-41	Sequence 41, App1
2	100.6	45.1	5875	4 US-09-354-147C-1	Sequence 1, App1
3	86.4	38.7	5822	4 US-09-354-147C-4	Sequence 4, App1
4	32.8	14.7	1214	3 US-09-224-426-3	Sequence 3, App1
5	32.8	14.7	1214	3 US-09-478-601-3	Sequence 3, App1
6	32.8	14.7	1214	3 US-09-478-602-3	Sequence 3, App1
7	31	13.9	1152	4 US-09-489-039A-2256	Sequence 2256, Ap
8	31	13.9	1152	4 US-09-489-039A-4251	Sequence 4251, Ap
9	30.2	13.5	842	4 US-09-154-750A-72	Sequence 72, App1
10	30	13.5	425	4 US-09-621-976-9791	Sequence 9791, Ap
11	30	13.5	1147	3 US-08-061-376-2	Sequence 2, App1
12	30	13.5	1208	4 US-08-979-608A-16	Sequence 16, App1
13	30	13.5	1208	4 US-09-517-849-16	Sequence 16, App1
14	30	13.5	1208	4 US-09-616-289-16	Sequence 16, App1
15	30	13.5	2429	3 US-08-061-376-1	Sequence 1, App1
16	30	13.5	12425	4 US-09-616-289-50	Sequence 50, App1
17	29.4	13.2	274	4 US-09-313-294A-3811	Sequence 3811, Ap
18	29.2	13.1	2196	4 US-09-023-655-142	Sequence 15, App1
19	29.2	13.1	8252	1 US-08-046-585-15	Sequence 15, App1
20	29.2	13.1	8252	1 US-08-393-703-15	Sequence 15, App1
21	29.2	13.1	8252	5 PCT-US93-11721-15	Sequence 15, App1
22	29	13.0	90050	3 US-09-245-041-5	Sequence 15, App1
23	28.8	12.9	334	4 US-09-621-976-1499	Sequence 1499, App
24	28.8	12.9	629	4 US-09-016-434-130	Sequence 230, App
25	28.8	12.9	1482	4 US-09-149-476-258	Sequence 94, App1
26	28.8	12.9	1497	4 US-09-230-132-94	Sequence 94, App1
27	28.8	12.9	1542	4 US-09-149-476-106	Sequence 106, App

ALIGNMENTS

28	28.8	12.9	1812	4 US-09-023-655-430	Sequence 430, App
29	28.6	12.8	4079	4 US-09-016-434-1208	Sequence 1208, Ap
30	28.6	12.8	4132	4 US-09-300-958A-10	Sequence 10, App1
31	28.6	12.8	4204	4 US-09-023-655-1292	Sequence 1292, Ap
32	28.4	12.7	4704	4 US-09-543-681A-3486	Sequence 3486, Ap
33	28.4	12.7	3701	4 US-09-023-655-309	Sequence 309, App1
34	28.4	12.7	4503	2 US-08-770-301A-2	Sequence 2, App1
35	28.4	12.7	4503	3 US-09-175-581-2	Sequence 2, App1
36	28	12.6	271	4 US-09-313-294A-4585	Sequence 4585, Ap
37	28	12.6	343	1 US-08-080-255-2	Sequence 2, App1
38	28	12.6	343	3 US-08-465-713-2	Sequence 2, App1
39	28	12.6	343	5 PCT-US93-05857-2	Sequence 2, App1
40	28	12.6	1668	4 US-09-620-312D-127	Sequence 127, App
41	28	12.6	2271	1 US-09-904-615-52	Sequence 52, App1
42	28	12.6	4201	1 US-08-080-255-4	Sequence 4, App1
43	28	12.6	4201	3 US-08-465-713-4	Sequence 4, App1
44	28	12.6	4201	5 PCT-US93-05857-4	Sequence 4, App1
45	28	12.6	5751	4 US-09-023-655-1415	Sequence 1415, Ap

RESULT 1

US-09-354-147C-41  
Sequence 41, Application US/09354147C  
Patent No. 6573067  
GENERAL INFORMATION:  
APPLICANT: Dlb-Hajj, Sulayman  
APPLICANT: Maxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/09/354,147C  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: Full length cDNA sequence for human Nan  
US-09-354-147C-41

Query Match 90.0%; Score 200.6; DB 4; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 7.4e-58;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	5	CAAGGTGACCAAAATGACTTGGGAAACGCGCTCATTCACCACTCCAGACTCTTTGCA	64
DB	5295	CCAAGGTGACCAAAATGACTT-GGAAACGCGCTCATTCACCACTCCAGACTCTTTGCA	5353
QY	65	ATGGAAGCTTGTACTTGGGGTGGCCAAAGGCAAGTGCACCTGATGAGCCCTCA	124
DB	5354	ATGGAAGCTTGTACTTGGGGTGGCCAAAGGCAAGTGCACCTGATGAGCCCTCA	5413
QY	125	CCTCCAGCCTTACCTCATAGCTTCACAGCCTTCTGAGCCTTGAGCTCCAGGGGTCA	184
DB	5414	CCTCCAGCCTTACCTCATAGCTTCACAGCCTTCTGAGCCTTGAGCTCCAGGGGTCA	5473
QY	185	GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT	223
DB	5474	GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT	5512

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RESULT 2
US-09-354-147C-1
; Sequence 1, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; NAME/KEY: unsure
; LOCATION: (1996)..(4042)
; OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
; OTHER INFORMATION: or Lys.
US-09-354-147C-1
Query Match 45.1%; Score 100.6; DB 4; Length 5875;
Best Local Similarity 74.3%; Pred. No. 4.5e-24;
Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 15 CAAATGACTGGGAAAGGGCCCATTCACCACTCCAGACTCTTCGATGAGACTT 74
DB 5236 CAAATGAGGCTGAAGAGAGGTCAAGTTCATCGACAGAGGTGTTTCAGATGAGACTT 5295
QY 75 GTCTAGCTTTGGGGTGGCCAGAGGCGAAGTCCACTGTGACTGAGCCCTCCAGCCG 134
DB 5296 GTCCAGCTTGATGTGGCCAGAGGTCAAGTTCAGATGAGTCAATGAGTCCAGCCG 5355
QY 135 TACCTCATAGCTTCACAGGCTTGCCTTACGCTCTGAGCTCCAGGGGTGAG 185
DB 5356 TACCTCACTGGCTTCACAGCTTACGCTCCAGCCTCTGGGAGAGGCGGCGAG 5406

RESULT 3
US-09-354-147C-4
; Sequence 4, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
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; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; NAME/KEY: unsure
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-09-354-147C-4
Query Match 38.7%; Score 86.4; DB 4; Length 5822;
Best Local Similarity 71.1%; Pred. No. 2.8e-19;
Matches 128; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

QY 7 AGTGACCAAAATGACTTGGGAAAGGGCCCTGATTCACCACTCCAGACTCTTGAAT 66
DB 5206 AAGATGATCAAGCTGAAGCTGAAGAGAGGTCAAGTTCATGCTCCAGAGTCTTGAAT 5265
QY 67 GGAGACTTGTCTAGCTTTGGGGTGGCCAGAGGCAAGTCACTGTGACTG-AGCCTGAC 125
DB 5266 GGAGACTTGTCTAGCTTGAATGTGCCAAGATCAAGGTGATGTGACTGAAACCCCGAC 5325
QY 126 CTCACGCTTACCTCAATGCTTACAGGCTTGCCTTACGCTCTGAGCTCCAGGGGTGAG 185
DB 5326 CTGCACGCTTACCTCAAGCTTCAAGCTCAGCCCGCCTCTGCGGAACAAAGCGCGG 5385

RESULT 4
US-09-224-426-3/C
; Sequence 3, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/jpw/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: rat
US-09-224-426-3
Query Match 14.7%; Score 32.8; DB 3; Length 1214;
Best Local Similarity 52.1%; Pred. No. 0.19;
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTTTTGCAATGAGACTGTCTAGCTTTGGGGTGGCCAAAGGCAAGT 104
DB 1138 ATCTCTCCCGACGGTTTGATGGGGTGGCTGTGACTTGAGGCGACTGGGAATTGTCAAGT 1079
QY 105 CCACGTGACGAGCCCTCCAGCTCCAGGCTTACAGCTTACAGGCTTGCCTTCAG 164
DB 1078 GCTTTGCTTTCTCTCTCTCTCTATATGACTGTGTGAGCGTTGCTGACCGTGGAGAGCTG 1019
QY 165 CCTGTGAGCTCCAGGGGTCA 184
DB 1018 CCCTGGGGCTTCAGGCTTCA 999

RESULT 5
US-09-478-601-3/C
; Sequence 3, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
```

APPLICANT: Wilson, Amy E.  
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
FILE REFERENCE: 574532\JFW  
CURRENT APPLICATION NUMBER: US/09/478,601  
CURRENT FILING DATE: 2000-01-06  
EARLIER APPLICATION NUMBER: 09/224,426  
EARLIER FILING DATE: 1998-12-31  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1214  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-478-601-3

Query Match 14.7%; Score 32.8; DB 3; Length 1214;  
Best Local Similarity 52.1%; Pred. No. 0.19;  
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTCTTTCAGATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGGT 104  
DB 1138 ATCTCTCCCGAGGTTTGATGGGGCTGAGCTTGGAGCGACTGGGAATTGTCAAGT 1079  
QY 105 CCACTGTGACTGAGCCCTCACTCCAGGCTTACTTCACTTACAGCCTTGGCTTCAAG 164  
DB 1078 GCCTTGTCTTGTCTCTCTCTATCATCAGCTGTCTGAGCGTTGCTGACCGTGGGAGCTG 1019  
QY 165 CCTGTGAGCTCCAGGGGTCA 184  
DB 1018 CCCCTGGGCTGCAGGCTTCA 999

RESULT 6  
US-09-478-602-3/c  
Sequence 3; Application US/09478602  
Patent No. 6291195  
GENERAL INFORMATION:  
APPLICANT: Salon, John A.  
APPLICANT: Laz, Thomas M.  
APPLICANT: Nagorny, Ralae  
APPLICANT: Wilson, Amy E.  
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
FILE REFERENCE: 574532\JFW  
CURRENT APPLICATION NUMBER: US/09/478,602  
CURRENT FILING DATE: 2000-01-06  
EARLIER APPLICATION NUMBER: 09/224,426  
EARLIER FILING DATE: 1998-12-31  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1214  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-478-602-3

Query Match 14.7%; Score 32.8; DB 3; Length 1214;  
Best Local Similarity 52.1%; Pred. No. 0.19;  
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTCTTTCAGATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGGT 104  
DB 1138 ATCTCTCCCGAGGTTTGATGGGGCTGAGCTTGGAGCGACTGGGAATTGTCAAGT 1079  
QY 105 CCACTGTGACTGAGCCCTCACTCCAGGCTTACTTCACTTACAGCCTTGGCTTCAAG 164  
DB 1078 GCCTTGTCTTGTCTCTCTCTATCATCAGCTGTCTGAGCGTTGCTGACCGTGGGAGCTG 1019  
QY 165 CCTGTGAGCTCCAGGGGTCA 184  
DB 1018 CCCCTGGGCTGCAGGCTTCA 999

RESULT 7  
US-09-489-039A-2256/c  
Sequence 2256; Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 2256  
LENGTH: 1152  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2256

Query Match 13.9%; Score 31; DB 4; Length 1152;  
Best Local Similarity 52.8%; Pred. No. 0.77;  
Matches 67; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 92 CCAAGGCGAAGTCTGATGAGCCCTCACTCCAGGCTTACTTCACTTACATTCACACA 151  
DB 286 CGAGGGGCGAAGCGCTCCCGACACATCATATTTCTCCAGACCGCTTCTGCTGATTA 227  
QY 152 GCCTTGTCTTACAGCTCTGAGCTCCAGGGGTGAGCAGCTTAGTATCAACAGGAGTGG 211  
DB 226 ACCCGGAAAGCTTCCCTTCAAGCGGCGAGCGGTGAGAGTGAGTATTAATATTGG 167  
QY 212 ATTACC 218  
DB 166 ATTACC 160

RESULT 8  
US-09-489-039A-4251/c  
Sequence 4251; Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 4251  
LENGTH: 1152  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4251

Query Match 13.9%; Score 31; DB 4; Length 1152;  
Best Local Similarity 52.8%; Pred. No. 0.77;  
Matches 67; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 92 CCAAGGCGAAGTCTGATGAGCCCTCACTCCAGGCTTACTTCACTTACATTCACACA 151  
DB 286 CGAGGGGCGAAGCGCTCCCGACACATCATATTTCTCCAGACCGCTTCTGCTGATTA 227  
QY 152 GCCTTGTCTTACAGCTCTGAGCTCCAGGGGTGAGCAGCTTAGTATCAACAGGAGTGG 211  
DB 226 ACCCGGAAAGCTTCCCTTCAAGCGGCGAGCGGTGAGAGTGAGTATTAATATTGG 167  
QY 212 ATTACC 218  
DB 166 ATTACC 160

## RESULT 9

US-09-154-750A-72/c  
; Sequence 72, Application US/09154750A  
; Patent No. 6432640  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kenneth  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 842  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-72

Query Match 13.5%; Score 30.2; DB 4; Length 842;  
Best Local Similarity 53.9%; Pred. No. 1.3;  
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 56 CTCTTGGAGATGAGACTTGTCTACCTTGGGGTGGCCAGGAGGTCACCTGTGACT 115  
DB 398 CTCCTGGAGCTGAGATGATGATCTGGGTGGATGGGAGGATGGGGGCGAGAGCCA 339  
OY 116 GAGCCCTGACCTTCACGCGCTTACCTGATAGCTTACAGCGCTTGCCTTCACTCTG 170  
DB 338 GCCCCACCCACCCAGCCTTGCCTTCATCATCTTCTTCAAGCAGCGCTCTG 284

## RESULT 10

US-09-621-976-9791  
; Sequence 9791, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 9791  
; LENGTH: 425  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-9791

Query Match 13.5%; Score 30; DB 4; Length 425;  
Best Local Similarity 54.5%; Pred. No. 1.1;  
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 81 CTTTGGGTGGCCAGGAGGAGTCACTGTGACTGAGCCCTTACCTCCAGCTTACTC 140  
DB 196 CTTTGGAGATGATGACCCCGATGGCTTCTTGGCTGAGGCGCCAGCCTCACCCCTGCCCC 255  
OY 141 ATAGCTCACAGGCTTGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 190  
DB 256 AGCCATTCGGGCCCCCATCTCCAGCAAGATCCCCCAGAGTCCAGAGCT 305

## RESULT 11

US-08-061-376-2/c  
; Sequence 2, Application US/08061376  
; Patent No. 6175000  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; APPLICANT: Djabali, Malek  
; APPLICANT: Selleri, Lucia  
; APPLICANT: Parry, Pauline  
; TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/061,376  
; FILING DATE: 13-MAY-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9387  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)546-4737  
; TELEFAX: (619)546-9392  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1147 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-08-061-376-2

Query Match 13.5%; Score 30; DB 3; Length 1147;  
Best Local Similarity 50.0%; Pred. No. 1.7;  
Matches 75; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

OY 15 CAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGGCAATGAGACTT 74  
DB 1017 CAACAAAAGCTGTGAGAACTGCTTCAGAGAAATCTGAGCTCTTTTCAAGGGCCAGTC 958  
OY 75 GTTACGCTTTGGGGTGGCCAGGAGGAGTCACTGTGACTGAGCCCTTCACTCCAGCC 134  
DB 957 GCCACTCTGACGGGTGGCGCTCAGTACAGTTCACACAAAGTGTAGGCCACACTTCTGCA 898  
OY 135 TACTCATAGCTTCAAGCTTGCCTTCAAG 164  
DB 897 GATTAGATGAATCTCATCATCTCATCTG 868

## RESULT 12

US-08-979-608A-16  
; Sequence 16, Application US/08979608A  
; Patent No. 6355451  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
; TREATING ATHEROSCLEROSIS  
; NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-08-979-608A-16  
Query Match 13.5%; Score 30; DB 4; Length 1208;  
Best Local Similarity 54.5%; Pred. No. 1.7;  
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 81 CTTGGGGTGGCCAGGAGGCAAGTCCACTGTGACTGAGCCCTCACTCCACGCCCTACTC 140  
DB 618 CTTTGAGGATGATGACCCCGATGCTTTAGGCTGAGCGCCCGACCTCACCCTGCCCC 677  
QY 141 ATAGCTTCACAGCCTTGCCCTTCAGCCTCTGAGCTCCAGGGGTAGACGCT 190  
DB 678 AGCCCATTCGGGCCCATCTCACCAGATCCCGCCAGAGTCCAGAGGCT 727  
RESULT 13  
US-09-517-849-16  
Sequence 16, Application US/09517849  
Patent No: 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-517-849-16  
Query Match 13.5%; Score 30; DB 4; Length 1208;  
Best Local Similarity 54.5%; Pred. No. 1.7;  
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 81 CTTGGGGTGGCCAGGAGGCAAGTCCACTGTGACTGAGCCCTCACTCCACGCCCTACTC 140  
DB 618 CTTTGAGGATGATGACCCCGATGCTTTAGGCTGAGCGCCCGACCTCACCCTGCCCC 677  
QY 141 ATAGCTTCACAGCCTTGCCCTTCAGCCTCTGAGCTCCAGGGGTAGACGCT 190  
DB 678 AGCCCATTCGGGCCCATCTCACCAGATCCCGCCAGAGTCCAGAGGCT 727  
RESULT 14  
US-09-616-289-16  
Sequence 16, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
FILING DATE: 2000-07-14  
PRIORITY APPLICATION NUMBER: US 09/517,849  
PRIORITY FILING DATE: 2000-03-02  
PRIORITY APPLICATION NUMBER: US 08/979,608  
PRIORITY FILING DATE: 1997-11-26  
PRIORITY APPLICATION NUMBER: US 60/031,930  
PRIORITY FILING DATE: 1996-11-27  
PRIORITY APPLICATION NUMBER: US 60/048,547  
PRIORITY FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

LOCATION: (1)...(651)  
US-09-616-289-16

Query Match 13.5%; Score 30; DB 4; Length 1208;  
Best Local Similarity 54.5%; Pred. No. 1.7;  
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 897 GATTAGATAGAAATCTCATACATCTCATCTG 868

Search completed: March 22, 2004, 23:17:57  
Job time : 34.3955 secs

OY 81 CTTTGGGGTGCCCAAGGGCAGGTCACACTGATGATGAGCCCTCAGCCCTCAGCCCTACCTC 140  
DB 618 CTTTGGAGATATGACCCCGATGGCTTTTGGCTGAGCGCCCAAGCTCAGCCCTGCCCC 677

OY 141 ATAGCTCACAGCTTGGCTTCAGCTCTGAGCTTCAGGGGTGACAGCT 190  
DB 678 AGCCATTCCGCGCCCATCTACCCCAAGATCCCCCAAGTCCAGAGCT 727

RESULT 15  
US-08-061-376-1/c  
Sequence 1, Application US/08061376

Patent No. 6175000

GENERAL INFORMATION:

APPLICANT: Evans, Glen A.

APPLICANT: Djabali, Malek

APPLICANT: Selleri, Lucia

APPLICANT: Parry, Pauline

TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23

TITLE OF INVENTION: TRANSLATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/061.376

FILING DATE: 13-MAY-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9387

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 546-4737

TELEFAX: (619) 546-9392

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2429 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: DNA (genomic)

US-08-061-376-1

Query Match 13.5%; Score 30; DB 3; Length 2429;  
Best Local Similarity 50.0%; Pred. No. 2.3;  
Matches 75; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

OY 15 CAAATGACTTGGGAAACGGGCTCATTCACACTCCAGACTCTTGGCATGAGACTT 74  
DB 1017 CAACAAAGCTCTGAGACTTCTTCAAGAAATCTGACAGCTCTTTTCAAGGCCAGTC 958

OY 75 GTTACGCTTTGGGGTGCCCAAGGTCACAGTGTGACTGAGCCCTCAGCCCTCAGCC 134  
DB 957 GCCACTCTGACGGGTGCGCTCAGTACAGTTCACACAAAGTGTAGGCCACACTTCTGGCA 898

OY 135 TACCTCATAGCTTCAAGCTTGCTTCAG 164



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# OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 1143.57 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-11

Sequence: 1 cagacatgagaacccgc.....caacggtacgctcgagag 215

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Genbank: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: gb\_ba: \*  
16: em\_fun: \*  
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20: em\_om: \*  
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24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_hlg\_hum: \*  
31: em\_hlg\_inv: \*  
32: em\_hlg\_other: \*  
33: em\_hlg\_mus: \*  
34: em\_hlg\_pln: \*  
35: em\_hlg\_rod: \*  
36: em\_hlg\_mam: \*  
37: em\_hlg\_vtc: \*  
38: em\_sy: \*  
39: em\_hlgo\_hum: \*  
40: em\_hlgo\_mus: \*  
41: em\_hlgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	215	100.0	215	6	AX017227	AX017227 Sequence
2	215	100.0	215	6	BD138449	BD138449 Mammalian
3	168.6	78.4	167476	9	AC116038	AC116038 Homo sapi
4	90.2	42.0	3701	6	AR340648	AR340648 Sequence
5	90.2	42.0	3701	6	BD217793	BD217793 Regulatio
6	90.2	42.0	5419	9	HSAA17790	AA17790 Homo sapi
7	90.2	42.0	5728	6	BD012083	BD012083 Human bod
8	90.2	42.0	5728	6	BD082952	BD082952 Human bod
9	90.2	42.0	5728	6	AF150882	AF150882 Homo sapi
10	90.2	42.0	5860	6	AR340678	AR340678 Sequence
11	90.2	42.0	6237	9	AF188679	AF188679 Homo sapi
12	90.2	42.0	6528	6	BD012082	BD012082 Human bod
13	90.2	42.0	6528	6	BD082951	BD082951 Human bod
14	90.2	42.0	6528	6	AF109737	AF109737 Homo sapi
15	63.6	29.6	241289	2	AC124662	AC124662 Mus muscu
16	59	27.4	210800	2	AC127824	AC127824 Rattus no
17	59	27.4	243048	2	AC127215	AC127215 Rattus no
18	47.4	22.0	5822	6	AR340647	AR340647 Sequence
19	47.4	22.0	5822	6	BD217792	BD217792 Regulatio
20	47.4	22.0	5858	10	AF118044	AF118044 Mus muscu
21	47.4	22.0	5921	10	AB031389	AB031389 Mus muscu
22	45.8	21.3	5334	6	E36125	E36125 Nucleic aci
23	45.8	21.3	5849	10	RNO237852	RNO237852 Rattus no
24	45.8	21.3	5875	6	AR340646	AR340646 Sequence
25	45.8	21.3	5875	6	BD217791	BD217791 Regulatio
26	45.8	21.3	5897	6	AX017217	AX017217 Sequence
27	45.8	21.3	5897	6	BD138440	BD138440 Mammalian
28	45.8	21.3	5905	10	AF059030	AF059030 Rattus no
29	45.8	21.3	5908	6	E36122	E36122 Nucleic aci
30	37.6	17.5	182506	9	AL359077	AL359077 Human DNA
31	37.6	17.5	194050	2	AL354658	AL354658 Homo sapi
32	36.4	16.9	171363	2	BX470146	BX470146 Dario rer
33	36	16.7	172879	9	BS000213	BS000213 Pan trogl
34	35.4	16.5	170212	9	AC058822	AC058822 Homo sapi
35	35.4	16.5	184092	2	AC027114	AC027114 Homo sapi
36	34.8	16.2	166018	2	EX649313	EX649313 Dario rer
37	34.8	16.2	176761	2	AC112689	AC112689 Mus muscu
38	34.8	16.2	221979	5	BX005310	BX005310 Zebrafish
39	34.8	16.2	247221	2	BX470211	BX470211 Dario rer
40	34.8	16.2	248639	2	AC135768	AC135768 Rattus no
41	34.8	16.2	253625	2	AC098417	AC098417 Rattus no
42	34.6	16.1	169207	10	AC119813	AC119813 Mus muscu
43	34.6	16.1	233925	2	AC118930	AC118930 Mus muscu
44	34.4	16.0	202214	2	AC135818	AC135818 Rattus no
45	34.4	16.0	243500	2	AC100177	AC100177 Mus muscu

## ALIGNMENTS

RESULT 1	AX017227	215 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX017227				
DEFINITION	Sequence 11 from Patent WO9947670.				
ACCESSION	AX017227				
VERSION	AX017227.1	GI:10042147			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	1				
TITLE	Tate, S.N., Grose, D.T. and Hick, C.A.				
JOURNAL	Mammalian sodium channel proteins				
	Patent: WO 9947670-A 11 23-SEP-1999;				

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS (GB) ; HICK CAROLINE ANNE (GB)  
 FEATURES  
 Location/Qualifiers  
 1. 215  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 215; DB 6; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-54;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACATGAGAACTCCGTACTACTATGATGTAAGAAGGCTTTGTAAGGACACCCC 60  
 DB 1 CAGACATGAGAACTCCGTACTACTATGATGTAAGAAGGCTTTGTAAGGACACCCC 60  
 QY 61 TTCTTTTGTCTGATGTCAGAGAGTCTGATGTTACAGATATATCAGAAATGAGC 120  
 DB 61 TTCTTTTGTCTGATGTCAGAGAGTCTGATGTTACAGATATATCAGAAATGAGC 120  
 QY 121 CATGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTCCCAAGAAAATTTCC 180  
 DB 121 CATGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTCCCAAGAAAATTTCC 180  
 QY 181 AGCGATTTTGTGATCCAAAGCTTACGCTTCGAGG 215  
 DB 181 AGCGATTTTGTGATCCAAAGCTTACGCTTCGAGG 215

RESULT 2  
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 LOCUS BD138449 215 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Mammalian sodium channel protein.  
 ACCESSION BD138449  
 VERSION BD138449.1 GI:22323394  
 KEYWORDS JP 2002508941-A/10.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 215)  
 GROSE, D.T., HICK, C.A. and Tate, S.N.  
 Mammalian sodium channel protein  
 Patent: JP 2002508941-A 10 26-MAR-2002;  
 GLAXO GROUP LTD

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 OS Homo sapiens (human)  
 PN JP 2002508941-A/10  
 PD 26-MAR-2002  
 PR 18-MAR-1999 JP 2000536853  
 PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
 C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
 C12N1/15,  
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 CC Mammalian sodium channel protein  
 FH Key  
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FEATURES  
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QY 1 CAGACATGAGAACTCCGTACTACTATGATGTAAGAAGGCTTTGTAAGGACACCCC 60  
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 QY 121 CATGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTCCCAAGAAAATTTCC 180  
 DB 121 CATGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTCCCAAGAAAATTTCC 180  
 QY 181 AGCGATTTTGTGATCCAAAGCTTACGCTTCGAGG 215  
 DB 181 AGCGATTTTGTGATCCAAAGCTTACGCTTCGAGG 215

RESULT 3  
 AC116038/c  
 LOCUS AC116038 167476 bp DNA linear PRI 07-OCT-2003  
 DEFINITION Homo sapiens chromosome 3 clone RP11-134J21, complete sequence.  
 ACCESSION AC116038  
 VERSION AC116038.3 GI:37537604  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 167476)  
 KAUL, R.K., OLSON, M.V., ZHOU, Y., JAMES, R.A., ROUSE, G., WU, Z.,  
 SAENPHIMMACHAK, C., BUCKLEY, D., KIBUKAWA, M., RAYMOND, C. and  
 HAUGEN, E.D.  
 Direct Submission  
 Box 352145, Seattle, WA 98195, USA

## REFERENCE

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 JOURNAL  
 COMMENT  
 OS Homo sapiens (human)  
 PN JP 2002508941-A/10  
 PD 26-MAR-2002  
 PR 18-MAR-1999 JP 2000536853  
 PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
 C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
 C12N1/15,  
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 CC Mammalian sodium channel protein  
 FH Key  
 Location/Qualifiers  
 FT source 1. 215  
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TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
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 OS Homo sapiens (human)  
 PN JP 2002508941-A/10  
 PD 26-MAR-2002  
 PR 18-MAR-1999 JP 2000536853  
 PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
 C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
 C12N1/15,  
 PC C12N1/19, C12N1/21, C12N5/10, C12Q1/02, G01N33/15, G01N33/50, G01N33/PC  
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 CC Mammalian sodium channel protein  
 FH Key  
 Location/Qualifiers  
 FT source 1. 215  
 /organism="Homo sapiens (human)"  
 /db\_xref="taxon:9606"

Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web Site: <http://www.genome.washington.edu>  
 Contact: [uwgchgs@u.washington.edu](mailto:uwgchgs@u.washington.edu)  
 Project Information  
 Center project name: chr-3  
 Center clone name: RP11-134J21 (bc0780)  
 Summary Statistics  
 Sequencing vector: plasmid, 100% of reads  
 Chemistry: Dye-terminator ET, 4% of reads  
 Chemistry: Dye-terminator Big Dye, 5% of reads  
 Assembly program: Phrap, version 0.99019  
 Consensus quality: 167467 bases at least Q40  
 Consensus quality: 167476 bases at least Q30  
 Consensus quality: 167476 bases at least Q20  
 Insert size: 167476; sum-of-contigs  
 Quality coverage: 18.9x in Q20 bases; sum-of-contigs

## Overlapping Sequences:

5': RP11-1114A3 AC137625, 2001-bp overlap  
3': RP11-182A24 (UMGC:bco782) AC123903, 41341-bp overlap

## Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8629	2732	2741	2234	2259
6	<800	6382	6514	2067	2008
2248	2299	512	<800	5097	5007
9345	9792	449	<800	2317	2259
2016	2003	2707	2741	2813	2744
4889	4771	4809	4878	2537	2550
3455	3447	184	<800	1923	2008
245	<800	5818	5899	2486	2550
72	<800	1364	1346	4036	3992
4175	4167	999	990	2583	2550
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6640	6560	4721	4667	2738	2744
4710	4771	727	745	4704	4629
3468	3447	179	<800	2649	2744
687	<800	7123	7158	2550	2550
3049	3091	2078	2040	5020	4862
762	<800	1891	1888	6949	6960
553	<800	8072	8171	4636	4629

5080	5088	92	<800	3588	3544
6613	6560	3674	3639	604	<800
8963	9211	5478	5397	5748	6106
331	<800	240	<800	953	943
2328	2299	5050	4878	4728	4629
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712	<800	3231	3264	1222	1220
1368	1370	86	<800	694	<800
182	<800	5444	5397	3022	3007
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775	<800	438	<800	1294	1220
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2709	2686	5528	5397	3725	3544
19834	19753	475	<800	790	<800
8729	8629	2310	2371	4232	4223
2264	2299	5177	5089	396	<800
651	<800	391	<800	4714	4629
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8764	8629	316	<800	879	917
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QY 1 CAGACATGAGAACTCCGTTACTATGTCGAGAAAGGCTTGTAAAGGCAACCC 60  
 DB 119382 CAGACAAAGAACTCCGTTACTATGTCGAGAAAGGCTTGTAAAGGCAACCC 119323  
 QY 61 TTCCTTTGTTCTGATGTCGAGAACTGTTACCATATATCATGAGATGAGAC 120  
 DB 119322 TTCGTTTGTGATGTCGAGAACTGTTACCATATATCATGAGATGAGAC 119263  
 QY 121 CATTGATCTTCAGATGTCGTTGATGTTACCTGAGATGTTCCCAAGAAAA 175  
 DB 119262 CATTGATCTTCAGATGTCGTTGATGTTACCTGAGATGTTCCCAAGAAAA 119208

RESULT 4  
 AR340648 3701 bp DNA linear PAT 17-AUG-2003  
 LOCUS AR340648  
 DEFINITION Sequence 6 from patent US 6573067.  
 ACCESSION AR340648  
 VERSION AR340648.1 GI:33732380  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3701)  
 AUTHORS Dlb-Hajj,S. and Waxman,S.G.  
 TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
 JOURNAL Patent: US 6573067-A 6 03-JUN-2003;  
 FEATURES location/Qualifiers  
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QY 81 AGAAGTCGATGTTACCATATATCATGAGATGAGCAATGATCTTCAGATGCT 140  
 DB 2351 AGAAGTCGATGTTACCATATATCATGAGATGAGCAATGATCTTCAGATGCT 2410  
 QY 141 TTGATGTTACCTGAGATGTTCCCAAGAAAA 175  
 DB 2411 TTGATGTTACCTGAGATGTTCCCAAGAAAA 2445

RESULT 5  
 BD217793 3701 bp DNA linear PAT 17-JUL-2003  
 LOCUS BD217793  
 DEFINITION Regulation of sodium channel in posterior root ganglion.  
 ACCESSION BD217793  
 VERSION BD217793.1 GI:33027563  
 KEYWORDS JP 2002509860-A/3.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 3701)  
 Hajj,S.D. and Waxman,S.  
 Regulation of sodium channel in posterior root ganglion  
 Patent: JP 2002509860-A 3 02-APR-2002;  
 JOURNAL YALE UNIVERSITY

REFERENCE OS Homo sapiens (human)  
 AUTHORS PN JP 2002509860-A/3  
 TITLE PD 02-APR-2002  
 JOURNAL PF 23-JAN-1999 JP 2000529355  
 PR 23-JAN-1998 US 60/072990,20-NOV-1998 US 60/109402 PI  
 SULAIMAN DIB HAJJ,STEPHEN WAXMAN

PC C07K14/435,A61K38/00,A61K39/395,A61K45/00,A61P25/04,A61P43/00,  
 PC C07K16/18,  
 PC C12N5/10,C12N15/09,C12P21/02,G01N33/566,G01N33/84,A61K37/02,  
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 FH Key Location/Qualifiers  
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 FT unsure  
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 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 81 AGAAGTCGATGTTACCATATATCATGAGATGAGCAATGATCTTCAGATGCT 140  
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 DB 2411 TTGATGTTACCTGAGATGTTCCCAAGAAAA 2445

RESULT 6  
 HSA417790 5419 bp mRNA linear PRI 09-OCT-2002  
 LOCUS HSA417790  
 DEFINITION HSA417790 mRNA for voltage-gated sodium channel (NAV1.9 gene).  
 ACCESSION AU417790  
 VERSION AU417790.1 GI:22796539  
 KEYWORDS NAV1.9 gene; voltage-gated sodium channel.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
 AUTHORS Blum,R., Kafitz,K.W. and Konnerth,A.  
 TITLE Neurotrophin-evoked depolarization requires the sodium channel  
 JOURNAL Nature 419 (6908), 687-693 (2002)  
 MEDLINE 22272672  
 PUBMED 12384689  
 REFERENCE 2 (bases 1 to 5419)  
 AUTHORS Blum,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-OCT-2001) Blum R., Institut fuer Physiologie,  
 Ludwig-Maximilians-Universitaet, Biedersteiner Strasse 29, Geb.  
 608, 80802 Muenchen, GERMANY

## FEATURES

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 1..5376  
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 /evidence=experimental  
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ORIGIN

Query Match 42.0%; Score 90.2; DB 9; Length 5419;  
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Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 81 AGAGTGTGATGTTACCGATATCATCAGATGAGACCATGATCTTCAGATGGCT 140  
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Db 2448 AGAAGTGTGATGTTACCGATATCATCAGATGAGACCATGATCTTCAGATGGCT 3007  
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Qy 141 TTGGATGTTACTGAGATGTTCCCAAGAAAA 175  
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Db 3008 TTGGATGTTACTGAGATGTTCCCAAGAAAA 3042  
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RESULT 7  
LOCUS BD012083 5728 bp DNA linear PAT 02-AUG-2002  
DEFINITION Human sodium channel SCN12A and SCN8A.  
ACCESSION BD012083  
VERSION BD012083.1 GI:22092272  
KEYWORDS WO 0190355-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 5728)  
kanazawa, I., Goto, U., and Jeong, S. Y.  
Human sodium channel SCN12A and SCN8A  
Patent: WO 0190355-A 2 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON  
YONG JEONG  
OS Homo sapiens (human)  
PN WO 0190355-A/2  
PD 29-NOV-2001  
PF 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085  
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
PC C12N15/12, C07K14/47, C07K16/18

CC FH Key Location/Qualifiers  
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ORIGIN

Query Match 42.0%; Score 90.2; DB 6; Length 5728;  
Best Local Similarity 96.8%; Pred. No. 1.5e-16;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 3147 AGAAGTGTGATGTTACCGATATCATCAGATGAGACCATGATCTTCAGATGGCT 3206  
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Qy 141 TTGGATGTTACTGAGATGTTCCCAAGAAAA 175  
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Db 3207 TTGGATGTTACTGAGATGTTCCCAAGAAAA 3241  
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RESULT 8  
LOCUS BD082952 5728 bp DNA linear PAT 27-AUG-2002  
DEFINITION Human sodium channel SCN12A.  
ACCESSION BD082952  
VERSION BD082952.1 GI:22628562  
KEYWORDS JP 2001327294-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 5728)  
kanazawa, I., Goto, U., and Jeon, Y.  
Human sodium channel SCN12A  
Patent: JP 2001327294-A 2 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
OS Homo sapiens (human)  
PN JP 2001327294-A/2  
PD 27-NOV-2001  
PF 23-MAY-2000 JP 2000152085  
PR ICHIRO KANAZAWA, JUN GOTO, YOSHIOHRO TEI  
PI C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
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Best Local Similarity 96.8%; Pred. No. 1.5e-16;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 81 AGAGTGTGATGTTACCGATATCATCAGATGAGACCATGATCTTCAGATGGCT 140  
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Db 3147 AGAAGTGTGATGTTACCGATATCATCAGATGAGACCATGATCTTCAGATGGCT 3206  
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Qy 141 TTGGATGTTACTGAGATGTTCCCAAGAAAA 175  
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Db 3207 TTGGATGTTACTGAGATGTTCCCAAGAAAA 3241  
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RESULT 9  
LOCUS AF150882 5728 bp mRNA linear PRI 15-JAN-2000  
DEFINITION Homo sapiens voltage-gated sodium channel alpha subunit, alternate  
splice variant SCN12A-s (SCN12A) mRNA, complete cds.

ACCESSION AF150882  
VERSION AF150882.1 GI:6693704  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Homo sapiens  
Hitachi, S., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,  
Hitachi, M., Ishihara, K., Uchiyama, Y., and Kanazawa, I.  
TITLE Identification of a novel human voltage-gated sodium channel alpha  
subunit gene, SCN12A  
JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
MEDLINE 20090626  
PUBMED 10623608  
REFERENCE 2 (bases 1 to 5728)  
AUTHORS Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, J.,  
and Kanazawa, I.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,  
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan  
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## ORIGIN

Query Match 42.0%; Score 90.2; DB 9; Length 5728;  
Best Local Similarity 96.8%; Pred. No. 1.5e-16;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

81 AGAAGTCTGATGTTACCGATGATCTATCGAATGTGACACCATTTGTTGAGAGGCT 140  
DB 3147 AGAAGTCTGATGTTACCGATGATCTATCGAATGTGACACCATTTGTTGAGAGGCT 3206

Qy 141 TTGATGTTACTCTGAGATGTTCCCAAGAAAA 175  
Db 3207 TTGATGTTACTCTGAGATGTTCCCAAGAAAA 3241

## RESULT 10

AR340678 5860 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 41 from patent US 6573067.  
ACCESSION AR340678  
VERSION AR340678.1 GI:33732410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5860)  
AUTHORS Dib-Hajj, S. and Waxman, S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 41 03-JUN-2003;  
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## ORIGIN

Query Match 42.0%; Score 90.2; DB 6; Length 5860;  
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## RESULT 11

AF188679 6237 bp mRNA linear PRI 14-DEC-1999  
LOCUS Homo sapiens voltage-gated sodium channel type XI alpha subunit  
DEFINITION (SCN11A) mRNA, complete cds.  
ACCESSION AF188679  
VERSION AF188679.1 GI:6572949  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Homo sapiens  
Hitachi, S., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, M., Goto, J.,  
Hitachi, M., Ishihara, K., Uchiyama, Y., and Kanazawa, I.  
TITLE Identification of a novel human voltage-gated sodium channel alpha  
subunit gene, SCN12A  
JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
MEDLINE 20090626  
PUBMED 10623608  
REFERENCE 2 (bases 1 to 6237)  
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A., Wood, P.M., and  
Waxman, S.G.  
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root  
ganglion neurons  
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)  
PUBMED 10580103

## ORIGIN

Query Match 42.0%; Score 90.2; DB 9; Length 5728;  
Best Local Similarity 96.8%; Pred. No. 1.5e-16;  
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2978 AGAAGTCTGATGTTACAGTATCTATCAGATGTAGCACCATGATCTTCAGAGTGCT 3037  
Qy 141 TTGATGTTACTGATGATGTTCCCAAGAAAA 175  
Db 3038 TTGATGTTACTGATGATGTTCCCAAGAAAA 3072  
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LOCUS Definition Human sodium channel SCN12A and SCN8A.  
BD012082  
ACCESSION BD012082.1 GI:22092271  
VERSION MO 0190355-A/1.  
KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 6528)  
TITLE Kanazawa, I., Goto, J. and Jeong, S.Y.  
JOURNAL Human sodium channel SCN12A and SCN8A  
Patent: WO 0190355-A 1 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON  
YONG JEONG  
COMMENT  
OS Homo sapiens (human)  
PN WO 0190355-A/1  
PD 29-NOV-2001  
PE 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085  
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
CC C12N15/12, C07K14/47, C07K16/18  
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Qy 141 TTGATGTTACTGATGATGTTCCCAAGAAAA 175  
Db 3207 TTGATGTTACTGATGATGTTCCCAAGAAAA 3241  
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BD082951  
ACCESSION BD082951.1 GI:22628561  
VERSION JP 2001327294-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 6528)  
TITLE Kanazawa, I., Goto, J. and Tel, Y.  
JOURNAL Human sodium channel SCN12A  
Patent: JP 2001327294-A 1 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT  
OS Homo sapiens (human)  
PN JP 2001327294-A/1  
PD 27-NOV-2001  
PE 23-MAY-2000 JP 2000152085  
PI ICHIRO KANAZAWA, JUN GOTO, YOSHITIRO TEI  
PC C12N15/09, C07K14/47, C07K16/18, C12P21/02, C12P21/08, C12N15/00  
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Best Local Similarity 96.8%; Pred. No. 1.5e-16;

Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 81 AGAAGTCTGATGTTACCACTATCTATGAGATGAGACCATGATTTAGAGATGCT 140  
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QY 141 TTGGATGGTTACTGAGATGTTCCCAAGAAAA 175  
 DB 3207 TTGGATGGTTACTGAGATGTTCCCAAGAAAA 3241

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 LOCUS Homo sapiens voltage-gated sodium channel alpha subunit SCN12A  
 DEFINITION (SCN12A) mRNA, complete cds.  
 ACCESSION AF109737  
 VERSION AF109737.1 GI:6693696  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 1 (bases 1 to 6528)  
 Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,  
 Hirai, M., Ishihara, K., Uchiyama, Y. and Kanazawa, I.  
 Identification of a novel human voltage-gated sodium channel alpha  
 subunit gene, SCN12A  
 Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
 2 (bases 1 to 6528)  
 Jeong, S.Y., Suzuki, T., Hashida, H., Masuda, N., Goto, J. and  
 Kanazawa, I.  
 Direct Submission  
 Submitted (27-NOV-1998) Neurology, Graduate School of Medicine,  
 Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

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ORIGIN

Query Match 42.0%; Score 90.2; DB 9; Length 6528;  
 Best Local Similarity 96.8%; Pred. No. 1.5e-15;  
 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 81 AGAAGTCTGATGTTACCACTATCTATGAGATGAGACCATGATTTAGAGATGCT 140  
 DB 3147 AGAAGTCTGATGTTACCACTATCTATGAGATGAGACCATGATTTAGAGATGCT 3206

QY 141 TTGGATGGTTACTGAGATGTTCCCAAGAAAA 175  
 DB 3207 TTGGATGGTTACTGAGATGTTCCCAAGAAAA 3241

RESULT 15  
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 LOCUS Mus musculus chromosome 9 clone RP24-409K22 map 9, \*\*\* SEQUENCING  
 DEFINITION IN PROGRESS \*\*\*, 11 unordered pieces.  
 AC124662.5 GI:38490569  
 AC124662 HTG: PHASE1; HTG: FULLTOP; HTG: ACTIVEFIN.  
 VERSION HTG: PHASE1; HTG: FULLTOP; HTG: ACTIVEFIN.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 241289)  
 Birren, B., Nussbaum, C. and Lander, E.  
 Mus musculus chromosome 9, clone RP24-409K22  
 Unpublished  
 2 (bases 1 to 241289)  
 Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,  
 Anderson, S., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L.,  
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 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacombe, K.,  
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 Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 241289)  
 Birren, B., Nussbaum, C., Lander, E., Abouelell, A., Allen, N.,  
 Anderson, M., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T.,



**ORIGIN**

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:33:04 ; Search time 155.624 Seconds  
(without alignments)  
5869.049 Million cell updates/sec

Title: US-09-646-224A-11

Perfect score: 215  
Sequence: 1 cagacatggaacacccg.....caacgttaccgttcgaagg 215

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002s:\*  
7: Geneseq2003as:\*  
8: Geneseq2003bs:\*  
9: Geneseq2003cs:\*  
10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	215	2	AAZ21489 Human sen
2	90.2	42.0	3638	2	AAx87602 Human sod
3	90.2	42.0	3701	4	AAf30104 Human sod
4	90.2	42.0	5728	6	AAf42750 Human sod
5	90.2	42.0	5860	4	AAf30101 Human sod
6	90.2	42.0	5860	4	ADD32193 Human Na
7	90.2	42.0	6528	6	AAf42749 Human sod
8	47.4	22.0	5822	4	AAx87601 Mouse sod
9	47.4	22.0	5822	4	AAf30103 Mouse sod
10	47.4	22.0	5822	9	ADD32195 Mouse Na
11	45.8	21.3	5298	9	ADD32209 Rat Na v
12	45.8	21.3	5334	2	AAx60244 Stab11ise
13	45.8	21.3	5875	2	AAx87600 Rat sodiu
14	45.8	21.3	5875	2	AAf30102 Rat sodiu
15	45.8	21.3	5897	2	AAZ21480 Rat senso
16	45.8	21.3	5905	2	ADb52929 Primary r
17	45.8	21.3	5905	9	ADD32191 Rat Na v
18	45.8	21.3	5908	2	AAx60241 CDNA enco
19	34	15.8	3073	5	ABV22473 Human pro
20	34	15.8	3073	5	ABV26134 Human pro
21	34	15.8	3073	5	ABV20302 Human pro
22	34	15.8	3073	5	ABV28288 Human pro
23	32.6	15.2	96589	8	ADA02708 Human ZFH

C	24	32.6	15.2	96589	9	ADB72446 Human ZFH
C	25	32.4	15.1	5504	4	ABf29845 Drosophil
C	26	31.4	14.6	800	7	ADA69948 Rice gene
C	27	31.4	14.6	2219	4	AAh14881 Human CDN
C	28	31.4	14.6	3994	5	AAH90054 Human bon
C	29	31.4	14.6	4062	5	AAH90106 Human bon
C	30	31.4	14.6	4062	8	ADB48438 Novel hum
C	31	31.4	14.6	4661	8	AAH89941 Human bon
C	32	31.4	14.6	5220	9	ADCl10001 Human NOV
C	33	31.2	14.5	11426	4	ABf03100 Drosophil
C	34	31.2	14.5	349901	9	ADc86940 Human GPC
C	35	31.2	14.5	349938	9	ADc87621 Human GPC
C	36	31.2	14.4	15363	2	AAx13216 Enterococ
C	37	31	14.4	15363	6	ABs99011 Enterococ
C	38	31	14.4	32134	4	ABK42170 Genomic s
C	39	31	14.4	32134	4	AAf37170 Human mus
C	40	31	14.4	32134	4	AAf03669 Human rep
C	41	31	14.4	32134	4	ABA07858 Human ova
C	42	31	14.4	32134	7	ABx60158 CDNA enco
C	43	31	14.4	32134	8	ADB60326 Connectiv
C	44	31	14.4	56632	4	AAK65581 Human imm
C	45	31	14.4	94191	9	ADe11169_3 Continuation (4 of

#### ALIGNMENTS

RESULT 1  
AAZ21489 standard; CDNA; 215 BP.  
ID AAZ21489  
XX AAZ21489;

DT 03-DEC-1999 (first entry)

DE Human sensory neurone specific 2a nucleotide sequence fragment #9.

KV Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;

KW voltage gated; hypersensitivity; ss.

OS Homo sapiens.

PN WO9947670-A1.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-GH000838.

PR 18-MAR-1998; 98GB-00005793.

PA (GLAX ) GLAXO GROUP LTD.

PI Grose DT, Hick CA, Tate SN;

DR WPI; 1999-562112/47.

PT Mammalian sodium channel protein for treating pain and hypersensitivity.

PS Claim 6; Page 67; 73pp; English.

XX AAZ21481 to AAZ21495 represent fragments of the human sensory neurone

CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel

CC protein. SNS-2a can be used in a method for the identification of a

CC modulator of a sodium channel, and for assaying for compounds which

CC modulate sodium flux. The sodium channel modulators can be used in a

CC medicament for the treatment of pain or hypersensitivity

XX Sequence 215 BP; 61 A; 44 C; 48 G; 62 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 215; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 5.6e-61;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 42.0%; Score 90.2; DB 2; Length 3638;  
 Best Local Similarity 96.8%; Pred. No. 2.8e-19;  
 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 1 CAGACAATGAGAACTCCGCTACTATGATGTAAGAGAGTCTAGTAAAGCACCACC 60  
 CC 1 CAGACAATGAGAACTCCGCTACTATGATGTAAGAGAGTCTAGTAAAGCACCACC 60  
 CC 61 TTCTTTTGTGTTGATGTCAGAGAGTGTGATGTTACCGATATATCATCATGAGATGTCAC 120  
 CC 61 TTCTTTTGTGTTGATGTCAGAGAGTGTGATGTTACCGATATATCATCATGAGATGTCAC 120  
 CC 121 CATTCATCTTCAGAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTC 180  
 CC 121 CATTCATCTTCAGAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTC 180  
 CC 181 AGCGATTTTTCGTTACCAACGCTTACGCTTTCGAGAG 215  
 CC 181 AGCGATTTTTCGTTACCAACGCTTACGCTTTCGAGAG 215

RESULT 2  
 AAX87602  
 ID AAX87602 standard; cDNA; 3638 BP.  
 AC AAX87602;  
 XX 26-OCT-1999 (first entry)  
 XX 26-OCT-1999 (first entry)  
 DE Human sodium channel NaN partial cDNA.  
 KM NaN, sodium channel; ion transport; human; dorsal root ganglia; pain;  
 KW paresthesia; hyperexcitability; therapy; SCN1A gene; ss.  
 OS Homo sapiens.  
 XX MO9938889-A2.  
 XX 05-AUG-1999.  
 PD 29-JAN-1999; 99WO-US002008.  
 XX 29-JAN-1999; 99WO-US002008.  
 PF 29-JAN-1998; 98US-0072990P.  
 PR 20-NOV-1998; 98US-0109402P.  
 XX (UYVA ) UNIV YALE.  
 PA DiB-Hajj S, Waxman S;  
 PI WPI; 1999-479168/40.  
 DR P-PSDB; AAY06598.  
 XX New isolated nucleic acids encoding sodium channels, used to develop  
 PT products for treating acute or chronic pain or hyperexcitability  
 PT phenomena.  
 XX Claim 1; Fig 8A1-2; 91pp; English.  
 PS This is the nucleotide sequence of a partial cDNA clone which codes for a  
 CC portion (see AAY06596) of human NaN, a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The NaN channel cDNA was obtained from human DRG tissue  
 CC cDNA by PCR amplification (see also AAX87620-22). Rat, mouse and human  
 CC NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98)  
 CC are provided. The invention also includes expression vectors and  
 CC transformed host cells, methods for identifying tissues and cells that  
 CC express NaN, methods for identifying agents that modulate NaN channel  
 CC activity or NaN channel mRNA transcription or translation, and a method  
 CC for using such agents to treat acute or chronic pain, paresthesia and  
 CC hyperexcitability phenomena. The preferential expression of NaN in  
 CC sensory DRG and trigeminal neurons provides a target for selectively  
 CC modifying the behaviour of these nerve cells while not affecting other  
 CC nerve cells in the brain and spinal cord. The gene is named SCN1A  
 CC Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;

Query Match 42.0%; Score 90.2; DB 2; Length 3638;  
 Best Local Similarity 96.8%; Pred. No. 2.8e-19;  
 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 81 AGAAGTCTGATGTTACCAAGTATCTATCAGAAATGTAGACCATGATCTTAGAGATGGCT 140  
 CC 2351 AGAAGTCTGATGTTACCAAGTATCTATCAGAAATGTAGACCATGATCTTAGAGATGGCT 2410  
 CC 141 TTGATGCTTACCTGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTC 175  
 CC 2411 TTGATGCTTACCTGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTCAGATGCTTTC 2445

RESULT 3  
 AAF30104  
 ID AAF30104 standard; cDNA; 3701 BP.  
 AC AAF30104;  
 XX 30-APR-2001 (first entry)  
 XX 30-APR-2001 (first entry)  
 DE Human sodium channel NaN partial cDNA.  
 KM Sodium channel; NaN; human; tetrodotoxin resistant; pain; paresthesia;  
 KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 1..3699  
 XX FT /\*tag= a  
 XX FT /partial  
 XX MO200105831-A1.  
 XX 25-JAN-2001.  
 PD 14-JUL-2000; 2000WO-US019342.  
 PF 14-JUL-2000; 2000WO-US019342.  
 XX 16-JUL-1999; 99US-00354147.  
 PR (UYVA ) UNIV YALE.  
 PA DiB-Hajj S, Waxman SG;  
 PI WPI; 2001-103147/11.  
 DR P-PSDB; AAB20125.  
 XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 PT channels, useful for preventing, diagnosing and treating pain,  
 PT paresthesia and/or hyperexcitability phenomena.  
 XX Example 4; Fig 8A; 162pp; English.  
 PS The present sequence is that of a partial cDNA for a novel human  
 CC tetrodotoxin resistant sodium channel, termed NaN (see AAB20125). The  
 CC cDNA was isolated from a human dorsal root ganglia tissue cDNA library by  
 CC PCR amplification (see also AAF30122-23). A full-length sequence is given  
 CC in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium  
 CC channel protein family and produces a TTX-R sodium current. Such channels  
 CC underlie the generation and propagation of impulses in excitable cells  
 CC such as neurons and muscle fibres. Preferential expression of NaN on  
 CC sensory neurons innervating the body (dorsal root ganglia) and the face  
 CC (trigeminal ganglia), but not on other neurons, makes it a very useful  
 CC target for diagnostic and/or therapeutic uses in relation to acute and/or  
 CC chronic pain pathologies. A claimed method of treating pain, paresthesia  
 CC and/or hyperexcitability phenomena in a human or animal subject involves  
 CC administering an agent that alters sodium current flow through NaN  
 CC channels, or which modulates transcription or translation of NaN mRNA, in  
 CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in  
 CC gene therapy to correct disorders associated with decreased sodium  
 CC channel expression or (antisense) to down-regulate NaN expression, in the  
 CC diagnosis of disease, and in the recombinant production of NaN

CC polypeptides  
XX Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;  
SQ Query Match 42.0%; Score 90.2; DB 4; Length 3701;  
Best Local Similarity 96.8%; Pred. No. 2.8e-19;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 81 AGAAGTGTGATGTTACCTGATATCTATCAGATGTAGCACCATTGATCTTCAGATGGCT 140  
DB 2351 AGAAGTGTGATGTTACCTGATATCTATCAGATGTAGCACCATTGATCTTCAGATGGCT 2410  
QY 141 TTGGATGTTACTGATGATGTTCCCAAGAAAA 175  
DB 2411 TTGGATGTTACTGATGATGTTCCCAAGAAAA 2445  
RESULT 4  
AAL42750 ID AAL42750 standard; cDNA; 5728 BP.  
XX AAL42750;  
XX AC  
XX DT 19-JUL-2002 (first entry)  
XX DE Human sodium channel subunit SCN12A-s coding sequence.  
XX KM Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
KW human nervous system; chromosome 3p23-21.3; excitatory cell;  
KM drug development; familial hyperglycaemia; QT extending syndrome type 3;  
KW motor endplate disease.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 200..4534  
FT /\*tag= a  
FT /product= "Human sodium channel subunit SCN12A-s"  
XX WO200190355-A1.  
XX PN 29-NOV-2001.  
XX PD 11-JUL-2000; 2000WO-JP004629.  
XX PF 23-MAY-2000; 2000JP-00152085.  
XX PR (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX PA Kanazawa I, Goto J, Jeong S;  
XX PI  
XX P1  
XX WPI; 2002-393394/42.  
XX DR P-PSDS; AAO14926.  
XX PT Sodium channel alpha subunits SCN12A and SCN8A of human nervous system  
PT together with splicing variants, useful in studying physiological  
PT mechanism relating to excitatory cells and in drug development.  
XX PS Claim 7; Page 55-70; 118bp; Japanese.  
XX  
XX CC The invention comprises the amino acid and coding sequence of three  
CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s  
CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and  
CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
CC subunit proteins are useful in studying physiological mechanisms relating  
CC to excitatory cells and in drug development. The sodium ion channel  
CC subunit proteins are useful for treating diseases such as familial  
CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.  
CC The present cDNA sequence encodes the human SCN12A-s sodium channel  
XX subunit  
XX Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;

Query Match 42.0%; Score 90.2; DB 6; Length 5728;  
Best Local Similarity 96.8%; Pred. No. 3.3e-19;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 81 AGAAGTGTGATGTTACCTGATATCTATCAGATGTAGCACCATTGATCTTCAGATGGCT 140  
DB 3147 AGAAGTGTGATGTTACCTGATATCTATCAGATGTAGCACCATTGATCTTCAGATGGCT 3206  
QY 141 TTGGATGTTACTGATGATGTTCCCAAGAAAA 175  
DB 3207 TTGGATGTTACTGATGATGTTCCCAAGAAAA 3241  
RESULT 5  
AAF30101 ID AAF30101 standard; cDNA; 5860 BP.  
XX AAF30101;  
XX AC  
XX DT 30-APR-2001 (first entry)  
XX DE Human sodium channel Nan cDNA.  
XX KM Sodium channel; Nan; human; tetrodotoxin resistant; pain; paraesthesia;  
KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 31..5402  
FT /\*tag= a  
XX WO200105831-A1.  
XX PN 25-JAN-2001.  
XX PD 14-JUL-2000; 2000WO-US019342.  
XX PF 16-JUL-1999; 99US-00354147.  
XX PR (UYVA ) UNIV YALE.  
XX PA  
XX PI Dib-Hajj S, Waxman SG;  
XX PT  
XX DR WPI; 2001-103147/11.  
XX DR P-PSDS; AAB20121.  
XX PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
PT channels, useful for preventing, diagnosing and treating pain,  
PT paraesthesia and/or hyperexcitability phenomena.  
XX PS Claim 1; Fig 11A; 162pp; English.  
XX  
XX CC The present sequence is that of cDNA encoding a novel human tetrodotoxin  
CC resistant sodium channel, termed Nan (see AAB20121). The cDNA was  
CC isolated from a human dorsal root ganglia tissue cDNA library by PCR  
CC amplification (see also AAF30122-23). Nan belongs to the a-subunit  
CC voltage-gated sodium channel protein family and produces a TTX-R sodium  
CC current. Such channels underlie the generation and propagation of  
CC impulses in excitable cells such as neurons and muscle fibres.  
CC Preferential expression of Nan on sensory neurons innervating the body  
CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
CC neurons, makes it a very useful target for diagnostic and/or therapeutic  
CC uses in relation to acute and/or chronic pain pathologies. A claimed  
CC method of treating pain, paraesthesia and/or hyperexcitability phenomena  
CC in a human or animal subject involves administering an agent that alters  
CC sodium current flow through Nan channels, or which modulates  
CC transcription or translation of Nan mRNA, in dorsal root ganglia or  
CC trigeminal neurons. Nan nucleic acids are used in gene therapy to correct  
CC disorders associated with decreased sodium channel expression or  
CC (antisense) to down-regulate Nan expression, in the diagnosis of disease,  
CC and in the recombinant production of Nan polypeptides  
XX

SQL Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;

Query Match 42.0%; Score 90.2; DB 4; Length 5860;  
Best Local Similarity 96.8%; Pred. No. 3,3e-19;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 81 AGAAGTGTGATGTTACCTGATATCATATCAGATGAGACCATGATGCTTCAGATGGCT 140  
DB 2978 AGAAGTGTGATGTTACCTGATATCATATCAGATGAGACCATGATGCTTCAGATGGCT 3037  
OY 141 TTGATGGTTACCTGATGATGGTTCCTCAAGAAAA 175  
DB 3038 TTGATGGTTACCTGATGATGGTTCCTCAAGAAAA 3072

RESULT 6  
ADD32193 ID ADD32193 standard; cDNA; 5860 BP.  
AC ADD32193;  
AD32193;  
DT 15-JAN-2004 (first entry)  
DE Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
XX expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH 31.5406  
FT CDS /tag=a  
FT /product="Na v 1.9 sodium channel protein"  
XX  
XX WO2003080570-A2.  
XX  
XX  
XX 02-OCT-2003.  
XX  
XX 20-MAR-2003; 2003WO-US008611.  
XX  
XX 20-MAR-2002; 2002US-0365550P.  
XX  
XX (TRAN-) TRANSMOLECULAR INC.  
XX  
XX Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
XX P-PSDB; ADD32194.  
XX  
XX Expression vector useful for stable cloning and expression of Nav1.9  
XX sodium channel at the mRNA and protein levels comprises a nucleic acid  
XX sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
XX fragment.  
XX  
XX Disclosure; SEQ ID NO 3; 125bp; English.  
XX  
XX The present invention describes an expression vector comprising a nucleic  
XX acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
XX its fragment, and producing a sodium current when transfected in a cell.  
XX Also described: (1) a recombinant cell comprising the plasmid selected  
XX from pRAN, pCMV-Na-GFP, pL338XN-rNan and the plasmid described above;  
XX (2) a method of making a cell or cell line that produces a Na v 1.9  
XX sodium channel-dependent sodium current by: (a) providing a cell that has  
XX been transfected with the expression vector; and (b) culturing the cell  
XX under conditions that allow expression of Na v 1.9 sodium channel protein  
XX to produce a sodium current into the transfected cell; (3) a method of  
XX screening for an agent that modulates sodium current in a cell by: (a)  
XX exposing the cell or cell line produced by the method to the agent; and  
XX (b) measuring sodium current following exposure to the agent, where an  
XX alteration in the level of sodium current is indicative of an agent  
XX capable of modulating sodium current in a cell; and (4) a recombinant  
XX cell comprising the expression vector. The expression vectors are useful

CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a human Na v 1.9 sodium channel protein, which  
CC is used in the exemplification of the present invention.  
XX  
XX SQL Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
XX  
XX Query Match 42.0%; Score 90.2; DB 9; Length 5860;  
XX Best Local Similarity 96.8%; Pred. No. 3,3e-19;  
XX Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 81 AGAAGTGTGATGTTACCTGATATCATATCAGATGAGACCATGATGCTTCAGATGGCT 140  
DB 2978 AGAAGTGTGATGTTACCTGATATCATATCAGATGAGACCATGATGCTTCAGATGGCT 3037  
OY 141 TTGATGGTTACCTGATGATGGTTCCTCAAGAAAA 175  
DB 3038 TTGATGGTTACCTGATGATGGTTCCTCAAGAAAA 3072

RESULT 7  
AAL42749 ID AAL42749 standard; cDNA; 6528 BP.  
AC AAL42749;  
AD42749;  
DT 19-JUL-2002 (first entry)  
DE Human sodium channel subunit SCN12A coding sequence.  
XX  
XX Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
XX human nervous system; chromosome 3p23-21.3; excitatory cell;  
XX human nervous system; familial hyperglycaemia; QT extending syndrome type 3;  
XX motor endplate disease.  
XX  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH 200.5575  
FT CDS /tag=a  
FT /product="Human sodium channel subunit SCN12A"  
XX  
XX WO200190355-A1.  
XX  
XX  
XX 29-NOV-2001.  
XX  
XX 11-JUL-2000; 2000WO-JP004629.  
XX  
XX 23-MAY-2000; 2000JP-00152085.  
XX  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
XX Kanazawa I, Goto J, Jeong S;  
XX  
XX WPI; 2002-393394/42.  
XX P-PSDB; AAO14925.  
XX  
XX Sodium channel alpha subunits SCN12A and SCN8A of human nervous system  
XX together with splicing variants, useful in studying physiological  
XX mechanism relating to excitatory cells and in drug development.  
XX  
XX Claim 6; Page 29-46; 118pp; Japanese.  
XX  
XX The invention comprises the amino acid and coding sequence of three  
XX sodium channel subunits from the human nervous system (SCN12A, SCN12A-s  
XX and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and  
XX the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
XX subunit proteins are useful in studying physiological mechanisms relating  
XX to excitatory cells and in drug development. The sodium ion channel  
XX subunit proteins are useful for treating diseases such as familial  
XX hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.  
XX The present cDNA sequence encodes the human SCN12A sodium channel subunit







PN W02003080570-A2.  
XX 02-OCT-2003.  
XX 20-MAR-2003; 2003WO-US008611.  
XX 20-MAR-2002; 2002US-0365550P.  
XX (TRAN-) TRANSMOLECULAR INC.  
XX Gonda MA, Greenwood JD;  
XX WPI; 2003-876895/81.  
XX P-PSDB; ADD32210.  
XX  
XX Expression vector useful for stable cloning and expression of Nav1.9  
XX PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
XX PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
XX PT fragment.

PS Claim 13; SEQ ID NO 19; 125pp; English.

XX The present invention describes an expression vector comprising a nucleic  
XX acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
XX its fragment, and producing a sodium current when transfected in a cell.  
XX Also described: (1) a recombinant cell comprising the plasmid selected  
XX from pRAN, pCMV-rhan-gfp, pUC338X-rhan and the plasmid described above;  
XX (2) a method of making a cell or cell line that produces a Na v 1.9  
XX sodium channel-dependent sodium current by: (a) providing a cell that has  
XX been transfected with the expression vector; and (b) culturing the cell  
XX under conditions that allow expression of Na v 1.9 sodium channel protein  
XX to produce a sodium current into the transfected cell; (3) a method of  
XX screening for an agent that modulates sodium current in a cell by: (a)  
XX exposing the cell or cell line produced by the method to the agent; and  
XX (b) measuring sodium current following exposure to the agent, where an  
XX alteration in the level of sodium current is indicative of an agent  
XX capable of modulating sodium current in a cell; and (4) a recombinant  
XX cell comprising the expression vector. The expression vectors are useful  
XX for the stable cloning and expression of the Na v 1.9 sodium channel at  
XX the mRNA and protein levels, and for producing sodium channel currents  
XX characteristic of native currents in dorsal root ganglion neurons. The  
XX present sequence encodes a rat Na v 1.9 sodium channel protein, which is  
XX used in the exemplification of the present invention.

SQ Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other;

Query Match 21.3%; Score 45.8; DB 9; Length 5298;  
Best Local Similarity 61.2%; Pred. No. 0.00016;  
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 81 AGAAGTGTGATGTTACCGATATCTATCAGATGTAGACCATTTGATCTTCAGATGCT 140  
DB 2879 AGAAGTGTGACGAGTGTGATGCTCTCGAATGACAGACATGACCTGAATGATATCT 2938  
QY 141 TTGGATGCTTACCTGAGATGTTCCCAAGAAAATTTCCAGCATTTTTCGTCCACG 200  
DB 2939 TTGAAAATTACAGAAAACAGTTTCCCAAAAAGCAGCAGATGATGCTTTCCCAAG 2998  
QY 201 G 201  
DB 2999 G 2999

RESULT 12  
ID AAX60244  
XX AAX60244 standard; cDNA; 5334 BP.  
XX  
AC AAX60244;  
XX  
DT 11-AUG-1999 (first entry)  
XX  
DE Stabilised cDNA encoding type 5 sodium channel protein designated PNS.  
XX

KW Type 5 sodium channel; PNS; nervous system; plexiform;  
KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
KW neuropathic pain; migraine; headache; ss.  
XX  
OS Synthetic.  
OS Rattus sp.  
XX  
XX FR2771103-A1.  
XX  
XX 21-MAY-1999.  
XX  
XX 19-NOV-1998; 98FR-00014551.  
XX  
XX 20-NOV-1997; 97US-0066225P.  
XX  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
XX  
XX Dietrich PS, Fish LM, Khare R, Robert DK, Sangameswaran L;  
XX WPI; 1999-315739/27.  
XX  
XX Isolated DNA encoding sodium channel of the nervous system.

PS Example 7; Fig 5A-E; 90pp; French.

XX The present sequence encodes a type 5 sodium channel protein designated  
XX CNS. The protein is a sodium ion channel of the nervous system, and is  
XX highly expressed in plexiform and dorsal root ganglia. The protein can be  
XX used to identify inhibitors of sodium channel proteins that are resistant  
XX to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
XX epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
XX neuropathy, and especially neuropathic pain, e.g. migraine and headache  
XX  
SQ Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;

Query Match 21.3%; Score 45.8; DB 2; Length 5334;  
Best Local Similarity 61.2%; Pred. No. 0.00016;  
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 81 AGAAGTGTGATGTTACCGATATCTATCAGATGTAGACCATTTGATCTTCAGATGCT 140  
DB 2902 AGAAGTGTGACGAGTGTGATGCTCTCGAATGACAGACATGACCTGAATGATATCT 2961  
QY 141 TTGGATGCTTACCTGAGATGTTCCCAAGAAAATTTCCAGCATTTTTCGTCCACG 200  
DB 2962 TTGAAAATTACAGAAAACAGTTTCCCAAAAAGCAGCAGATGATGCTTTCCCAAG 3021  
QY 201 G 201  
DB 3022 G 3022

RESULT 13  
ID AAX87600  
XX AAX87600 standard; cDNA; 5875 BP.  
XX  
AC AAX87600;  
XX  
DT 26-OCT-1999 (first entry)  
XX  
XX Rat sodium channel Nan cDNA.  
XX  
XX NAN; sodium channel; ion transport; rat; dorsal root ganglia; pain;  
XX paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.  
XX  
OS Rattus sp.  
XX  
XX  
XX Key Location/Qualifiers  
XX FH 41..5338  
XX CDS /\*tag= a  
XX FT 5551..5600  
XX FT misc\_feature /\*tag= b

/note= "these bases represent nucleotides missing from the sequence given in Fig 1 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

MO938889-A2.  
05-AUG-1999.  
29-JAN-1999; 99WO-US002008.  
29-JAN-1998; 98US-0072990P.  
20-NOV-1998; 98US-0109402P.  
(UYVA ) UNIV YALE.  
Dib-Hajj S, Waxman S;  
WPI: 1999-479168/40.  
P-PSDB; AAY06596.  
New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability phenomena.  
Claim 1; Fig 1A-D; 91pp; English.

This is the nucleotide sequence of an isolated nucleic acid which encodes the rat Na<sup>v</sup> channel (see AAY06596), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The Na<sup>v</sup> channel cDNA was obtained from Sprague-Dawley rat DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse and human Na<sup>v</sup> nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express Na<sup>v</sup>, methods for identifying agents that modulate Na<sup>v</sup> channel activity or Na<sup>v</sup> channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of Na<sup>v</sup> in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The Na<sup>v</sup> gene has been named Scn11a

Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;

Query Match 21.3%; Score 45.8; DB 2; Length 5875;  
Best Local Similarity 61.2%; Pred. No. 0.00016;  
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

81 AGAAGTCTGATGTTACCACTATCTATCAGAAATGTAAGCAACATTGATCTTCAGATGCT 140  
2919 AGAAGTCTGACGACGAGCATGCTCTCGAATGACGACCAATTGACGATGATATCT 2978  
141 TTGGATGTTACTGAGATGTTCCCAAGAAAAATTTCCAGCGATTTTTCGTACCAAG 200  
2979 TTAGAAATTACAGAAAAAGTTTCCCAAAAAAGCAGATGATGCTTTCCCAAG 3038  
201 G 201  
3039 G 3039

RESULT 14  
AAFP30102  
ID AAFP30102 standard; cDNA; 5875 BP.

XX AAFP30102;  
XX AAFP30102;  
XX 30-APR-2001 (first entry)  
XX

Rat sodium channel Na<sup>v</sup> cDNA.

Sodium channel; Na<sup>v</sup>; rat; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.

Rattus norvegicus.

Key Location/Qualifiers  
CDS 41..5338  
/\*tag= a

MO200105831-A1.

25-JAN-2001.

14-JUL-2000; 2000WO-US019342.

16-JUL-1999; 99US-00354147.

(UYVA ) UNIV YALE.

Dib-Hajj S, Waxman SG;

WPI: 2001-103147/11.

P-PSDB; AAB20122, AAB20123.

Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.

Example 1; Fig 1; 162pp; English.

The present sequence is that of cDNA encoding a novel rat tetrodotoxin resistant sodium channel, termed Na<sup>v</sup> (see AAB20122). The cDNA was isolated from a dorsal root ganglia tissue cDNA library by PCR amplification using generic primers (from conserved regions of a-subunit sodium channel proteins) and Na<sup>v</sup>-specific primers (see also AAFP30105-19), and RACE amplification. The open reading frame shows 73% similarity to the human Na<sup>v</sup> sequence (see AAFP30101). Na<sup>v</sup> belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of Na<sup>v</sup> on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through Na<sup>v</sup> channels, or which modulates transcription or translation of Na<sup>v</sup> mRNA, in dorsal root ganglia or trigeminal neurons. Na<sup>v</sup> nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate Na<sup>v</sup> expression. In the diagnosis of disease, and in the recombinant production of Na<sup>v</sup> polypeptides

Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;

Query Match 21.3%; Score 45.8; DB 4; Length 5875;  
Best Local Similarity 61.2%; Pred. No. 0.00016;  
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

81 AGAAGTCTGATGTTACCACTATCTATCAGAAATGTAAGCAACATTGATCTTCAGATGCT 140  
2919 AGAAGTCTGACGACGAGCATGCTCTCGAATGACGACCAATTGACGATGATATCT 2978  
141 TTGGATGTTACTGAGATGTTCCCAAGAAAAATTTCCAGCGATTTTTCGTACCAAG 200  
2979 TTAGAAATTACAGAAAAAGTTTCCCAAAAAAGCAGATGATGCTTTCCCAAG 3038  
201 G 201  
3039 G 3039

XX 3039 G 3039  
XX



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# OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 19:33:04 ; Search time 131.682 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-11

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Sequence: 1 cagacgaatgagaactccgct.....caacggttaacgctcgaagg 215

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match length	DB ID	Description
1	90.2	42.0	3701 15 US-10-388-470-6	Sequence 6, Appl1
2	90.2	42.0	5860 15 US-10-388-470-41	Sequence 41, Appl1
3	47.4	22.0	5822 15 US-10-388-470-41	Sequence 4, Appl1
4	45.8	21.3	5875 15 US-10-388-470-1	Sequence 1, Appl1
5	35	16.3	651 15 US-10-027-632-273499	Sequence 273499,
6	34.4	16.0	3673778 14 US-10-312-841-1	Sequence 1, Appl1
7	33.2	15.4	536 15 US-10-027-632-241203	Sequence 241203,
8	33.2	15.4	536 15 US-10-027-632-241204	Sequence 241204,
9	33.2	15.4	586 15 US-10-027-632-221451	Sequence 221451,
10	33.2	15.4	586 15 US-10-027-632-221452	Sequence 221452,
11	32.2	15.0	1581 14 US-10-198-846-6480	Sequence 6480, Ap
12	32	14.9	539 15 US-10-027-632-91590	Sequence 91590, A
13	32	14.9	539 15 US-10-027-632-91591	Sequence 91591, A
14	32	14.9	539 15 US-10-027-632-317742	Sequence 317742,
15	32	14.9	539 15 US-10-027-632-317743	Sequence 317743,

C 16	31.4	14.6	4062	14 US-10-037-270-348	Sequence 348, App
C 17	31.4	14.6	4062	15 US-10-117-722-348	Sequence 348, App
C 18	31.2	14.5	822900	12 US-10-292-798-1393	Sequence 1393, App
C 19	31	14.4	1405	12 US-10-424-599-63251	Sequence 63251, A
C 20	31	14.4	15363	9 US-09-070-927A-279	Sequence 279, App
C 21	31	14.4	32134	9 US-09-764-847-1057	Sequence 1057, Ap
C 22	31	14.4	32134	9 US-09-764-877-3535	Sequence 3535, Ap
C 23	31	14.4	32134	10 US-09-764-891-6357	Sequence 6357, Ap
C 24	31	14.4	32134	14 US-10-092-154-1057	Sequence 1057, Ap
C 25	31	14.4	32134	14 US-10-205-428-653	Sequence 653, App
C 26	31	14.4	32134	15 US-10-242-515-3535	Sequence 3535, Ap
C 27	30.4	14.1	4793	14 US-10-097-340-90	Sequence 90, Appl
C 28	30.2	14.0	758	15 US-10-027-632-12557	Sequence 12557, A
C 29	30.2	14.0	780	8 US-08-781-986A-736	Sequence 736, App
C 30	30.2	14.0	780	12 US-10-329-624-736	Sequence 736, App
C 31	30.2	14.0	176080	12 US-10-235-192A-43	Sequence 43, Appl
C 32	30	14.0	2021	15 US-10-027-632-99112	Sequence 99112, A
C 33	30	14.0	7945	14 US-10-138-098-49	Sequence 49, Appl
C 34	29.8	13.9	387	12 US-10-424-599-109491	Sequence 109491,
C 35	29.8	13.9	1095	15 US-10-027-632-9059	Sequence 9059, Ap
C 36	29.8	13.9	5544	9 US-09-843-676-68	Sequence 676, Ap
C 37	29.8	13.9	5544	9 US-09-766-253-68	Sequence 253, Ap
C 38	29.8	13.9	5544	10 US-09-438-486-68	Sequence 486, Ap
C 39	29.8	13.9	5544	14 US-10-053-758-68	Sequence 758, Appl
C 40	29.8	13.9	5544	14 US-10-054-295-68	Sequence 295, Ap
C 41	29.8	13.9	5544	14 US-10-054-611-68	Sequence 611, Ap
C 42	29.8	13.9	5544	14 US-10-044-692-111	Sequence 692, Ap
C 43	29.6	13.8	459	14 US-10-044-539-111	Sequence 539, Ap
C 44	29.6	13.8	459	15 US-10-027-632-39269	Sequence 39269, A
C 45	29.4	13.7	430	15 US-10-027-632-55537	Sequence 55537, A

## ALIGNMENTS

RESULT 1  
US-10-388-470-6  
Sequence 6, Application US/10388470  
Publication No. US2003022862A1  
GENERAL INFORMATION:  
APPLICANT: Ddb-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is  
OTHER INFORMATION: Leu.  
US-10-388-470-6  
Query Match 42.0%; Score 90.2; DB 15; Length 3701;  
Best Local Similarity 96.8%; Pred. No. 5.2e-20;

	Matches	92;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	81	AGAGTCGAGTGTACCAAGTATACATAGAGATGAGACACCATGATTTGCAGATGCGT	140							
Db	2351	AGAACTCTGAGTATCCAGTATACATAGATGAGATGAGACACCATGATTTGCAGATGCGT	2410							
QY	141	TTGGATGCTTACCTGAGATGGTTCCCAAAAGAAAA	175							
Db	2411	TTGGATGGTTACCTGAGATGGTTCCCAAAAGCCAA	2445							

RESULT 2  
US-10-388-470-41  
; Sequence 41, Application US/10388470  
; Publication No. US20030228662A1

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GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 3860
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human Nav
US-10-388-470-41

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Query Match 42.0%; Score 90.2; DB 15; length 5860;
Best Local Similarity 96.8%; Pred. No. 6,4e-20;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0

OY      81  AGAACTCGATGTTACCGATATACTATCAGAAATGAGCACCATTGATCTTCAGATGCT 140
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OY      141  TTGATGTTACCTCGATGCTTTCCCAAGAAAA 175
DB      3038  TTGATGTTACCTGATGATGTTCCCAAAAGCAA 3072

RESULT 3
US-10-388-470-4
; Sequence 4, Application US//10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008

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? PRIOR FILING DATE: 1999-01-29
? NUMBER OF SEQ. ID NOS: 44
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 4
? LENGTH: 5822
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (19)..(5313)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (5804)
? OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or g or t
US-10-388-470-4

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	Query Match	22.0%	Score 47.4	DB 15	Length 5822
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Db	2960	TTGAAATTTTACGAAAAACAGTTTCC	CCCCAAAAAGCACACAGATGATGCTTCCCAAAG	3019	
Qy	201	GTTACGCTT	209		
Db	3020	GCCTCAGTT	3028		

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RESULT 4
US-10-388-470-1
Sequence 1, Application US/10388470
Publication No. US20030228662A1
GENERAL INFORMATION:
APPLICANT: Maxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
PRIOR FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 5875
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: cDNA sequence for rat Nan
FEATURE:
NAME/KEY: unsure
LOCATION: (1996)..(4042)
OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.
US-10-388-470-1
Query Match 21.3%; Score 45.8; DB 15; Length 5875;
Best Local Similarity 61.2%; Pred. No. 0.0001;
Matches 74; Conservative 0; Mismatches 47; Indels 0; Gaps 0.

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Query Match	Best Local Similarity	16.3%	Score 35	DB 15	Length 651
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Db	380	CTTACACATAAATGTGAGAACCCGTGGAATVAAAAACCCCTCTATTATTAGGTTTAGAT	439		
QY	78	TGCAGAACTCTGATGTTTACAGATATACATATCAGAATGTAGACACCTTATGATCTTCAGGATG	137		
Db	440	TCATTGGTCTGATCTCTCAACCAAGAAAAAATGTCGTGAAAGCCCTTTTATTTCGAATG	499		
QY	138	GCTTT	142		
Db	500	AAITTT	504		

Query Match	Similarity	15.4%	Score 33.2	DB 15	Length 536
Best Local	Similarity	51.3%	Pred. No. 0.7		
Matches	77	Conservative	0	Mismatches	73
				Indels	0
				Gaps	0
QY	6	AATGAGAACTCCGTACTACTATGTAAGAAAGGTCTTAGTAAGAAGCACCCTTCTCT	65		
DB	435	ATTGTGCACTCACAAATTTCTTTTCAAAATATTTTGGGAAAGTTTACCTTAGT	376		
QY	66	TTTGTTTCGANGTGCAGAAAGTCATGTTTACAGATACTATCAAGATGTGACCAATTG	125		
DB	375	TTTCTTTCTATATATAGAAATAATATATATAATATTGGACAAATATAGAGTACTG	316		
QY	126	ATCTCAGATGGCTTGAGATGTTACCTG	155		





Db 285 TTCTCTATATATAGAAATAATTAATAATTTGAGAAATATAGACTG 226  
Cy 126 ATCTCAGATGCGTTGGATGTTACTG 155  
Db 225 CTTGAGGTAGATTATTATGTAGCAG 196

RESULT 11  
US-10-198-6480  
; Sequence 6480, Application US/10198846  
; Publication No. US200300999741  
; GENERAL INFORMATION:  
; APPLICANT: Little, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6480  
; LENGTH: 1581  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 4, 36, 52, 60, 70, 76, 80, 82, 102, 108, 112, 114, 116, 118,  
; LOCATION: 120, 122, 124, 126, 128, 136, 138, 142, 150, 156, 158, 167,  
; LOCATION: 173, 175, 183, 185, 189, 197, 199, 213, 218, 226, 262,  
; LOCATION: 264, 265, 268, 275, 276, 307, 325, 337, 339, 349  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
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; LOCATION: 353, 357, 373, 382, 400, 402, 408, 414, 424, 428, 436, 438,  
; LOCATION: 451, 453, 457, 493, 499, 504, 505, 525, 530, 541, 560, 620,  
; LOCATION: 640, 665, 666, 693, 718, 728, 776, 787, 805, 823, 871, 895,  
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; OTHER INFORMATION: n = A,T,C or G  
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; LOCATION: 11407, 1153, 1159, 1216, 1231, 1236, 1249, 1264, 1276, 1280,  
; LOCATION: 1301, 1302, 1319, 1333, 1342, 1375, 1380, 1382, 1419, 1422,  
; LOCATION: 1424, 1434, 1438, 1448, 1450, 1492, 1535, 1556, 1567, 1571,  
; LOCATION: 1573, 1576  
; OTHER INFORMATION: n = A,T,C or G  
US-10-198-6480

Query Match 15.0%; Score 32.2; DB 14; Length 1581;  
Best Local Similarity 47.9%; Pred. No. 2.6; Matches 86; Indels 0; Gaps 0;  
Matches 79; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Db 37 AAGCTCTAGTAAGGACCCCTCTCTTTGTTCTATGTGAGAGTGTATAC 96  
Cy 862 AAGGTTTCAAGGCCCCCCCCCTTTTNTTGGGGGGCCCTTTGGAAAAAATT 921  
Db 97 CAGTATATATCAGATAGTACCATGATCTTCAGATGCGTTGGATGTTACTG 156  
Cy 922 TTTTTCCTTTCCAAAGAGCCCTTTAAATTCTTTTNCCTTNGGGGTGAAGGCG 981  
Db 157 GATGTTCCCAAGAAATTTCCAGATTTTTCGTACCAAG 201  
Cy 982 TTTTTCCTTTCCAAAGATTTTCCCAATTTTNGGCCAAAG 1026

RESULT 12  
US-10-027-632-91590  
; Sequence 91590, Application US/10027632

; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91591  
; LENGTH: 539  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-91590

Query Match 14.9%; Score 32; DB 15; Length 539;  
Best Local Similarity 58.3%; Pred. No. 1.8; Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Db 26 TATGTAAAGAGGTCTTAAGGACCCCTCTCTTTGTTCTGATGTCAGAG 85  
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Db 86 TCTGATCTTACAGTATCTATCTGAAATGTAGCACC 121  
Cy 147 CCTAAAGCAGTATATATACCAATGTAAACAGCACC 182

RESULT 13  
US-10-027-632-91591  
; Sequence 91591, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91591  
; LENGTH: 539  
; TYPE: DNA

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; ORGANISM: Human
US-10-027-632-31591
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Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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DB 87 TATGTTGACAGATGTTAGTAAACATATATTTCTTGTCTGAGTGGAGAG 146
QY 86 TCTGATTTACCAATATCTATCAGATGTAGCACC 121
DB 147 CCTAAAGCAGTAATATACCATATGTAACAAGCACC 182

RESULT 14
US-10-027-632-317742
; Sequence 317742, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317742
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317742
Query Match
Best Local Similarity 14.9%; Score 32; DB 15; Length 539;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 26 TATGTTGAAGAAGTCTTAGTAAAGCACCCTTCTTGTCTGATGTCAGAG 85
DB 87 TATGTTGACAGATGTTAGTAAACATATATTTCTTGTCTGAGTGGAGAG 146
QY 86 TCTGATTTACCAATATCTATCAGATGTAGCACC 121
DB 147 CCTAAAGCAGTAATATACCATATGTAACAAGCACC 182

RESULT 15
US-10-027-632-317743
; Sequence 317743, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
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; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317743
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317743
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Query Match
Best Local Similarity 14.9%; Score 32; DB 15; Length 539;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 26 TATGTTGAAGAAGTCTTAGTAAAGCACCCTTCTTGTCTGATGTCAGAG 85
DB 87 TATGTTGACAGATGTTAGTAAACATATATTTCTTGTCTGAGTGGAGAG 146
QY 86 TCTGATTTACCAATATCTATCAGATGTAGCACC 121
DB 147 CCTAAAGCAGTAATATACCATATGTAACAAGCACC 182
```

Search completed: March 23, 2004, 05:12:00  
Job time : 217.682 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:45:54 ; Search time 1620.11 Seconds  
(Without alignments)  
4669.435 Million cell updates/sec

Title: US-09-646-224A-11

Perfect score: 215  
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Sequence: 1 cagacatggaacccgt.....caacgttaccgtcgaagg 215

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	215	100.0	215	27	US-09-646-224A-11	Sequence 11, Appl
2	170.2	79.2	437	72	US-60-169-841-129	Sequence 129, App
3	170.2	79.2	30565	77	US-60-213-846-31	Sequence 31, Appl
4	170.2	79.2	33768	77	US-60-213-846-334	Sequence 334, App
5	170.2	79.2	32768	77	US-60-213-846-335	Sequence 335, App
6	170.2	79.2	32768	77	US-60-213-846-336	Sequence 336, App
7	170.2	79.2	32768	77	US-60-213-846-337	Sequence 337, App
8	170.2	79.2	32768	77	US-60-213-846-338	Sequence 338, App
9	170.2	79.2	32768	77	US-60-213-846-339	Sequence 339, App
10	169.8	79.1	15159	103	US-60-466-412-84151	Sequence 84151, A
11	163.6	76.0	201	103	US-60-466-412-152259	Sequence 152259, A
12	118	54.9	3194	77	US-60-213-846-1109	Sequence 1109, Ap
13	99	46.0	201	103	US-60-466-412-152339	Sequence 152339, A
14	92.8	43.2	3163	77	US-60-213-846-1412	Sequence 1412, Ap
15	90.2	42.0	3701	1	PCT-US00-19342-6	Sequence 6, Appl
16	90.2	42.0	3701	1	PCT-US99-02008-6	Sequence 6, Appl
17	90.2	42.0	3701	50	US-10-388-470-6	Sequence 6, Appl
18	90.2	42.0	5080	46	US-10-170-335-13985	Sequence 13985, A
19	90.2	42.0	5080	102	US-60-453-050-2171	Sequence 2171, Ap
20	90.2	42.0	5080	102	US-60-453-135-2171	Sequence 2171, Ap
21	90.2	42.0	5080	103	US-60-466-412-2171	Sequence 2171, Ap
22	90.2	42.0	5728	47	US-10-219-0518-910	Sequence 910, App
23	90.2	42.0	5728	48	US-10-296-130-3	Sequence 3, Appl
24	90.2	42.0	5860	1	PCT-US00-19342-31	Sequence 41, Appl
25	90.2	42.0	5860	1	PCT-US03-08611-9	Sequence 3, Appl
26	90.2	42.0	5860	50	US-10-388-470-81	Sequence 41, Appl
27	90.2	42.0	5860	93	US-60-365-550-3	Sequence 317, Appl
28	90.2	42.0	6237	108	US-60-516-609-317	Sequence 317, Appl
29	90.2	42.0	6499	38	US-09-770-175-8399	Sequence 8399, Ap
30	90.2	42.0	6528	42	US-10-296-130-1	Sequence 1, Appl
31	90.2	42.0	6528	105	US-60-485-101-251	Sequence 251, Appl
32	51.2	23.8	201	102	US-60-453-050-33591	Sequence 33591, A
33	51.2	23.8	201	102	US-60-453-135-33591	Sequence 33591, A
34	51.2	23.8	201	103	US-60-466-412-33591	Sequence 33591, A
35	47.4	22.0	5822	1	PCT-US00-19342-4	Sequence 4, Appl
36	47.4	22.0	5822	1	PCT-US03-08611-5	Sequence 4, Appl
37	47.4	22.0	5822	1	PCT-US99-02008-4	Sequence 5, Appl
38	47.4	22.0	5822	50	US-10-388-470-4	Sequence 4, Appl
39	47.4	22.0	5822	93	US-60-365-550-5	Sequence 5, Appl
40	47.4	22.0	5833	45	US-10-144-771-19000	Sequence 19000, A
41	47.4	22.0	5833	93	US-60-360-207-19000	Sequence 19000, A
42	47.4	22.0	5858	46	US-10-180-934-1	Sequence 1, Appl
43	47.4	22.0	5858	105	US-10-377-139-15	Sequence 15, Appl
44	47.4	22.0	5858	105	US-60-485-101-345	Sequence 345, Appl
45	45.8	21.3	5298	1	PCT-US03-08611-19	Sequence 19, Appl

## ALIGNMENTS

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RESULT 1
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: GENERAL INFORMATION:
: APPLICANT: Glaxo Wellcome PLC
: APPLICANT: Tate, Simon N
: APPLICANT: Grose, David T
: APPLICANT: Hicks, Caroline A
: TITLE OR INVENTION: Ion Channels
: FILE REFERENCE: PG3432
: CURRENT APPLICATION NUMBER: US/09/646,224A
: CURRENT FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: GB 9805793.8
: PRIOR FILING DATE: 1998-03-18
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
:
: LENGTH: 215
: TYPE: DNA

```

ORGANISM: Homo sapiens  
US-09-646-224A-11

Query Match	100.0%;	Score 215;	DB 27;	Length 215;
Best Local Similarity	100.0%;	Pred. No. 3.8e-57;		
Matches 215; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	CAGACAAATAGAAAATCCGGTACTACTATGATGGAAAAGAGCTCTAGTAAAAAGGACACCCC	60
Db	1	CAGACAAATAGAAAATCCGGTACTACTATGATGGAAAAGAGCTCTAGTAAAAAGGACACCCC	60
QY	61	TTCCCTTTTGTCTGATGTGCAGAAAGTCTGATGTTCACGATATCTATCAGATGTAGCAC	120
Db	61	TTCCCTTTTGTCTGATGTGCAGAAAGTCTGATGTTCACGATATCTATCAGATGTAGCAC	120
QY	121	CATTGATCTTCAGAGATGCGTTTGGATATGGTATCCCTGAGATGGTCCCAAGAAAATTTCC	180
Db	121	CATTGATCTTCAGAGATGCGTTTGGATATGGTATCCCTGAGATGGTCCCAAGAAAATTTCC	180
QY	181	AGCGATTTTTCGTAACCAACGATTAAGCTTCGAGAG	215
Db	181	AGCGATTTTTCGTAACCAACGATTAAGCTTCGAGAG	215

RESULT 2  
US-60-169-841-129  
; Sequence 129, Application US/60169841

```

APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO000153
CURRENT APPLICATION NUMBER: US/60/169,841
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 2910
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129
LENGTH: 437
TYPE: DNA
ORGANISM: Human
US-60-169-841-129

```

Query Match	79.2%	Score 170.2;	DB 72;	Length 437;
Best Local Similarity	98.3%;	Pred. No. 7.3e-43;		
Matches 172; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

Oy		CAGACAAATGAGAACTCCGTACTCACTATGGTGAAGAAGGCTTGTTGTAAAAGCACC	60
Db	194	CAGACAATGAGAACTCCGTACTCACTATGGTGAAGAAGGCTTGTTGTAAAAGCACC	25
Oy	61	TTCCTTTGTTCGATGTGCAGAGCTCATGTATCCAGTATTACATCAGATGTAGCAC	120
Db	254	TTCCTTTGTTCGATGTGCAGAGCTCATGTATCCAGTATTACATCAGATGTAGCAC	31
Oy	121	CATTGATCTTCAGATGCGTTTGGATGGTTACCTGAGATGTTTTCCCAAAGAAAA	175
Db	314	CATTGATCTTCAGATGCGCTTTGGATGGTTACCTGAGATGTTTTCCCAAAGAACAA	368

```

RESULT 3
US-60-213-846-31
; Sequence 31, Application US/60213846
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000703
; CURRENT APPLICATION NUMBER: US/60/213,846
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 31  
LENGTH: 30565  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (30565)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-31

Query Match 79.2%; Score 170.2; DB 77; Length 30565;  
Best Local Similarity 98.3%; Pred. No. 2.9e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 60  
22214 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 22273  
Qy 61 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 120  
Db 22274 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 22333  
Qy 121 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 175  
Db 22334 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 22388

RESULT 4  
US-60-213-846-334  
Sequence 334, Application US/60213846  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
FILE REFERENCE: C1000703  
CURRENT APPLICATION NUMBER: US/60/213,846  
CURRENT FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 334  
LENGTH: 32768  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (32768)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-334

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 60  
Db 24417 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 24476  
Qy 61 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 120  
Db 24477 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 24536  
Qy 121 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 175  
Db 24537 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 24591

RESULT 5  
US-60-213-846-335  
Sequence 335, Application US/60213846  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
FILE REFERENCE: C1000703  
CURRENT APPLICATION NUMBER: US/60/213,846  
CURRENT FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 335  
LENGTH: 32768  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (32768)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-335

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: C1000703  
CURRENT APPLICATION NUMBER: US/60/213,846  
CURRENT FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 335  
LENGTH: 32768  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (32768)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-335

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 60  
Db 24417 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 24476  
Qy 61 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 120  
Db 24477 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 24536  
Qy 121 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 175  
Db 24537 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 24591

RESULT 6  
US-60-213-846-336  
Sequence 336, Application US/60213846  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
FILE REFERENCE: C1000703  
CURRENT APPLICATION NUMBER: US/60/213,846  
CURRENT FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 336  
LENGTH: 32768  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (32768)  
OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-336

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 60  
Db 24417 CAGCAATGAGAACTCCGTACTACTATGTGAAAGAGGCTTTAGTAAAGGCAACCC 24476  
Qy 61 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 120  
Db 24477 TTCTTTTGTCTGATGTCAGAGTCTGATGTTACCACTATCTACAGATGTAGCAC 24536  
Qy 121 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 175  
Db 24537 CATTGATCTTCAGAGTGGCTTTGGATGGTTACCTGAGATGGTTCCCAAGAAAA 24591

## RESULT 7

US-60-213-846-337  
; Sequence 337, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 337  
; LENGTH: 32768  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(32768)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-337

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 60  
DB 24417 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 24476  
OY 61 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 120  
DB 24477 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 24536  
OY 121 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 175  
DB 24537 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 24591

## RESULT 8

US-60-213-846-338  
; Sequence 338, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 338  
; LENGTH: 32768  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(32768)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-338

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 60  
DB 24417 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 24476  
OY 61 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 120

DB 24477 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 24536

OY 121 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 175  
DB 24537 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 24591

## RESULT 9

US-60-213-846-339  
; Sequence 339, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 339  
; LENGTH: 32768  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(32768)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-213-846-339

Query Match 79.2%; Score 170.2; DB 77; Length 32768;  
Best Local Similarity 98.3%; Pred. No. 3e-42;  
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 60  
DB 24417 CAGACAATGAGAACTCCGTACTACTATGTTGAAAGAGTCTTAGTAAAGGACACCC 24476  
OY 61 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 120  
DB 24477 TTCCTTTGTTCTGATGTCGACAAAGTCTGATGTTACCCGTAATACATGAGATGAGAC 24536  
OY 121 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 175  
DB 24537 CATTGATCTTCAGATGAGCTTTGATGTTACCTGAGATGTTCCCAAGAAAA 24591

## RESULT 10

US-60-466-412-84151  
; Sequence 84151, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84151  
; LENGTH: 115159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(115159)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-466-412-84151

Query Match 79.0%; Score 169.8; DB 103; Length 115159;  
Best Local Similarity 97.7%; Pred. No. 5.9e-42;

Matches 177; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 60  
DB 71063 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 71122

QY 61 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGC 120  
DB 71123 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGC 71182

QY 121 CATTGATCTTCAGATGAGCTTGTGATGTTACTGATGTTCCCAAGAAAA 175  
DB 71183 CATTGATCTTCAGATGAGCTTGTGATGTTACTGATGTTCCCAAGAAAA 71237

RESULT 11  
US-60-466-412-152259  
; Sequence 152259, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 152259  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-152259

Query Match 76.1%; Score 163.6; DB 103; Length 201;  
Best Local Similarity 99.4%; Pred. No. 7e-41;  
Matches 163; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 60  
DB 38 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 97

QY 61 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGC 120  
DB 98 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGC 157

QY 121 CATTGATCTTCAGATGAGCTTGTGATGTTACTGATGTTCCCAAGAAAA 175  
DB 158 CATTGATCTTCAGATGAGCTTGTGATGTTACTGATGTTCCCAAGAAAA 201

RESULT 12  
US-60-213-846-1109  
; Sequence 1109, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1109  
; LENGTH: 3194  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-213-846-1109

Query Match 54.9%; Score 118; DB 77; Length 3194;  
Best Local Similarity 100.0%; Pred. No. 4.6e-26;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGAAGAAGGCTTGTAGTAAAGGACCCCTTCTTTTGTCTGATGTCAGAAATGTGA 90  
DB 2097 TGAAGAAGGCTTGTAGTAAAGGACCCCTTCTTTTGTCTGATGTCAGAAATGTGA 2156

QY 91 TGTACCAAGTATCTATACAGAAATGTAGCAGATGTTCCCAAGAAAA 175  
DB 2157 TGTACCAAGTATCTATACAGAAATGTAGCAGATGTTCCCAAGAAAA 1822

RESULT 13  
US-60-466-412-152339  
; Sequence 152339, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 152339  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-152339

Query Match 46.0%; Score 99; DB 103; Length 201;  
Best Local Similarity 100.0%; Pred. No. 2e-20;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 60  
DB 103 CAGACAATGAGAACTCCGTACTAATAAGTGTGAAAGAGGCTTGTAGTAAAGGACACCC 162

QY 61 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCAAG 99  
DB 163 TTCCTTTTGTCTGATGTCAGAAAGTCTGATGTTACCAAG 201

RESULT 14  
US-60-213-846-1412  
; Sequence 1412, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1412  
; LENGTH: 3163  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-213-846-1412

Query Match 43.2%; Score 92.8; DB 77; Length 3163;  
Best Local Similarity 93.3%; Pred. No. 4.4e-18;  
Matches 97; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 72 CTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGCAGATGTTCC 131  
DB 1719 CTGATGTCAGAAAGTCTGATGTTACCACTATACAGAAATGTAGCAGATGTTCC 1778

QY 132 AGATGCTTGTGATGTTACTGATGTTCCCAAGAAAA 175  
DB 1779 AGATGCTTGTGATGTTACTGATGTTCCCAAGAAAA 1822

```
RESULT 15
PCT-US00-19342-6
; Sequence 6, Application PC/TUS0019342
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: DiB-Hajj, Sulayman
; APPLICANT: Maxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-02-WO
; CURRENT APPLICATION NUMBER: PCT/US00/19342
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/354,147
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3699)
; OTHER INFORMATION: partial human Nan cDNA sequence
; NAME/KEY: unsure
; LOCATION: (922)
; OTHER INFORMATION: Y = C or T
PCT-US00-19342-6

Query Match          42.0%; Score 90.2; DB 1; Length 3701;
Best Local Similarity 96.8%; Pred. No. 3.1e-17;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      81 AGAATCTGATGTTACCACTATATCAGATGTAGCCACCTTGTCTTCGAGATGGCT 140
      |||
Db      2351 AGAAGTCTGATGTTACCACTATATCAGATGTAGCCACCTGATCTTCGAGATGGCT 2410

QY      141 TTGGATGGTTACCTGAGATGGTCCCAAGAAAA 175
      |||
Db      2411 TTGGATGGTTACCTGAGATGGTCCCAAGAAAA 2445
```

Search completed: March 23, 2004, 04:00:02  
Job time : 1638.26 secs





LOCATION: (1)...(1790242)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-767-471-10805

Query Match 14.1%; Score 30.4; DB 6; Length 1790242;  
Best Local Similarity 49.4%; Pred. No. 15;  
Matches 79; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 19 GTACTACTATGTTGAAGAAGCTTACTTAAGAACACCCCTTCTTGTCTGATGT 78  
DB 1700597 GTTATATTGTGGCAAAATAGATCAGTAAACCAATTAATTTTGTCTTGTAGT 1700538

QY 79 GCAGAAGTCTGATGTTTACAGATATCTACTAGATAGTACACCATTTGATCTTCAAGATGG 138  
DB 1700537 AAAACAGACTATTTCTTCCAGACCTTATTAAGTCTGAAGATTATATTTTGTGTGTA 1700478

QY 139 CTTTGATGTTTACTCTGAGATGTTCCCAAGAAAAATTT 178  
DB 1700477 TTTTACTGAAACATATAATATACAAACATTTATTTGT 1700438

RESULT 3  
US-10-767-701-13578  
Sequence 13578, Application US/10767701  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
FILE REFERENCE: 38-21(5353)B  
CURRENT APPLICATION NUMBER: US/10/767,701  
CURRENT FILING DATE: 2004-01-29  
NUMBER OF SEQ ID NOS: 63128  
SEQ ID NO 13578  
LENGTH: 1051  
TYPE: DNA  
ORGANISM: Sorghum bicolor  
FEATURE:  
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41987\_1  
US-10-767-701-13578

Query Match 14.0%; Score 30; DB 6; Length 1051;  
Best Local Similarity 52.4%; Pred. No. 1.6;  
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 69 GTTCTGATGTGCAAGATCTGATGTTACCATATCTATCAGATGTAGACACCATTTGATC 128  
DB 692 GTTCTGCTCGGATGCTCTCTGCTGTACCATATCTAGTTGTAAGTGTCTCCCGGTCTC 751

QY 129 TTCAGATGGCTTTGGATGGTATCTGAGATGTTCCCAAGAAAAATTTCCAGCATTT 188  
DB 752 AATGACATCATGATGATCTCTGTAGAATGTATATCATATATGCTGTACCGAAC 811

QY 189 TTGCTA 194  
DB 812 TCGCTA 817

RESULT 4  
US-10-767-701-6590  
Sequence 6590, Application US/10767701  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
FILE REFERENCE: 38-21(5353)B  
CURRENT APPLICATION NUMBER: US/10/767,701  
CURRENT FILING DATE: 2004-01-29  
NUMBER OF SEQ ID NOS: 63128  
SEQ ID NO 6590

LENGTH: 865  
TYPE: DNA  
ORGANISM: Sorghum bicolor  
FEATURE:  
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS4834\_1  
US-10-767-701-6590

Query Match 13.4%; Score 28.8; DB 6; Length 865;  
Best Local Similarity 58.0%; Pred. No. 3.9;  
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 122 ATGATCTTCAGATGCTTTGATGTTTACCTGATGTTCCCAAGAAAAATTTCCA 181  
DB 655 ATGCTATTGAGAGCTTCTGTTAAGTGGCAAGATGTTGCTAAACCAAGTTGCA 714

QY 182 GCGATTTTTCGTACCAACGTTAGCTT 209  
DB 715 ACTATTTTCTGTATTAACACTATGATT 742

RESULT 5  
US-10-796-280-12202  
Sequence 12202, Application US/10796280  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001510  
CURRENT APPLICATION NUMBER: US/10/796,280  
CURRENT FILING DATE: 2004-03-10  
NUMBER OF SEQ ID NOS: 68533  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12202  
LENGTH: 303523  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(303523)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-796-280-12202

Query Match 13.3%; Score 28.6; DB 6; Length 303523;  
Best Local Similarity 48.5%; Pred. No. 34;  
Matches 79; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 25 CTATGTAAGAAAGAGCTTTAGTAAGAAAGCAACCCCTTCTTTGTTCTGATGTCAGAA 84  
DB 224151 CAACGTGGGAAACAGAAAGACTCTTATCAGGCTTCTTGTGTTGTAAGTCACTC 224210

QY 85 GTCTGATGTTTACCATATCTATCATCATGATGTAGACACCATTTGATCTTCAGATGGCTTTGG 144  
DB 224211 TGTGTTTAAACAAATAATAGAAAAAACAACCAATTTCTATGTAAGATCTTGA 224270

QY 145 ATGTTACCTGAGATGTTCCCAAGAAAAATTTCCAGCATTT 187  
DB 224271 TTCACTCCATCTGAATCTACTAAACAGTATTTGGAATT 224313

RESULT 6  
US-09-969-034-2460  
Sequence 2460, Application US/09969034  
GENERAL INFORMATION:  
APPLICANT: Burgess, Christopher C.  
APPLICANT: Astle, Jon H.  
APPLICANT: Carroll, Eddie III  
APPLICANT: Catino, Theodore J.  
APPLICANT: Diwedi, Poornima  
APPLICANT: Molino, Gary A.  
APPLICANT: Thigalingam, Arunthathi  
APPLICANT: Lewis, Marcia E.  
TITLE OF INVENTION: Nucleic Acid Sequences Differentially  
TITLE OF INVENTION: Expressed in Cancer Tissue

FILE REFERENCE: 1657/1032  
CURRENT APPLICATION NUMBER: US/09/969,034  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/237,271  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 4494  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2460  
LENGTH: 299  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 217,267, 271, 279, 298  
OTHER INFORMATION: n = A,T,C or G  
US-09-969-034-2460

Query Match 13.1%; Score 28.2; DB 5; Length 299;  
Best Local Similarity 53.2%; Pred. No. 3.7;  
Matches 59; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 ACATGAGAACTCCGACTACTGATGTTGAAAGAGCTTTAGTAAAGGACCCCTTC 63  
DB 139 AAATGTCAAGCTGATCAAGACTGACAGCAGCTTAGTGAATGACCCACTTC 198  
QY 64 CTTTGTCTGATGTGCAAGTCTGATGTTACAGTATCTATCAGATG 114  
DB 199 GTTTAAGCTCATCCANCAATATGATGCAAGTTGAGCTTGAGATG 249

RESULT 7  
US-10-793-479-20110/C

Sequence 120110, Application US/10793479  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J. B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J. Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/10/793,479  
CURRENT FILING DATE: 2004-03-03  
PRIOR APPLICATION NUMBER: US/09/513,999  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 20110  
LENGTH: 164  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 86  
OTHER INFORMATION: m=a or c  
US-10-793-479-20110

Query Match 13.1%; Score 28.2; DB 6; Length 164;  
Best Local Similarity 55.7%; Pred. No. 3.5;  
Matches 54; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 65 TTTTGTCTGATGTGCAAGTCTGATGTTACCAAGTATCTATCAGATGATG 124  
DB 133 TTGCATTCGAAATTAAGAAATTTGATATACCATTAATGTTTAAAGKCTAGAAACAT 74  
QY 125 GATCTTCAGATGAGCTTTGATGTTACCTGAGATG 161  
DB 73 TTGGAAGCATATTTTGTGTTTCTTCTGAGATG 37

RESULT 8  
US-60-548-091-2104  
Sequence 2104, Application US/60548091

GENERAL INFORMATION:  
APPLICANT: GARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2104  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-2104

Query Match 13.1%; Score 28.2; DB 7; Length 201;  
Best Local Similarity 51.2%; Pred. No. 3.7;  
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 45 AGTAAAGGACCCCTTCCTTTGTCTGATGTGAGAGTGTGATGTTACAGATATAC 104  
DB 37 AATTAAGTGTATTTCTACTCTCTGATCTCAGAGGCTATCTGAGACAGCTTGAC 96  
QY 105 TATCAGATGTAGCACCATTGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTG 164  
DB 97 TACATGCTATTTTACCAATGATTTTCAAGTGAAGCTGGCTAGTATTTAACTGGGTC 156  
QY 165 CCAAGAAA 173  
DB 157 TTTATATAA 165

RESULT 9  
US-60-548-091-2114

Sequence 2114, Application US/60548091  
GENERAL INFORMATION:  
APPLICANT: GARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2114  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-2114

Query Match 13.1%; Score 28.2; DB 7; Length 201;  
Best Local Similarity 51.2%; Pred. No. 3.7;  
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 45 AGTAAAGGACCCCTTCCTTTGTCTGATGTGAGAGTGTGATGTTACAGATATAC 104  
DB 37 AATTAAGTGTATTTCTACTCTCTGATCTCAGAGGCTATCTGAGACAGCTTGAC 96  
QY 105 TATCAGATGTAGCACCATTGATCTTCAGAGTGGCTTTGATGTTACCTGAGATGTTG 164  
DB 97 TACATGCTATTTTACCAATGATTTTCAAGTGAAGCTGGCTAGTATTTAACTGGGTC 156  
QY 165 CCAAGAAA 173  
DB 157 TTTATATAA 165

RESULT 10  
US-60-548-091-2125  
Sequence 2125, Application US/60548091  
GENERAL INFORMATION:  
APPLICANT: GARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2125
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-2125

```

```

Query Match      13.1%; Score 28.2; DB 7; Length 201;
Best Local Similarity 51.2%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 63;

```

```

QY 45 AGTAAAGGACACCCCTTCCTTTGTTCTGATGTGCAGAAAGTCTGATGTTACCAATATAC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 37 AATAAGATGTAATTCACCTCCCTTGATCTCAAGGCGTAACCTGGAAGCACAGCTTGAC 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 TATCAGAAATGTAACCAATGATCTTCAGATGCGTTTGATGCTTACCTGAGATGTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 TACAVGTCAATTTTACCAATGATTTTCAGGTGACCTGGGCTAAGTCATTTAACTGGGTC 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 CCAAGAAA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 TTTATATAA 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 11

```

US-60-548-091-2142
; Sequence 2142, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2142
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-2142

```

```

Query Match      13.1%; Score 28.2; DB 7; Length 201;
Best Local Similarity 51.2%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 63;

```

```

QY 45 AGTAAAGGACACCCCTTCCTTTGTTCTGATGTGCAGAAAGTCTGATGTTACCAATATAC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 37 AATAAGATGTAATTCACCTCCCTTGATCTCAAGGCGTAACCTGGAAGCACAGCTTGAC 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 TATCAGAAATGTAACCAATGATCTTCAGATGCGTTTGATGCTTACCTGAGATGTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 TACAVGTCAATTTTACCAATGATTTTCAGGTGACCTGGGCTAAGTCATTTAACTGGGTC 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 CCAAGAAA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 TTTATATAA 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 12

```

US-60-548-091-2155
; Sequence 2155, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091

```

```

; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2155
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-2155

```

```

Query Match      13.1%; Score 28.2; DB 7; Length 201;
Best Local Similarity 51.2%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 63;

```

```

QY 45 AGTAAAGGACACCCCTTCCTTTGTTCTGATGTGCAGAAAGTCTGATGTTACCAATATAC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 37 AATAAGATGTAATTCACCTCCCTTGATCTCAAGGCGTAACCTGGAAGCACAGCTTGAC 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 TATCAGAAATGTAACCAATGATCTTCAGATGCGTTTGATGCTTACCTGAGATGTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 TACAVGTCAATTTTACCAATGATTTTCAGGTGACCTGGGCTAAGTCATTTAACTGGGTC 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 CCAAGAAA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 TTTATATAA 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 13

```

US-60-548-091-2164
; Sequence 2164, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2164
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-2164

```

```

Query Match      13.1%; Score 28.2; DB 7; Length 201;
Best Local Similarity 51.2%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 63;

```

```

QY 45 AGTAAAGGACACCCCTTCCTTTGTTCTGATGTGCAGAAAGTCTGATGTTACCAATATAC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 37 AATAAGATGTAATTCACCTCCCTTGATCTCAAGGCGTAACCTGGAAGCACAGCTTGAC 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 TATCAGAAATGTAACCAATGATCTTCAGATGCGTTTGATGCTTACCTGAGATGTTTC 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 TACAVGTCAATTTTACCAATGATTTTCAGGTGACCTGGGCTAAGTCATTTAACTGGGTC 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 CCAAGAAA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 TTTATATAA 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 14

```

US-60-548-091-2179
; Sequence 2179, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 2179  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-2179

Query Match 13.1%; Score 28.2; DB 7; Length 201;  
Best Local Similarity 51.2%; Pred. No. 3.7;  
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 45 AGTAAAGGACCCCTTCTTGTCTGATGTGACAAAGCTGATGTTACAGATATAC 104  
DB 37 AATAAGATGTAATTTCTACTCCCTTGATCTCAAGGCGTAACCTGGAAGCAGACTTGAC 96  
QY 105 TATCAGATGTAGACCAATTGATCTTCAGATGGCTTTGATGGTTAAGTATGTTTC 164  
DB 97 TACAATGTCATTTTACCAATGATTTTACAGTGAAGCTGGCTAAGTCAATTTAACTGGGTC 156  
QY 165 CCAAGAAA 173  
DB 157 TTTATATAA 165

## RESULT 15

US-60-548-091-2187  
; Sequence 2187, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001506  
; CURRENT APPLICATION NUMBER: US/60/548,091  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2187  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-2187

Query Match 13.1%; Score 28.2; DB 7; Length 201;  
Best Local Similarity 51.2%; Pred. No. 3.7;  
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 45 AGTAAAGGACCCCTTCTTGTCTGATGTGACAAAGCTGATGTTACAGATATAC 104  
DB 37 AATAAGATGTAATTTCTACTCCCTTGATCTCAAGGCGTAACCTGGAAGCAGACTTGAC 96  
QY 105 TATCAGATGTAGACCAATTGATCTTCAGATGGCTTTGATGGTTAAGTATGTTTC 164  
DB 97 TACAATGTCATTTTACCAATGATTTTACAGTGAAGCTGGCTAAGTCAATTTAACTGGGTC 156  
QY 165 CCAAGAAA 173  
DB 157 TTTATATAA 165

Search completed: March 23, 2004, 04:48:14  
Job time : 322.461 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 1261.46 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-11

Perfect score: 215  
Sequence: 1 cagacatcgtgaactccgc.....caacggtacgcttcgaagg 215

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estin:\*  
4: em\_estma:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hc1:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc1:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_png:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90.2	42.0	3772	29	AY404476 Pan trogl
2	90.2	42.0	3772	29	AY404476 Homo sapi
3	46.4	21.6	4556	29	AY404477 Mus muscu
4	36.6	17.0	625	14	CA682659 wilm96.pko

C	5	36.4	16.9	931	29	CG117098	CG117098	PUPK0577B
C	7	35.8	16.9	948	29	CG117099	CG117099	PUPK0577D
C	6	35.8	16.7	866	29	CGN032A7	AL267352	Tetradon
C	8	35	16.3	380	14	CD200360	CD200360	MS1-01190
C	9	34.8	16.2	656	14	CB546546	AMGNNUC:N	CB546546
C	10	34.6	16.1	1103	14	CD244233	CD244233	AGENCOURT
C	11	34	15.8	481	13	BX507474	BX507474	DKFZP6860
C	12	34	15.8	531	9	AL700928	AL700928	DKFZP6860
C	13	34	15.8	569	13	CA126046	CA126046	SCRUR104
C	14	34	15.8	785	14	CD559574	CD559574	AGENCOURT
C	15	34	15.8	1837	29	AY411807	AY411807	Homo sapi
C	16	33.8	15.7	775	29	CC492373	CC492373	CH240_326
C	17	33.8	15.7	930	14	CK283422	CK283422	EST746144
C	18	33.6	15.6	551	10	BF041187	BF041187	BP250018B
C	19	33.6	15.6	554	28	AQ799654	AQ799654	HS_5270_A
C	20	33.6	15.6	579	28	BZ689367	BZ689367	PUBMH48TD
C	21	33.6	15.6	682	13	BM002597	BM002597	BM002597
C	22	33.6	15.6	754	14	CD559573	CD559573	AGENCOURT
C	23	33.6	15.6	778	14	CK130270	CK130270	AGENCOURT
C	24	33.6	15.6	779	14	CD109900	CD109900	AGENCOURT
C	25	33.6	15.6	801	14	CB960104	CB960104	AGENCOURT
C	26	33.6	15.6	821	14	CB988529	CB988529	AGENCOURT
C	27	33.6	15.6	1837	29	AY411808	AY411808	Pan trogl
C	28	33.4	15.5	473	9	AL712119	AL712119	DKFZP6860
C	29	33.4	15.5	942	29	CG043377	CG043377	PUPFW119TB
C	30	33.2	15.4	673	14	CF980598	CF980598	rs06003.Y
C	31	33.2	15.4	702	14	CF980526	CF980526	rs06007.Y
C	32	33.2	15.4	885	10	BF525356	BF525356	602069433
C	33	33.2	15.4	926	12	BG919167	BG919167	602817885
C	34	33	15.3	443	13	BY656623	BY656623	BY656623
C	35	33	15.3	506	28	AO235960	AO235960	HS_2056_A
C	36	33	15.3	840	28	BZ212482	BZ212482	CH230-475
C	37	32.8	15.3	468	14	CA466027	CA466027	AGENCOURT
C	38	32.6	15.2	410	9	AV667945	AV667945	AV667945
C	39	32.6	15.2	873	29	CNS02EDY	AL193615	Tetradon
C	40	32.4	15.1	1151	28	CC306586	CC306586	TAM32-168
C	41	32.2	15.0	539	10	BE696448	BE696448	MR1-CT039
C	42	32.2	15.0	562	28	AZ841422	AZ841422	2M0139P23
C	43	32.2	15.0	577	10	BF638051	BF638051	NP040407P
C	44	32.2	15.0	661	28	AZ722695	AZ722695	RP01-24-6
C	45	32.2	15.0	689	12	BI281265	BI281265	UI-R-DA0-

## ALIGNMENTS

RESULT 1	AY404476	3772 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY404476				
DEFINITION	Pan troglodytes SCN11A gene, VIRUTAL TRANSCRIPT, partial sequence,				
ACCESSION	AY404476				
VERSION	AY404476.1	GI:39760453			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.				
REFERENCE	1 (bases 1 to 3772)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Ferrreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 3772)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferrreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..3772

gene /organism="Pan troglodytes" /mol\_type="genomic DNA" /db\_xref="taxon:9598" <1..>3772 /gene="SCN11A" /locus\_tag="HCM1903"

ORIGIN

Query Match 42.0%; Score 90.2; DB 29; Length 3772;  
Best Local Similarity 96.8%; Pred. No. 2.5e-17;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 81 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 140  
DB 2681 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 2740

QY 141 TTGATGTTACCTGAGATGGTTCCCAAGAAAA 175  
DB 2741 TTGATGTTACCTGAGATGGTTCCCAAGAAAA 2775

RESULT 2  
AY0404475 4614 bp DNA linear GSS 16-DEC-2003  
LOCUS Homo sapiens SCN11A gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY0404475  
VERSION AY0404475.1 GI:39760452  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 4614)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
Location/Qualifiers  
1..4614  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>4614  
/gene="SCN11A"  
/locus\_tag="HCM1903"

ORIGIN

Query Match 42.0%; Score 90.2; DB 29; Length 4614;  
Best Local Similarity 96.8%; Pred. No. 2.6e-17;  
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 81 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 140

DB 2681 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 2740

QY 141 TTGATGTTACCTGAGATGGTTCCCAAGAAAA 175  
DB 2741 TTGATGTTACCTGAGATGGTTCCCAAGAAAA 2775

RESULT 3  
AY0404477 4556 bp DNA linear GSS 16-DEC-2003  
LOCUS Mus musculus SCN11A gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY0404477  
VERSION AY0404477.1 GI:39760454  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 4556)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
Location/Qualifiers  
1..4556  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>4556  
/gene="SCN11A"  
/locus\_tag="HCM1903"

ORIGIN

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Best Local Similarity 61.7%; Pred. No. 0.0016;  
Matches 74; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 81 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 140  
DB 2681 AGAAGTCGATGTTACCGATATACATGAGAAATGAGCAACATGATCTTCAGATGGCT 2740

QY 141 TTGATGTTACCTGAGATGGTTCCCAAGAAAAATTTCCAGCATTTTCTTACCAACG 200  
DB 2692 TTGATGTTACCTGAGATGGTTCCCAAGAAAAATTTCCAGCATTTTCTTACCAACG 2751

RESULT 4  
CA682659 625 bp mRNA linear EST 24-NOV-2002  
LOCUS wlm96-pk0005.e10 wlm96 Triticum aestivum cDNA clone  
DEFINITION wlm96-pk0005.e10 5' end, mRNA sequence.  
ACCESSION CA682659  
VERSION CA682659.1 GI:25268432  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 625)  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
/clone\_lib="ZM0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cor selected genomic DNA library"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Scott V. Tingey  
Crop Genetics  
E. I. Dupont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.  
Location/Qualifiers  
1..625  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Stephens"  
/db\_xref="taxon:4565"  
/clone="wim96.pk0005.e10"  
/cissue\_type="leaf"  
/clone\_lib="wim96"  
/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:  
XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after  
inoculation w/ E. graminis"

ORIGIN  
Query Match 17.0%; Score 36.6; DB 14; Length 625;  
Best Local Similarity 54.3%; Pred. No. 1.3;  
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 59 CCTTCCTTTGTTGATGTCAGAGCTGATGTTACCACTATACATCAGATGATG 118  
119 ACCATTGATCTTCAGATGCTTGGATGCTTACCTGATGATGTTCCCAAGAAA 174  
533 ACCATTGTTGTTGCGAGATTTTGATTTGATTTGATGTTGTTGCGAAGCTATA 478

RESULT 5  
CG117098 931 bp DNA linear GSS 20-AUG-2003  
LOCUS  
DEFINITION  
PUFK057TB ZM 0.6.1.0\_KB Zea mays genomic clone ZMMBtra0672117,  
genomic survey sequence.  
CG117098  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 931)  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
/clone\_lib="ZM0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cor selected genomic DNA library"

TITLE  
JOURNAL  
COMMENT  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..931  
/organism="Zea mays"

FEATURES  
SOURCE

/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBtra0672117"  
/clone\_lib="ZM 0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cor selected genomic DNA library"

ORIGIN  
Query Match 16.9%; Score 36.4; DB 29; Length 931;  
Best Local Similarity 53.5%; Pred. No. 1.6;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 61 TTCCCTTTGTTGATGTCAGAGCTGATGTTACCACTATACAGATGATGAC 120  
747 TTCAATGATTTTATAGTGCGAGAACTATCTCATACAGAGCTGTGTATCTTAAG 688  
QY 121 CATGATCTTCAGAGATGCTTGGATGTTACCTGATGATGTTCCCAAGAAAATTTC 180  
DB 687 TATTGACATTCAGCTGACCTGCTCATGAGATGATGATGATGTTCCCGCCAAAATTCT 628  
QY 181 AGCATTGTTTCGTACCAACCGT 202  
DB 627 AACCTGTTCTTAATAAATGCT 606

RESULT 6  
CG117099 948 bp DNA linear GSS 20-AUG-2003  
LOCUS  
DEFINITION  
PUFK057TB ZM 0.6.1.0\_KB Zea mays genomic clone ZMMBtra0672117,  
genomic survey sequence.  
CG117099  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 948)  
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/db\_xref="taxon:4577"  
/clone\_lib="ZM0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cor selected genomic DNA library"

TITLE  
JOURNAL  
COMMENT  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..948  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZM0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cor selected genomic DNA library"

ORIGIN  
Query Match 16.9%; Score 36.4; DB 29; Length 948;  
Best Local Similarity 53.5%; Pred. No. 1.6;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 61 TTCCCTTTGTTGATGTCAGAGCTGATGTTACCACTATACAGATGATGAC 120  
DB 327 TTCAATGATTTTATAGTGCGAGAACTATCTCATACAGAGCTGTGTATCTTAAG 366

QY 121 CATTGATCTTCAGATGCGCTTGGATGCTTACCTGAGATGCTTCCCAAGAAATTTCC 180  
 DB 387 TATTGACATTCAGCTGAACTGCTGATGAGATGATGATGTTGTCGCCCAAAATTTCT 446  
 QY 181 AGCATTTTTCGTACCAACGCT 202  
 DB 447 AACACTGTGCTTAAATAATGCT 468

## RESULT 7

CNS032A7/c 866 bp DNA linear GSS 01-SEP-2000  
 LOCUS Tetradon nigroviridis genome survey, sequence PUC-Ort end of clone  
 DEFINITION 070G05 of library G from Tetradon nigroviridis, genomic survey  
 sequence.  
 ACCESSION AL267352.1 GI:7989156  
 VERSION AL267352  
 KEYWORDS GSS, genome survey sequence.  
 SOURCE Tetradon nigroviridis  
 ORGANISM Tetradon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei;  
 Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Tetraodon.

## REFERENCE

## AUTHORS

1 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,  
 Saurin, W. and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis  
 using Tetradon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)

## TITLE

JOURNAL 20296633  
 MEDLINE 10835645  
 PUBMED 2

## REFERENCE

## AUTHORS

2 Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,  
 Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
 Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the  
 freshwater pufferfish Tetradon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)

## TITLE

JOURNAL 20359837  
 MEDLINE 10899143  
 PUBMED 3

## REFERENCE

## AUTHORS

## JOURNAL

3 (bases 1 to 866)  
 Genoscope.  
 Direct Submision  
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 This sequence is a single read and was generated as part of a large  
 scale clone-end sequencing project of the Tetradon nigroviridis  
 genome. For more information, please take a look at  
 http://www.genoscope.cns.fr/Tetradon.

## FEATURES

## source

1..866  
 /organism="Tetradon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="070G05"  
 /clone\_1lb="G"  
 /note="Genoscope sequence ID : COB8070AD03SPL-end :  
 PUC-Ort"

## ORIGIN

Query Match 16.7%; Score 35.8; DB 29; Length 866;  
 Best Local Similarity 48.5%; Pred. No. 2.5;  
 Matches 82; Conservative 5; Mismatches 82; Indels 0; Gaps 0;

QY 8 TGAAGAACTCCGACTACTATGCTGAAGAAGCTTGAAGAAAGCAACCCCTTCCTT 67  
 DB 812 TAAATATTCMGACATCATCGTTGCTTTGTTTATTTGACACGCTGGCATKTTAT 753

QY 68 TGTTCGATGTGAGAAAGTCTGATGTTACAGTATCTATCAGAAAGTATGACCATTTGAT 127

DB 752 TTTTTCATGACGATGATAGAAAAGTTMACATCTGATCCATTTGACCTGTTTCTT 693  
 QY 128 CTCGAGATGCTTTGGATGCTTACCTGAGATGCTTCCCAAGAAAT 176  
 DB 692 CTCGAGATGCTTGGCGCGCTGMAACATCTGCTTACCAATTAAGT 644

## RESULT 8

CD200360/c 380 bp mRNA linear EST 14-SEP-2003  
 LOCUS MS1-01190-D304-C03.U.B MS1-0119 Schistosoma mansoni cDNA clone  
 DEFINITION MS1-01190-D304-C03.B, mRNA sequence.  
 ACCESSION CD200360  
 VERSION CD200360  
 KEYWORDS EST.  
 SOURCE Schistosoma mansoni  
 ORGANISM Schistosoma mansoni  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.

## REFERENCE

## AUTHORS

1 (bases 1 to 380)  
 Verjovski-Almeida, S., Demarco, R., Martins, E.A.L., Guimaraes, P.E.M.,  
 Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,  
 Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,  
 Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,  
 Leite, R.A., Malaguar, L.C.C., Marques, R.C.P., Miyasato, P.A.,  
 Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,  
 Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,  
 Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,  
 Seubal, J.C., Leite, L.C.C. and Dias-Neto, E.  
 Transcriptome analysis of the acelomate human parasite Schistosoma  
 mansoni  
 Nat. Genet. 35 (2), 148-157 (2003)

## TITLE

JOURNAL 22879926  
 MEDLINE Contact: Dr. Sergio Verjovski-Almeida  
 COMMENT Departamento de Biogenetica - Universidade de Sao Paulo  
 Instituto de Quimica - Universidade de Quimica - 1200, 05508-900 Sao Paulo - SP,  
 Brasil

Tel: +55-11-3091-2173  
 Fax: +55-11-3091-2186  
 Email: verjovsk@usp.br  
 This sequence was derived from the FAPESP Schistosoma mansoni EST  
 Genome Project. All sequences in the project were assembled and  
 annotated. This entry and all the assembled sequences can be seen  
 in the following URL http://bioinfo.iq.usp.br/schisto/  
 Plate: MS1-01190-D304 row: 3 column: C.

## FEATURES

## source

1..380  
 Location/Qualifiers  
 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
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 /clone="MS1-01190-D304-C03.B"  
 /sex="mixed pool"  
 /dev\_stage="schistosomulum"  
 /lab\_host="in vitro culture"  
 /clone\_1lb="MS1-0119"  
 /note="Vector: pGEM T-easy"

## ORIGIN

Query Match 16.3%; Score 35; DB 14; Length 380;  
 Best Local Similarity 54.2%; Pred. No. 3.8;  
 Matches 71; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 73 TGAATGAGAAAGTGTATGATGTTACAGTATCTATCAGATGATGACCATTTGATCTTA 132  
 DB 176 TGAATTAAGAGTTTGAATCGGCTGCTAGATTCGAGAAAGTCGGCGATGGTTTGA 117

QY 133 GGAATGCTTGGATGCTTACCTGAGATGCTTCCCAAGAAATTTCCAGCATTTTGG 192  
 DB 116 ACATGAGATCGAAAATTAAGTATGATGATTAACGAGAGAAATCTGAAGTAACT 57

QY 193 TACCAACGGTT 203

Db 56 CAATTAAGCTT 46

RESULT 9  
LOCUS CBS46546/c  
DEFINITION ANGNNTC:RHVS-00295-C5-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhys-00295-c5 5', mRNA sequence.

ACCESSION CBS46546  
VERSION CBS46546.1 GI:29430487  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 656)  
Angen EST Program.  
Angen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Angen, Inc  
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00295 row: C column: 5.  
Location/Qualifiers  
1. 656  
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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypothalamus adult female Wistar rat avg. insert size 2.3 kb fraction 6 and 7"

ORIGIN

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Best Local Similarity 65.4%; Pred. No. 4.9;  
Matches 51; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 118 CACATTGATCTTGAGTGGCTTTGATGCTGACGATGGTCCCAAGAAAT 177  
Db 281 CTCCTATTGCTCATATGCTTGGTGGCTGGCGGTGAGGGTTTCCAGACACT 222

Qy 178 TCCAGCATTTTTCGTAC 195  
Db 221 TCCAGCTCTCTCTCAC 204

RESULT 10  
LOCUS CD244233  
DEFINITION BGENCOURT 14097420 NIH\_MGC\_180 Homo sapiens cDNA clone IMAGE:30378187 5', mRNA sequence.

ACCESSION CD244233  
VERSION CD244233.1 GI:31004697  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1103)  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-rc@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

FEATURES  
source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: ND443 row: 3 column: 20  
High quality sequence start: 73  
High quality sequence stop: 505.  
Location/Qualifiers  
1. 1103  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:30378187"  
/lab host="DH10B-Ton A (T1 and T5 phage resistances)"  
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC library."

ORIGIN

Query Match 16.1%; Score 34.6; DB 14; Length 1103;  
Best Local Similarity 53.8%; Pred. No. 6.2;  
Matches 70; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 57 CCCCTTCCTTTTGTCTGATGTCAGAGTCTGATGTTACCTGAGATGTTCCCAAGAAAT 116  
Db 732 CCTTAATTTTATTTTGTGAGGGCCCAATTAACCTTCCAGACCTTATTTTATGTC 791

Qy 117 GCACCATGATCTTCAGATGCTTGGATGCTTACCTGAGATGTTCCCAAGAAAT 176  
Db 792 GTAAATGGCCCTTGGAAAGAAAGATGCTCTCCAAATGCTTCCCAACAGAT 851

Qy 177 TTCACGCGAT 186  
Db 852 TTTTCTCTAT 861

RESULT 11  
LOCUS BX507474/c  
DEFINITION DKFZ686022259\_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone DKFZ686022259 5', mRNA sequence.

ACCESSION BX507474  
VERSION BX507474.1 GI:32040151  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 481)  
Biocker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Oanger, A., Pobo, G., Han, M., and Wiemann, S.  
EST (Biocker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by GBR (National Research Centre for Biotechnology of the Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFZ686022259) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1. 481  
/organism="Homo sapiens"  
/mol\_type="mRNA"

FEATURES  
source



RESULT 14  
LOCUS CD559574/c  
DEFINITION AGNCOURT 14496977 NIH MGC 195 Homo sapiens cDNA clone  
IMAGE:6971723 5', mRNA sequence.  
ACCESSION CD559574  
VERSION CD559574.2 GI:38559021  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 785)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585642.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: IRBK1 row: C column: 10  
High quality sequence stop: 717.  
Location/Qualifiers  
1..785  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="6971723"  
/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxp sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
a Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 15.8%; Score 34; DB 14; Length 785;  
Best Local Similarity 63.4%; Pred. No. 9; Mismatches 30; Indels 0; Gaps 0;  
Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 116 AGCACATTGATCTTCAGATGCTTTGGATGCTTACCTGAGATGTTCCCAAGAAAA 175  
DB 223 ATCTCCATTGATGCTCATCGCTTTGGTGCCTGCACTGAGAGGGTTTCCAGAGAGA 164  
QY 176 TTTCAGGCGATTTTTCGTACCA 197  
DB 163 TTTCAGGCGCTCATCTCCTCACTA 142

RESULT 15

AY411807/c  
LOCUS AY411807 1837 bp DNA linear GSS 12-DEC-2003  
DEFINITION Homo sapiens HCM4347 gene, VIRTUAL TRANSCRIPT, partial sequence.  
ACCESSION AY411807  
VERSION AY411807.1 GI:39767772  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1837)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D., and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652): 1960-1963 (2003)  
14671302  
JOURNAL PUBMED  
2 (bases 1 to 1837)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D., and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..1837  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>1837  
/locus\_tag="HCM4347"

ORIGIN  
Query Match 15.8%; Score 34; DB 29; Length 1837;  
Best Local Similarity 63.4%; Pred. No. 11; Mismatches 30; Indels 0; Gaps 0;  
Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 116 AGCACATTGATCTTCAGATGCTTTGGATGCTTACCTGAGATGTTCCCAAGAAAA 175  
DB 142 ATCTCCATTGATGCTCATCGCTTTGGTGCCTGCACTGAGAGGGTTTCCAGAGAGA 83  
QY 176 TTTCAGGCGATTTTTCGTACCA 197  
DB 82 TTTCAGGCGCTCATCTCCTCACTA 61

Search completed: March 22, 2004, 23:12:20  
Job time : 1277.46 secs

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 1840.35 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-12

Sequence: 1 ttgaatccgaatcctaac.....gagctcagcgaaggaattc 346

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_ov: *
22: em_or: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_hugo_hum: *
40: em_hugo_mus: *
41: em_hugo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	100.0	346	AX017228	AX017228 Sequence
2	346	100.0	346	BD138450	BD138450 Mammalian
3	255.2	73.8	167476	AC116038	AC116038 Homo sapi
4	53	15.3	241289	AC124662	AC124662 Mus muscu
5	46.8	13.5	856	E36123	E36123 Nucleic aci
6	46.8	13.5	3701	AR340648	AR340648 Sequence
7	46.8	13.5	3701	BD217793	BD217793 Regulatio
8	46.8	13.5	5419	HS417790	HS417790 Homo sapi
9	46.8	13.5	5728	BD012083	BD012083 Human sod
10	46.8	13.5	5728	BD082952	BD082952 Human sod
11	46.8	13.5	5728	AF150882	AF150882 Homo sapi
12	46.8	13.5	5860	AR340678	AR340678 Sequence
13	46.8	13.5	6237	AF188679	AF188679 Homo sapi
14	46.8	13.5	6528	BD012082	BD012082 Human sod
15	46.8	13.5	6528	BD082951	BD082951 Human sod
16	46.8	13.5	6528	AF109737	AF109737 Homo sapi
17	40.6	11.7	240544	AC108563	AC108563 Rattus no
18	40.6	11.7	253985	AC097242	AC097242 Rattus no
19	40	11.6	210800	AC127824	AC127824 Rattus no
20	38.2	11.0	139063	AC133563	AC133563 Homo sapi
21	37.6	10.9	168197	AC140520	AC140520 Homo sapi
22	37.4	10.8	104492	AC023358	AC023358 Homo sapi
23	37.4	10.8	184864	AC018927	AC018927 Homo sapi
24	37.2	10.8	164786	AL161423	AL161423 Human DNA
25	36.8	10.6	71821	AC010151	AC010151 Homo sapi
26	36.8	10.6	71821	AC036135	AC036135 Homo sapi
27	36.8	10.6	71821	AC036135	AC036135 Rattus no
28	36.8	10.6	71821	AC036135	AC036135 Rattus no
29	36.6	10.6	1785	MSU18238	MSU18238 Medicago sa
30	36.6	10.6	110000	AC115281_0	AC115281 Rattus no
31	36.6	10.6	110000	AC141403_1	AC141403 Rattus no
32	36.4	10.5	141331	AC009396	AC009396 Homo sapi
33	36.4	10.5	141331	AC009396	AC009396 Mouse DNA
34	36.4	10.5	164427	AC140859	AC140859 Homo sapi
35	36.4	10.5	185637	AC145547	AC145547 Homo sapi
36	36.4	10.5	185637	AC145547	AC145547 Homo sapi
37	36.4	10.5	185737	AC145616	AC145616 Homo sapi
38	36.4	10.5	207381	BX571731	BX571731 Danio rer
39	36.4	10.5	229785	AC144777	AC144777 Mus muscu
40	36.2	10.5	28331	AL139816	AL139816 Human DNA
41	36.2	10.5	143290	AC121964	AC121964 Mus muscu
42	36.2	10.5	177915	AC137451	AC137451 Rattus no
43	36.2	10.5	185138	AC135633	AC135633 Mus muscu
44	36.2	10.5	224686	AC110974	AC110974 Rattus no
45	36.2	10.5	250876	AC097179	AC097179 Rattus no

## ALIGNMENTS

RESULT 1  
LOCUS AX017228  
DEFINITION Sequence 12 from Patent WO9947670.  
ACCESSION AX017228  
VERSION AX017228.1 GI:10042148  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Tate, S.N., Grose, D.T. and Hick, C.A.  
Mammalian sodium channel proteins  
Patent: WO 9947670-A 12 25-SEP-1999;  
JOURNAL

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS (GB) ; HICK CAROLINE ANNE (GB)

## FEATURES

Location/Qualifiers  
1..346  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 346; DB 6; Length 346;  
Best Local Similarity 100.0%; Pred. No. 6,7e-96;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGAAATTCGGAAATCTAACCGCTGACGAGAAATCCGGAATCTTAATTAATGAAT 60  
1 TTAGAAATTCGGAAATCTAACCGCTGACGAGAAATCCGGAATCTTAATTAATGAAT 60  
61 AGAACCTTCGGATCTACGAGCACTGAGGCTCTGTCGCTGTCCAGTTTGAAGAA 120  
61 AGAACCTTCGGATCTACGAGCACTGAGGCTCTGTCGCTGTCCAGTTTGAAGAA 120  
121 GAAGGTACATCTCGAGAAAGATGGGTAGAGTTCAATTACAGAGAAAGTGAAAGAC 180  
121 GAAGGTACATCTCGAGAAAGATGGGTAGAGTTCAATTACAGAGAAAGTGAAAGAC 180  
181 CAACAGTTCTTTTGGGCTGAGATTCTTAATTTGCCAAGCTTTTCTGGGTTACTTAC 240  
181 CAACAGTTCTTTTGGGCTGAGATTCTTAATTTGCCAAGCTTTTCTGGGTTACTTAC 240  
241 CAGCTGCGCCAGTCTTGAATTTGAGGGGTAGAGAAAGCTTAAGATATACCTTCTAC 300  
241 CAGCTGCGCCAGTCTTGAATTTGAGGGGTAGAGAAAGCTTAAGATATACCTTCTAC 300  
301 CTAAGAGCTTCTGTGACAGCCAGATGAGCTGTAGCGAAGAAATTC 346  
301 CTAAGAGCTTCTGTGACAGCCAGATGAGCTGTAGCGAAGAAATTC 346

## RESULT 2

BD138450 1346 bp DNA linear PAT 18-SEP-2002  
LOCUS Mammalian sodium channel protein.  
DEFINITION BD138450.1 GI:23233395  
ACCESSION BD138450.1 GI:23233395  
VERSION JP 2002508941-A/11.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 346)  
Grose, D.T., Hick, C.A. and Tate, S.N.  
Mammalian sodium channel protein  
Patent: JP 2002508941-A 11 26-MAR-2002;  
GLAXO GROUP LTD

## COMMENT

OS Homo sapiens (human)  
PN JP 2002508941-A/11  
PD 26-MAR-2002 JP 2000536653  
PR 18-MAR-1999 JP 2000536653  
PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N1/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
C12N1/15,

PC C12N1/19, C12N1/21, C12N5/10, C1201/02, G01N33/15, G01N33/50, G01N33/ 68,  
C12N15/00, C12N5/00

CC Mammalian sodium channel protein  
FH Key Location/Qualifiers  
FT source 1..346  
/organism="Homo sapiens (human)"

## FEATURES

Location/Qualifiers  
1..346  
/organism="Homo sapiens"

/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 346; DB 6; Length 346;  
Best Local Similarity 100.0%; Pred. No. 6,7e-96;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGAAATTCGGAAATCTAACCGCTGACGAGAAATCCGGAATCTTAATTAATGAAT 60  
1 TTAGAAATTCGGAAATCTAACCGCTGACGAGAAATCCGGAATCTTAATTAATGAAT 60  
61 AGAACCTTCGGATCTACGAGCACTGAGGCTCTGTCGCTGTCCAGTTTGAAGAA 120  
61 AGAACCTTCGGATCTACGAGCACTGAGGCTCTGTCGCTGTCCAGTTTGAAGAA 120  
121 GAAGGTACATCTCGAGAAAGATGGGTAGAGTTCAATTACAGAGAAAGTGAAAGAC 180  
121 GAAGGTACATCTCGAGAAAGATGGGTAGAGTTCAATTACAGAGAAAGTGAAAGAC 180  
181 CAACAGTTCTTTTGGGCTGAGATTCTTAATTTGCCAAGCTTTTCTGGGTTACTTAC 240  
181 CAACAGTTCTTTTGGGCTGAGATTCTTAATTTGCCAAGCTTTTCTGGGTTACTTAC 240  
241 CAGCTGCGCCAGTCTTGAATTTGAGGGGTAGAGAAAGCTTAAGATATACCTTCTAC 300  
241 CAGCTGCGCCAGTCTTGAATTTGAGGGGTAGAGAAAGCTTAAGATATACCTTCTAC 300  
301 CTAAGAGCTTCTGTGACAGCCAGATGAGCTGTAGCGAAGAAATTC 346  
301 CTAAGAGCTTCTGTGACAGCCAGATGAGCTGTAGCGAAGAAATTC 346

## RESULT 3

AC116038 167476 bp DNA linear PRI 07-OCT-2003  
LOCUS Homo sapiens chromosome 3 clone RP11-134J21, complete sequence.  
DEFINITION AC116038  
ACCESSION AC116038  
VERSION HTG.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
Haugen, E.D.  
Direct Submission  
Unpublished

## TITLE

2 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.  
Direct Submission

Submitted (23-MAR-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA

## REFERENCE

3 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.  
and Haugen, E.D.  
Direct Submission

Submitted (28-JUN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA

## REFERENCE

## AUTHORS

4 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
Haugen, E.D.  
Direct Submission

Submitted (07-OCT-2003) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA

On Oct 7, 2003 this sequence version replaced gi:21622736.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC



Web site: <http://www.genome.washington.edu>  
 Contact: [uwgchgs@u.washington.edu](mailto:uwgchgs@u.washington.edu)  
 Project Information

Center Project name: chr-3  
 Center Clone name: Rp11-134U21 (bc0780)

#### Summary Statistics

Sequencing vector: plasmid; 100% of reads  
 Chemistry: Dye-terminator ET; 4% of reads  
 Chemistry: Dye-terminator Big Dye; 5% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 167467 bases at least Q40  
 Consensus quality: 167476 bases at least Q30  
 Consensus quality: 167476 bases at least Q20  
 Insert size: 167476; sum-of-contigs  
 Quality coverage: 18.9x in Q20 bases; sum-of-contigs

#### Overlapping Sequences:

5' : Rp11-114A3 AC137625, 2001-bp overlap  
 3' : Rp11-182A24 (UMC:bc0782) AC123903, 41341-bp overlap

#### Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

#### Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FgfrPrint	SeqDerMap	FgfrPrint	SeqDerMap	FgfrPrint
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6	<800	6382	6514	2067	2008
2248	2299	512	<800	5097	5007
9345	9792	449	<800	2317	2259
2016	2003	2707	2741	2813	2744
4889	4771	4809	4878	2537	2550
3455	3447	184	<800	1923	2008
245	<800	5818	5899	2486	2550
72	<800	1364	1346	4036	3992
4175	4167	999	990	2583	2550

72	<800	3014	3028	8136	8039
6640	6560	4721	4667	2738	2744
4710	4771	727	745	4704	4629
3468	3447	179	<800	2649	2744
687	<800	7123	7158	2550	2550
3049	3091	2078	2040	5020	4862
762	<800	1891	1888	6949	6960
553	<800	8072	8171	4636	4629
5080	5088	92	<800	3588	3544
6613	6560	3674	3639	604	<800
8963	9211	5478	5397	5748	6106
331	<800	240	<800	953	943
2328	2299	5050	4878	4728	4629
2038	2003	1053	1068	178	<800
712	<800	3231	3264	1222	1220
1368	1370	86	<800	694	<800
182	<800	5444	5397	3022	3007
1620	1560	1265	1228	4079	3992
775	<800	438	<800	1294	1220
2583	2686	1436	1408	2044	2008
2709	2686	5528	5397	3725	3544
19834	19753	475	<800	790	<800
8729	8629	2310	2371	4232	4223
2264	2299	5177	5089	396	<800
651	<800	391	<800	4714	4629
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6166	6159	3594	3639	14	<800
500	<800	1172	1188	4240	4223
8764	8629	316	<800	879	917
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3711	3718	324	<800	1198	1220
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560	<800	4463	4430	344	<800
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Query Match	73.8%	Score 255.2	DB 9	Length 167476
Best Local Similarity	96.3%	Pred. No. 1e-67		
Matches 283	Conservative 0	Mismatches 8	Indels 3	Gaps 2
QY	46	TAACCTTAATGGAAT--AGAACCTTCGGATTACGAGCAGTGGCTC-TCGTCGCT	102	
DB	106172	TAACCTTAATGGAATGAGTCCCTCCGACCTCTACGAGCAGTGGCTCCTTCGTCGCT	106113	
QY	103	GTCCAGTTTGAAGGAGTGAAGTCAATTCGACAGAGTGGTGAAGTTCAGTTTAC	162	
DB	106112	GTCCAGTTTGAAGGAGTGAAGTCAATTCGACAGAGTGGTGAAGTTCAGTTTAC	106053	
QY	163	AGAGAAAGTGAAGAGACCAACAGTCTTTTGGCTGAGATTTCTTAATTGCAAGC	222	
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QY	223	TTTTCTGCTTACTTACCAAGCTTCCGACGCTTGAATTTGAGGGGTGAAGAAAGC	282	
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RESULT 4				
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LOCUS				HTG 22-NOV-2003
DEFINITION				Mus musculus chromosome 9 clone RP24-409K22 map 9, *** SEQUENCING
ACCESSION				AC124662
VERSION				AC124662.5 GI:38490569
KEYWORDS				HTG; HTGS PHASE1; HTGS_FULUTOP; HTGS_ACTIVEFIN.
SOURCE				Mus musculus (house mouse)
ORGANISM				Mus musculus
REFERENCE				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS				1 (bases 1 to 241289)
JOURNAL				Mus musculus chromosome 9, clone RP24-409K22
AUTHORS				Unpublished
2 (bases 1 to 241289)				
Bitren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,				
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,				
Bouhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,				
Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,				
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dudge, S.,				
Faro, S., Fetzler, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,				
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,				
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,				
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K.,				
Lamaze, R., Lander, T., Lehotzky, J., Levine, R., Lindblad-Toh, K.,				
Liu, G., Maclean, C., Macdonald, P., Major, J., Margis, N.,				
Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Melitini, J.,				
Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,				
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,				

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
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 Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,  
 Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Strauss, N., Sudramanah, A., Talama, J., Testaye, S.,  
 Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
 Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 241289)  
 Bitren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,  
 Diaz, V.S., Dudge, S., Doolley, K., Dorris, L., Erickson, J., Faro, S.,  
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,  
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Lander, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Liu, X., Mabbitt, R., Maclean, C.,  
 Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M.,  
 Melitini, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,  
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,  
 O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Talama, J., Travers, M.,  
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 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (22-NOV-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 22, 2003 this sequence version replaced gi:38153914.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence.submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L26677  
 Center clone name: 409\_K\_22  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 56842: contig of 56842 bp in length  
 \* 56843 56842: gap of 100 bp  
 \* 56943 56946: contig of 39024 bp in length  
 \* 95967 96066: gap of 100 bp  
 \* 96067 133016: contig of 36950 bp in length  
 \* 133017 133116: gap of 100 bp  
 \* 133117 138788: contig of 5672 bp in length  
 \* 138789 138888: gap of 100 bp  
 \* 138889 157002: contig of 18114 bp in length  
 \* 157003 157102: gap of 100 bp  
 \* 157103 162695: contig of 5593 bp in length  
 \* 162696 162795: gap of 100 bp  
 \* 162796 165266: contig of 2471 bp in length  
 \* 165267 165366: gap of 100 bp  
 \* 165367 187706: contig of 22340 bp in length  
 \* 187707 210027: gap of 100 bp  
 \* 210027: contig of 22221 bp in length

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QY	103	GTCCCACTTTGAAGAAATGAAGGT	126										
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LOCUS	AR340648												
DEFINITION	AR340648												
ACCESSION	AR340648.1	GI:33732380											
VERSION													
KEYWORDS													
SOURCE	Unknown.												
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REFERENCE	Unclassified.												
AUTHORS	1 (bases 1 to 3701)												
TITLE	Db-Hajj,S. and Waxman,S.G.												
JOURNAL	Nucleic acid encoding sodium channels in dorsal root ganglia												
FEATURES	Patent: US 6573067-A 6 03-JUN-2003;												
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Db	2877	GTCCCACTTTGAAGAAATGAAGGT	2900										
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LOCUS	BD217793												
DEFINITION	BD217793												
ACCESSION	BD217793.1	GI:33027563											
VERSION													
KEYWORDS	JP 2002509860-A/3.												
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ORGANISM	Homio sapiens (human)												
REFERENCE	1 (bases 1 to 3701)												
AUTHORS	Hajj,S.D. and Waxman,S.												
TITLE	Regulation of sodium channel in posterior root ganglion												
JOURNAL	Patent: JP 2002509860-A 3 02-APR-2002;												
	VALE UNIVERSITY												
COMMENT	OS Homio sapiens (human)												
	PN JP 2002509860-A/3												
	PD 02-APR-2002												
	PF 29-JAN-1999 JP 2000529355												
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	SULAVANAN DIB HAJJ STEPHEN WAXMAN												
	PC C07K14/435,A61K38/00,A61K39/395,A61K45/00,A61P25/04,A61P43/00,												
	PC C07K16/18,												
	PC C12N5/10,C12N15/09,C12P21/02,G01N33/566,G01N33/84,A61K37/02,												
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	Key												
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Best Local Similarity 88.1%; Pred. No. 0.0032; Mismatches 7; Indels 3; Gaps 2;  
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Qy 46 TAACCTAATGGAAT--AGAACCTTCCGATCTACAGACCTGAGCCTC-TCTGCGCT 102  
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Qy 103 GTCCAGTTTGAAGATGAGGT 126  
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RESULT 8  
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LOCUS Homo sapiens mRNA for voltage-gated sodium channel (NAV1.9 gene).  
DEFINITION A417790  
ACCESSION A417790  
VERSION A417790.1 GI:22796539  
KEYWORDS NAV1.9 gene; voltage-gated sodium channel.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1 Blum, R., Kafitz, K.W. and Konnerth, A.  
TITLE Neurotrophin-evoked depolarization requires the sodium channel Na(V)1.9  
JOURNAL Nature 419 (6908), 687-693 (2002)  
MEDLINE 22272672  
PUBMED 12384689  
REFERENCE 2 (bases 1 to 5419)  
AUTHORS Blum, R.  
TITLE Direct Submision  
SUBMITTED (25-OCT-2001) Blum R., Institut fuer Physiologie,  
Ludwig-Maximilians-Universitaet, Biedersteiner Strasse 29, Geb.  
608, 80802 Muenchen, GERMANY  
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FEATURES source  
gene  
CDS

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ORIGIN

Query Match 13.5%; Score 46.8; DB 9; Length 5419;  
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Matches 74; Conservative 0;

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RESULT 9  
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LOCUS Human sodium channel SCN12a and SCN8A.  
DEFINITION BD012083  
ACCESSION BD012083  
VERSION BD012083.1 GI:22092272  
KEYWORDS WO 0190355-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 5728)  
TITLE Kanazawa, I., Goto, J. and Jeong, S. Y.  
HUMAN sodium channel SCN12a and SCN8A  
PATENT: WO 0190355-A 2 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP., ICHIRO KANAZAWA, JUN GOTO, EON  
YONG JEONG  
COMMENT OS Homo sapiens (human)  
PN WO 0190355-A/2  
PD 29-NOV-2001  
PF 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085  
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
PC C12N15/12, C07K14/47, C07K16/18  
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DEFINITION	BD082952			
ACCSSION	BD082952.1	GI:22628562		
VERSION	UP 2001327294-A/2.			
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
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ORIGIN				
Query Match	13.5%	Score 46.8;	DB 6;	Length 5728;
Beet Local Similarity	88.1%	Pred. No. 0.0032;		
Matches	74;	Conservative	0;	Mismatches 7;
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				Gaps 2;
QY	46	TAAGTAAATGAAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC--TCGTGGCT	102	
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Db	3673	GTCCAGTTGAGGAATGAGGT	3696	
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LOCUS	AF150882	Human sodium voltage-gated sodium channel alpha subunit, alternate splice variant SCN12A-s (SCN12A) mRNA, complete cds.	5728 bp	linear
DEFINITION	AF150882			
ACCSSION	AF150882			
VERSION	AF150882.1	GI:6693704		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
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ORIGIN				
Query Match	13.5%	Score 46.8;	DB 6;	Length 5728;
Beet Local Similarity	88.1%	Pred. No. 0.0032;		
Matches	74;	Conservative	0;	Mismatches 7;
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QY	46	TAAGTAAATGAAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC--TCGTGGCT	102	
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Db	3673	GTCCAGTTGAGGAATGAGGT	3696	
RESULT 11				
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DEFINITION	AF150882			
ACCSSION	AF150882			
VERSION	AF150882.1	GI:6693704		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
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Query Match	13.5%	Score 46.8;	DB 6;	Length 5728;
Beet Local Similarity	88.1%	Pred. No. 0.0032;		
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QY	46	TAAGTAAATGAAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC--TCGTGGCT	102	
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RESULT 11				
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FEATURES	source
TITLE	Hirai, M., Iwashara, K., Uchiyama, Y., and Kanazawa, I.
JOURNAL	Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A
MEDLINE	Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
PUBLISHED	20090626
REFERENCE	10623608
AUTHORS	2 (bases 1 to 5728)
	Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Maeda, M., Goto, J. and Kanazawa, I.
TITLE	Direct Submmission
JOURNAL	Submitted (12-MAY-1999) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan
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	WCRQNLPQKEVAGCGAQSODIPLVEMKRGSETQEBGLITISVPTLGVRHDT
	WLPALSEEDVDFSGEDNAQRITQEPPEQAAELHQENKPSORVQSVLEIMFSD
	EPHLTIQDPKKSVDTSIISEGSTIIDLQDFGLPEVPRKQPCRCLEPGCCPCPC
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	RTLRALPRLALSOPEGMKRVVNAVLGALPAILNLVLCILFVLPFCILGVYFSGKF
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	IYAAVDSTKEQOPEFESNLGYIVGFVPIIFSGFTPLNFIIVIIIDNFVQOQKLDGI
	ODIMEEOKKYNNAMKIGSKKPKOKRIPPLNKCQGLVDIVTSQIFDIILISLIL
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Query Match	13.5%: Score 46.8; DB 9; Length 5728;
Best Local Similarity	88.1%: Pct. No. 0.0032;
Matches	74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
QY	46 TAACTAATGAAATT-AGAACTTCGGATCTACGAGCACTGAGGCTC-TCGTGGCGT 102
DB	3613 TAACTAATGGAATTGAAGTCTCTCCGGACTCTACGAGCACTGAGGCTCTGTGGCGCT 3672
QY	103 GTCCCACTTTGAAGATGGAAGCT 126
DB	3673 GTCCCACTTTGAAGATGGAAGCT 3696
RESULT 12	
LOCUS	AR340678 5860 bp DNA linear PAT 17-AUG-2003
DEFINITION	Sequence 41 from patent US 6573067.

ACCESSION AR340678  
VERSION AR340678.1 GI:33732410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 5860)  
TITLE Dib-Hajj, S. and Waxman, S.G.  
JOURNAL Nucleic acid encoding sodium channels in dorsal root ganglia  
FEATURES  
source  
1..5860  
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ORIGIN  
Query Match 13.5%; Score 46.8; DB 6; Length 5860;  
Best Local Similarity 88.1%; Pred. No. 0.0032;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAATT-AGAACTTCGGATCTACGAGACTGAGGCGCTC-TCGTGCGCT 102  
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3444 TAACTTAATGGAATTGAAGTCTCTCCGACTCTACGAGACTGAGGCGCTCTTGCGCT 3503  
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QY 103 GTCCAGTTTGAAGATGAGGT 126  
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DB 3504 GTCCAGTTTGAAGATGAGGT 3527  
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RESULT 13  
AF188679 6237 bp mRNA linear PRI 14-DEC-1999  
LOCUS AF188679  
DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit  
(SCN11A) mRNA, complete cds.  
ACCESSION AF188679  
VERSION AF188679.1 GI:6572949  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 6237)  
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A., Wood, P.M. and  
Waxman, S.G.  
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root  
ganglion neurons  
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)  
MEDLINE 20047838  
PUBMED 10580103  
2 (bases 1 to 6237)  
REFERENCE 2 (bases 1 to 6237)  
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A. and Waxman, S.G.  
TITLE Direct Substitution  
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,  
Bldg. 34, 950 Campbell Ave., West Haven, CT 06516, USA  
location/Qualifiers  
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/note="Nan alpha subunit; TTX-R sodium channel"  
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VLISVSTWISTLENOEHIPEPPLFRVRLARIGRLRLVRAARGITLFLPAMSL  
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Best Local Similarity 88.1%; Pred. No. 0.0032;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAATT-AGAACTTCGGATCTACGAGACTGAGGCGCTC-TCGTGCGCT 102  
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DB 3444 TAACTTAATGGAATTGAAGTCTCTCCGACTCTACGAGACTGAGGCGCTCTTGCGCT 3503  
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QY 103 GTCCAGTTTGAAGATGAGGT 126  
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DB 3504 GTCCAGTTTGAAGATGAGGT 3527  
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RESULT 14  
BD012082 6528 bp DNA linear PAT 02-AUG-2002  
LOCUS BD012082  
DEFINITION Human sodium channel SCN12A and SCN8A.  
ACCESSION BD012082  
VERSION BD012082.1 GI:22092271  
KEYWORDS WO 0190355-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 6528)  
AUTHORS Kanazawa, I., Goto, J. and Jeong, S.Y.  
TITLE Human sodium channel SCN12A and SCN8A  
JOURNAL Patent: WO 0190355-A 1 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON  
YONG JEONG

## COMMENT

OS Homo sapiens (human)  
PN WO 0190355-A/1  
PD 29-NOV-2001  
PR 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085  
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
PC C12N15/12, C07K14/47, C07K16/18  
CC

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/db\_xref="taxon:9606"

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Query Match 13.5%; Score 46.8; DB 6; Length 6528;  
Best Local Similarity 88.1%; Pred. No. 0.0032;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 46 TAACTTAATGGAATT--AGAACTTCCGATCTACGACACTGAGGCTC-TCGTGGCT 102  
Db 3613 TAACTTAATGGAATTGAAGTCTCCGACTCTACGACACTGAGGCTCTTCGTGGCT 3672  
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Qy 103 GTCCCACTTTGAAGGAATGAAGT 126  
Db 3673 GTCCCACTTTGAAGGAATGAAGT 3696  
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RESULT 15  
BD082951 6528 bp DNA linear PAT 27-AUG-2002  
LOCUS Human sodium channel SCN12A.  
DEFINITION BD082951  
ACCESSION BD082951.1 GI:22628561  
VERSION JP 2001327294-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 6528)  
Kanazawa, I., Goto, U. and Tei, Y.  
Human sodium channel SCN12A  
Patent: JP 2001327294-A 1 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
OS Homo sapiens (human)  
PN JP 2001327294-A/1  
PD 27-NOV-2001  
PF 23-MAY-2000 JP 2000152085  
PI ICHIRO KANAZAWA, JUN GOTO, YOSHIIRO TEI  
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
CC

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

## FEATURES

FT Key Location/Qualifiers  
CDS (200)..(5575).  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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## ORIGIN

Query Match 13.5%; Score 46.8; DB 6; Length 6528;  
Best Local Similarity 88.1%; Pred. No. 0.0032;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 46 TAACTTAATGGAATT--AGAACTTCCGATCTACGACACTGAGGCTC-TCGTGGCT 102  
Db 3613 TAACTTAATGGAATTGAAGTCTCCGACTCTACGACACTGAGGCTCTTCGTGGCT 3672  
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Qy 103 GTCCCACTTTGAAGGAATGAAGT 126  
Db 3673 GTCCCACTTTGAAGGAATGAAGT 3696  
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Search completed: March 22, 2004, 19:32:29  
Job time : 1846.35 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:33:04 ; Search time 250.445 Seconds  
(without alignments)  
5869.049 Million cell updates/sec

Title: US-09-646-224A-12

Sequence: 1 ttagaattccgaattacc.....gagcttgcgaagaattcc 346

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*  
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2: Geneseq19908:\*  
3: Geneseq20008:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2003as:\*  
8: Geneseq2003bs:\*  
9: Geneseq2003cs:\*  
10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	100.0	346	2	AAZ21490
2	46.8	13.5	856	2	AAZ60242
3	46.8	13.5	3638	2	AAZ87602
4	46.8	13.5	3701	4	AAZ30104
5	46.8	13.5	5728	6	AAZ42750
6	46.8	13.5	5860	4	AAZ30101
7	46.8	13.5	5860	9	ADD32193
8	46.8	13.5	6528	6	AAZ42749
9	36	10.4	13578	4	AAZ81662
10	36	10.4	48203	4	AAZ82628
11	36	10.4	48203	4	AAZ81663
12	36	10.4	48204	4	AAZ70161
13	36	10.4	48204	4	AAZ81666
14	36	10.4	48204	4	AAZ82630
15	36	10.4	48204	4	AAZ70164
16	36	10.4	110000	6	AAZ08336_07
17	36	10.4	110000	6	AAZ08336_08
18	35.8	10.3	1915	3	AAZ47923
19	35.8	10.3	5298	9	ADD32209
20	35.8	10.3	5334	2	AAZ60244
21	35.8	10.3	5822	2	AAZ87601
22	35.8	10.3	5822	4	AAZ30103
23	35.8	10.3	5822	9	ADD32195

24	35.8	10.3	5875	2	AAZ87600	AAZ87600	Rat sodiu
25	35.8	10.3	5875	2	AAZ30102	AAZ30102	Rat sodiu
26	35.8	10.3	5875	4	AAZ221480	AAZ221480	Rat senso
27	35.8	10.3	5905	9	AAZ852929	AAZ852929	Primary r
28	35.8	10.3	5905	9	AAZ32191	AAZ32191	Rat Na v
29	35.8	10.3	5908	2	AAZ60241	AAZ60241	CDNA enco
30	35.6	10.3	5908	2	AAZ60241	AAZ60241	CDNA enco
31	35	10.1	1674	3	AAZ56355	AAZ56355	Escherich
32	35	10.1	915	7	AAZ33917	AAZ33917	Human pig
33	34.8	10.1	915	7	AAZ33917	AAZ33917	Human pig
34	34.8	10.1	659	7	AAZ71901	AAZ71901	Human can
35	34.8	10.1	2364	5	AAZ94358	AAZ94358	ADK64922
36	34.8	10.1	2364	6	AAZ64922	AAZ64922	DNA encod
37	34.2	10.1	110000	2	AAZ42063_00	AAZ42063_00	Haemophil
38	34.2	9.9	444	2	AAZ8188	AAZ8188	EST clone
39	34.2	9.9	24908	4	AAZ81665	AAZ81665	Human imm
40	34	9.8	1668	3	AAZ56360	AAZ56360	Escherich
41	33.8	9.8	1842	3	AAZ56349	AAZ56349	Escherich
42	33.8	9.8	51469	4	AAZ78813	AAZ78813	Human imm
43	33.8	9.8	51469	4	AAZ70270	AAZ70270	Human imm
44	33.2	9.6	51469	4	AAZ69322	AAZ69322	Human imm
45	33.2	9.6	1647	3	AAZ56338	AAZ56338	Escherich

## ALIGNMENTS

RESULT 1  
ID AAZ21490 standard; cDNA; 346 BP.  
AC AAZ21490;  
DT 03-DEC-1999 (first entry)  
DE Human sensory neuron specific 2a nucleotide sequence fragment #10.  
KW Sensory neuron specific 2a; SNS-2a; sodium channel protein; pain;  
RW voltage gated; hypersensitivity; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
PN W09947670-A1.  
PD 23-SEP-1999.  
PF 18-MAR-1999; 99WC-GB000838.  
PR 18-MAR-1998; 98GB-00005793.  
PA (GLAX ) GLAXO GROUP LTD.  
PI Grose DT, Hick CA, Tate SN;  
DR WPI; 1999-562112/47.  
PT Mammalian sodium channel protein for treating pain and hypersensitivity.  
PS Claim 6; Page 67; 73pp; English.  
CC AAZ21481 to AAZ21495 represent fragments of the human sensory neuron specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity.  
CC Sequence 346 BP; 101 A; 71 C; 82 G; 92 T; 0 U; 0 Other;  
XX Query Match 100.0%; Score 346; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.8e-105;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATTCGGAATCTAACCCGTCGTACGAGAAATCCGTAATCTTAATGGAAT 60  
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QY 121 GAAGTACATTTCTGCAAGAAATGGGTAGAAGTCAAGTTAACAAGAAAGGTGAAGAAG 180  
DB 121 GAAGTACATTTCTGCAAGAAATGGGTAGAAGTCAAGTTAACAAGAAAGGTGAAGAAG 180  
QY 181 CAGACGTTCTTTTGGGCTGAGATTTCTTAATTTGCCAAGCTTTTCCGTTACTTAC 240  
DB 181 CAGACGTTCTTTTGGGCTGAGATTTCTTAATTTGCCAAGCTTTTCCGTTACTTAC 240  
QY 241 CAGCCTGCCAGTCTTGAATTTGAAGGGTAGAGAAAAGCTTAAGATTAATCTTCTAC 300  
DB 241 CAGCCTGCCAGTCTTGAATTTGAAGGGTAGAGAAAAGCTTAAGATTAATCTTCTAC 300  
QY 301 CTAAAGCTTCTGTGACAGCCCAAGATGAGCTGTAGCGGAAGGAATTC 346  
DB 301 CTAAAGCTTCTGTGACAGCCCAAGATGAGCTGTAGCGGAAGGAATTC 346

## RESULT 2

AAK60242  
ID AAK60242 standard; cDNA; 856 BP.

AAK60242;

11-AUG-1999 (first entry)

CDNA encoding type 5 sodium channel protein designated PNS.

Type 5 sodium channel; PNS; nervous system; plexiform;  
dorsal root ganglia; tetradotoxin; TTX; epilepsy; stroke;  
diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
neuropathic pain; migraine; headache; ss.

Homo sapiens.

FR2771103-A1.

21-MAY-1999.

19-NOV-1998; 98FR-00014551.

20-NOV-1997; 97US-0066225P.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;

WPI; 1999-315739/27.

P-PSDB; AAY16577.

Isolated DNA encoding sodium channel of the nervous system.

Claim 1; Fig 3A; 90pp; French.

The present sequence encodes a type 5 sodium channel protein designated  
PNS. The protein is a sodium ion channel of the nervous system, and is  
highly expressed in plexiform and dorsal root ganglia. The protein can be  
used to identify inhibitors of sodium channel proteins that are resistant  
to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
neuropathy, and especially neuropathic pain, e.g. migraine and headache

Sequence 856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;

Query Match 13.5%; Score 46.8; DB 2; Length 856;  
Best Local Similarity 88.1%; Pred. No. 5.4e-05;

Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;  
QY 46 TAACCTTAATGGAAT--AGAACCTTCGGGATCTACGAGCACTGAGGCTC-TCGCGGCT 102  
DB 214 TAACCTTAATGGAATGGAAGTCTTCGACTCTACGAGCACTGAGGCTCTTCGCGCT 273  
QY 103 GTCCAGTTTGAAGGAATGGAAGT 126  
DB 274 GTCCAGTTTGAAGGAATGGAAGT 297

## RESULT 3

AAK87602  
ID AAK87602 standard; cDNA; 3638 BP.

AAK87602;

26-OCT-1999 (first entry)

Human sodium channel NAN partial cDNA.

NAN; sodium channel; ion transport; human; dorsal root ganglia; pain;  
paresthesia; hyperexcitability; therapy; SCN11a gene; ss.

Homo sapiens.

WO9338889-A2.

05-AUG-1999.

29-JAN-1999; 99WO-US002008.

29-JAN-1998; 98US-0072990P.

20-NOV-1998; 98US-0109402P.

(UYVA) UNIV YALE.

Dib-Hajj S, Waxman S;

WPI; 1999-479168/40.

P-PSDB; AAY06598.

New isolated nucleic acids encoding sodium channels, used to develop  
products for treating acute or chronic pain or hyperexcitability  
phenomena.

Claim 1; Fig 8A1-2; 91pp; English.

This is the nucleotide sequence of a partial cDNA clone which codes for a  
portion (see AAY06596) of human NAN, a previously unidentified voltage  
gated sodium channel protein that is preferentially expressed in dorsal  
root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
sodium current. The NAN channel cDNA was obtained from human DRG tissue  
cDNA by PCR amplification (see also AAK87600-02). Rat, mouse and human  
NAN nucleic acids (see AAK87600-02) and polypeptides (see AAY06596-98)  
are provided. The invention also includes expression vectors and  
transformed host cells, methods for identifying tissues and cells that  
express NAN, methods for identifying agents that modulate NAN channel  
activity or NAN channel mRNA transcription or translation, and a method  
for using such agents to treat acute or chronic pain, paresthesia and  
hyperexcitability phenomena. The preferential expression of NAN in  
CC sensory DRG and trigeminal neurons provides a target for selectively  
modifying the behaviour of these nerve cells while not affecting other  
nerve cells in the brain and spinal cord. The gene is named SCN11a

Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;

Query Match 13.5%; Score 46.8; DB 2; Length 3638;  
Best Local Similarity 88.1%; Pred. No. 0.0001; Indels 3; Gaps 2;  
Matches 74; Conservative 0; Mismatches 7;

QY 46 TAACCTTAATGGAAT--AGAACCTTCGGGATCTACGAGCACTGAGGCTC-TCGCGGCT 102  
|||||

Matches	74;	Conservative	0;	Mismatches	7;	Indels	3;	Gaps	2;
QY	46	TAACCTTAATGCAATT--AGAACCTTCGGATCTACGAGCACTGAGGCTC--TCGTGGGCT	102						
Db	2817	TAACCTTAATGCAATTGAAAGTCCTTCGGACTCTACGAGCACTGAGGCTCTCTGTGGCT	2876						
QY	103	GTCCCACTTTGAAGGAATGAAGGT	126						
Db	2877	GTCCCACTTTGAAGGAATGAAGGT	2900						
RESULT 5									
ID	AA142750								
XX	AA142750	standard; cDNA; 5728 BP.							
XX	AA142750;								
DT	19-JUL-2002	(first entry)							
XX									
DE	Human sodium channel subunit SCN12A-s coding sequence.								
XX									
KW	Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;								
KW	human nervous system; chromosome 3p23-21.3; excitatory cell;								
KW	drug development; familial hyperglycaemia; QT extending syndrome type 3;								
KW	motor endplate disease.								
XX									
OS	Homo sapiens.								
XX									
PH	Key	Location/Qualifiers							
FT	CDS	200..4534							
FT		/*tag= a							
FT		/product= "Human sodium channel subunit SCN12A-s"							
XX									
PN	WO200190355-A1.								
XX									
PD	29-NOV-2001.								
XX									
PF	11-JUL-2000; 2000MO-JP004629.								
XX									
PR	23-MAY-2000; 2000JP-00152085.								
XX									
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.								
XX									
PI	Kanazawa I, Goto J, Jeong S;								
XX									
DR	WPI; 2002-393394/42.								
DR	P-PSDB; AA014926.								
PT									
PT	Sodium channel alpha subunits SCN12A and SCN8A of human nervous system								
PT	together with splicing variants, useful in studying physiological								
PT	mechanism relating to excitatory cells and in drug development.								
XX									
PS	Claim 7; Page 55-70; 118pp; Japanese.								
XX									
CC	The invention comprises the amino acid and coding sequence of three								
CC	sodium channel subunits from the human nervous system (SCN12A, SCN12A-s								
CC	and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and								
CC	the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel								
CC	subunit proteins are useful in studying physiological mechanisms relating								
CC	to excitatory cells and in drug development. The sodium ion channel								
CC	subunit proteins are useful for treating diseases such as familial								
CC	hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.								
CC	The present cDNA sequence encodes the human SCN12A-s sodium channel								
XX	subunit								
XX									
SO	Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;								
	Query Match	13.5%; Score 46.8; DB 6; Length 5728;							
	Best Local Similarity	88.1%; Pred. No. 0.00012;							
	Matches	74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;							
QY	46	TAACCTTAATGCAATT--AGAACCTTCGGATCTACGAGCACTGAGGCTC--TCGTGGGCT	102						

DB 3613 TAACCTAATGGAATTGAAGTCTCTCCGACCTACAGAGACTGAGCCCTCTTCTGCGCT 3672  
 OY 103 GTCCCACTTTGAAGGAATGAAGCT 126  
 DB 3673 GTCCCACTTTGAAGGAATGAAGCT 3696

RESULT 6  
 AAF30101  
 ID AAF30101 standard; cDNA; 5860 BP.  
 AC AAF30101;  
 DT 30-APR-2001 (first entry)  
 DE Human sodium channel Na<sup>v</sup> cDNA.  
 XX  
 XX Sodium channel; Na<sup>v</sup>; human; tetrodotoxin resistant; pain; paraesthesia;  
 KM hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 31..5402  
 FT CDS /tag= a  
 FT  
 XX WO200105831-A1.  
 PN  
 XX  
 PD 25-JAN-2001.  
 PF 14-JUL-2000; 2000WO-US019342.  
 PR 16-JUL-1999; 99US-00354147.  
 XX (UYVA ) UNIV YALE.  
 PA  
 PI Dib-Hajj S, Waxman SG;  
 DR WPI; 2001-103147/11.  
 DR P-PSDB; AAB20121.  
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 PT channels, useful for preventing, diagnosing and treating pain,  
 PT paraesthesia and/or hyperexcitability phenomena.  
 PS Claim 1; Fig 11A; 162pp; English.  
 XX  
 XX The present sequence is that of cDNA encoding a novel human tetrodotoxin  
 CC resistant sodium channel, termed Na<sup>v</sup> (see AAB20121). The cDNA was  
 CC isolated from a human dorsal root ganglia tissue cDNA library by PCR  
 CC amplification (see also AAF30122-23). Na<sup>v</sup> belongs to the a-subunit  
 CC voltage-gated sodium channel protein family and produces a TTX-R sodium  
 CC current. Such channels underlie the generation and propagation of  
 CC impulses in excitable cells such as neurons and muscle fibres.  
 CC Preferential expression of Na<sup>v</sup> on sensory neurons innervating the body  
 CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
 CC neurons, makes it a very useful target for diagnostic and/or therapeutic  
 CC uses in relation to acute and/or chronic pain pathologies. A claimed  
 CC method of treating pain, paraesthesia and/or hyperexcitability phenomena  
 CC in a human or animal subject involves administering an agent that alters  
 CC sodium current flow through Na<sup>v</sup> channels, or which modulates  
 CC transcription or translation of Na<sup>v</sup> mRNA, in dorsal root ganglia or  
 CC trigeminal neurons. Na<sup>v</sup> nucleic acids are used in gene therapy to correct  
 CC disorders associated with decreased sodium channel expression or  
 CC (antisense) to down-regulate Na<sup>v</sup> expression, in the diagnosis of disease,  
 CC and in the recombinant production of Na<sup>v</sup> polypeptides  
 XX  
 SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;

Query Match 13.5%; Score 46.8; DB 4; Length 5860;  
 Best Local Similarity 88.1%; Pred. No. 0.00013;  
 Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

OY 46 TAACCTAATGGAATT--AGAACTCTCCGACTACAGACACTGAGGCTC-TCGTGCGCT 102  
 DB 3444 TAACCTAATGGAATTGAAGTCTCTCCGACTCTACAGACTGAGGCTCTCTGTGGCT 3503  
 OY 103 GTCCCACTTTGAAGGAATGAAGCT 126  
 DB 3504 GTCCCACTTTGAAGGAATGAAGCT 3527

RESULT 7  
 ADD32193  
 ID ADD32193 standard; cDNA; 5860 BP.  
 AC ADD32193;  
 DT 15-JAN-2004 (first entry)  
 DE Human Na<sup>v</sup> 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
 XX  
 XX expression vector; Na<sup>v</sup> 1.9 sodium channel protein;  
 KM sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 31..5406  
 FT CDS /tag= a  
 FT /product= "Na<sup>v</sup> 1.9 sodium channel protein"  
 FT  
 XX WO2003080570-A2.  
 PN  
 XX  
 PD 02-OCT-2003.  
 PF 20-MAR-2003; 2003WO-US008611.  
 PR 20-MAR-2002; 2002US-0365550P.  
 XX (TRAN-) TRANSMOLECULAR INC.  
 PA  
 PI Gonda MA, Greenwood JD;  
 DR WPI; 2003-876895/81.  
 DR P-PSDB; ADD32194.  
 PT Expression vector useful for stable cloning and expression of Na<sup>v</sup> 1.9  
 PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
 PT sequence that encodes a mammalian Na<sup>v</sup> 1.9 sodium channel protein or its  
 PT fragment.  
 PS Disclosure; SEQ ID NO 3; 125pp; English.  
 XX  
 XX The present invention describes an expression vector comprising a nucleic  
 CC acid sequence that encodes a mammalian Na<sup>v</sup> 1.9 sodium channel protein or  
 CC its fragment, and producing a sodium current when transfected in a cell.  
 CC Also described: (1) a recombinant cell comprising the plasmid selected  
 CC from pNa<sup>v</sup>, pCMV-rNa<sup>v</sup>-GFP, pG338XM-rNa<sup>v</sup> and the plasmid described above;  
 CC (2) a method of making a cell or cell line that produces a Na<sup>v</sup> 1.9  
 CC sodium channel-dependent sodium current by: (a) providing a cell that has  
 CC been transfected with the expression vector; and (b) culturing the cell  
 CC under conditions that allow expression of Na<sup>v</sup> 1.9 sodium channel protein  
 CC to produce a sodium current into the transfected cell; (3) a method of  
 CC screening for an agent that modulates sodium current in a cell by: (a)  
 CC exposing the cell or cell line produced by the method to the agent; and  
 CC (b) measuring sodium current following exposure to the agent, where an  
 CC alteration in the level of sodium current is indicative of an agent  
 CC capable of modulating sodium current in a cell; and (4) a recombinant  
 CC cell comprising the expression vector. The expression vectors are useful  
 CC for the stable cloning and expression of the Na<sup>v</sup> 1.9 sodium channel at  
 CC the mRNA and protein levels, and for producing sodium channel currents  
 CC characteristic of native currents in dorsal root ganglion neurons. The  
 CC present sequence encodes a human Na<sup>v</sup> 1.9 sodium channel protein, which  
 CC is used in the exemplification of the present invention.  
 XX

SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
Query Match 13.5%; Score 46.8; DB 9; Length 5860;  
Best Local Similarity 88.1%; Pred. No. 0.00013;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;  
QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGCGCT 102  
DB 3444 TAACTTAATGGAATGGAATGACTCTCCGACTCTACGAGCACTGAGGCTCTTCGTCGCT 3503  
QY 103 GTCCCACTTTGAAGAAATGAAGT 126  
DB 3504 GTCCCACTTTGAAGAAATGAAGT 3527  
RESULT 8  
AAL42749 standard; cDNA; 6528 BP.  
XX AAL42749;  
AC AAL42749;  
XX 19-JUL-2002 (first entry)  
XX Human sodium channel subunit SCN12A coding sequence.  
DE Human sodium channel subunit SCN12A coding sequence.  
XX Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
KW human nervous system; chromosome 3p23-21.3; excitatory cell;  
KW drug development; familial hyperklycaemia; QT extending syndrome type 3;  
KW motor endplate disease.  
XX Homo sapiens.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 200..5575  
FT /tag= a  
FT /product= "Human sodium channel subunit SCN12A"  
XX WO200190355-A1.  
XX 29-NOV-2001.  
XX 11-JUL-2000; 2000WO-JP004629.  
XX 23-MAY-2000; 2000JP-00152085.  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX Kanazawa I, Goto J, Jeong S;  
PI WPI; 2002-393394/42.  
DR P-PSDB; AAO14925.  
XX Sodium channel alpha subunits SCN12A and SCN8A of human nervous system  
PT together with splicing variants, useful in studying physiological  
PT mechanism relating to excitatory cells and in drug development.  
XX Claim 6; Page 29-46; 118pp; Japanese.  
XX The invention comprises the amino acid and coding sequence of three  
CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s  
CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and  
CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
CC subunit proteins are useful in studying physiological mechanisms relating  
CC to excitatory cells and in drug development. The sodium ion channel  
CC subunit proteins are useful for treating diseases such as familial  
CC hyperklycaemia, QT extending syndrome type 3 and motor endplate diseases.  
CC The present cDNA sequence encodes the human SCN12A sodium channel subunit  
XX Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;  
Query Match 13.5%; Score 46.8; DB 6; Length 6528;  
Best Local Similarity 88.1%; Pred. No. 0.00013;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGCGCT 102  
DB 3613 TAACTTAATGGAATGGAATGACTCTCCGACTCTACGAGCACTGAGGCTCTTCGTCGCT 3672  
QY 103 GTCCCACTTTGAAGAAATGAAGT 126  
DB 3673 GTCCCACTTTGAAGAAATGAAGT 3696  
RESULT 9  
AAK81662 standard; DNA; 13578 BP.  
ID AAK81662  
XX AAK81662;  
AC AAK81662;  
XX 07-NOV-2001 (first entry)  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36474.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36474.  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX Homo sapiens.  
XX WO200157182-A2.  
XX 09-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001354.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
XX 02-MAR-2000; 2000US-0186350P.  
XX 16-MAR-2000; 2000US-0189874P.  
XX 17-MAR-2000; 2000US-0190076P.  
XX 18-APR-2000; 2000US-0198123P.  
XX 19-MAY-2000; 2000US-0205515P.  
XX 07-JUN-2000; 2000US-0209467P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 30-JUN-2000; 2000US-0215135P.  
XX 07-JUL-2000; 2000US-0216647P.  
XX 07-JUL-2000; 2000US-0216880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225213P.  
XX 14-AUG-2000; 2000US-0225214P.  
XX 14-AUG-2000; 2000US-0225266P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225757P.  
XX 14-AUG-2000; 2000US-0225758P.  
XX 14-AUG-2000; 2000US-0225759P.  
XX 18-AUG-2000; 2000US-0226279P.  
XX 22-AUG-2000; 2000US-0226681P.  
XX 22-AUG-2000; 2000US-0226686P.  
XX 22-AUG-2000; 2000US-0227182P.  
XX 23-AUG-2000; 2000US-0227009P.  
XX 30-AUG-2000; 2000US-0228924P.  
XX 01-SEP-2000; 2000US-0229287P.  
XX 01-SEP-2000; 2000US-0229343P.  
XX 01-SEP-2000; 2000US-0229344P.  
XX 01-SEP-2000; 2000US-0229345P.  
XX 05-SEP-2000; 2000US-0229509P.  
XX 05-SEP-2000; 2000US-0229513P.

PR	06-SEP-2000;	2000US-0230437P.
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PR	14-SEP-2000;	2000US-0232398P.
PR	14-SEP-2000;	2000US-0232399P.
PR	14-SEP-2000;	2000US-0232401P.
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PR	20-OCT-2000;	2000US-0241785P.
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PR	08-DEC-2000;	2000US-0251990P.
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PR	05-JAN-2001;	2001US-0259678P.
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM,	

[illegible]

PR	14-SEP-2000	2000US-0232400P
PR	14-SEP-2000	2000US-0232401P
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PR	05-DEC-2000	2000US-0251030P
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PR	05-DEC-2000	2000US-0256119P









expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (1) by expressing inactive proteins or to  
CC supplement the patients own production of (1). Additionally, (1)  
CC polynucleotides may be used to produce the secreted (1), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (1) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX

Sequence 48203 BP; 15690 A; 10292 C; 9074 G; 13147 T; 0 U; 0 Other;

Query Match 10.4%; Score 36; DB 4; Length 48203;  
Best Local Similarity 55.6%; Pred. No. 1.3;  
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY 208 CTTAATTTGCCAAGCTTTTCTCGGTTACTTACCAAGCTGCCAGTCTTAGAATTGAG 267  
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QY 268 GGGT 271  
Db 31005 GGGT 31002

RESULT 13  
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ID AAK81666 standard; DNA; 48204 BP.  
XX  
AC AAK81666;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36478.  
XX  
XX Human; immune: haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
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PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-483426/52.  
  
Nucleic acids encoding human immune/hematopoietic antigen polypeptides;  
useful for preventing, diagnosing and/or treating cancers and metastasis.  
  
Disclosure; SEQ ID NO 36478; 3071pp + Sequence Listing; English.  
  
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic  
activity, and can be used in gene therapy and vaccine production. (I)  
proteins and polynucleotides may be used in the prevention, diagnosis and  
treatment of diseases associated with inappropriate (I) expression. For  
example, they may be used to treat disorders associated with decreased  
expression by rectifying mutations or deletions in a patient's genome  
that affect the activity of (I) by expressing inactive proteins or to  
supplement the patient's own production of (I). Additionally, (I)  
polynucleotides may be used to produce the secreted (I), by inserting the  
nucleic acids into a host cell and culturing the cell to express the  
protein. (I) proteins and polynucleotides may be used to prevent,  
diagnose and treat immune/haematopoietic-related diseases, especially  
cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
to AAK67694 represent human immune/haematopoietic antigen genomic  
sequences from the present invention. AAK54942 to AAK54950 and AAK62169  
represent sequences used in the exemplification of the present invention

Query Match 10.4%; Score 36; DB 4; Length 48204;  
Best Local Similarity 55.6%; Pred. No. 1.3;  
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
  
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Qy 208 CTTAAATGCTTCAAGCTTTCTGCTTACTTACCTACAGCTGCTGCTTGAATTGGAG 267  
Db 17140 ATTAAGTTCAGTTAACAAGAAAGGTGAAAGCCACAGTCTTTTGGCTGAGATTTC 17199  
  
Qy 268 GGGT 271  
Db 17200 GGGT 17203  
  
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XX  
AC AAK82630;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37442.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
XX  
KW Cytostatic; gene therapy; vaccine; metastasis; ds.  
OS Homo sapiens.  
XX  
FN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 17-JAN-2001; 2001WO-US001354.  
XX  
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OY 268 GCGT 271  
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Db 31005 GCGT 31002

RESULT 15  
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XX AAK70164;  
AC  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24976.  
XX  
KW Human; immune; hematopoietic; immune/haematopoietic antigen; cancer;  
XX cytostatic; gene therapy; vaccine; metastasis; ds.  
OS Homo sapiens.  
XX  
XX MO200157182-A2.  
XX  
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PR 29-SEP-2000; 2000US-0236466P.  
PR 29-SEP-2000; 2000US-0236467P.  
PR 29-SEP-2000; 2000US-0236468P.  
PR 29-SEP-2000; 2000US-0236469P.  
PR 29-SEP-2000; 2000US-0236470P.  
PR 29-SEP-2000; 2000US-0236471P.  
PR 29-SEP-2000; 2000US-0236472P.  
PR 29-SEP-2000; 2000US-0236473P.  
PR 29-SEP-2000; 2000US-0236474P.  
PR 29-SEP-2000; 2000US-0236475P.  
PR 29-SEP-2000; 2000US-0236476P.  
PR 29-SEP-2000; 2000US-0236477P.  
PR 29-SEP-2000; 2000US-0236478P.  
PR 29-SEP-2000; 2000US-0236479P.  
PR 29-SEP-2000; 2000US-0236480P.  
PR 29-SEP-2000; 2000US-0236481P.  
PR 29-SEP-2000; 2000US-0236482P.  
PR 29-SEP-2000; 2000US-0236483P.  
PR 29-SEP-2000; 2000US-0236484P.  
PR 29-SEP-2000; 2000US-0236485P.  
PR 29-SEP-2000; 2000US-0236486P.  
PR 29-SEP-2000; 2000US-0236487P.  
PR 29-SEP-2000; 2000US-0236488P.  
PR 29-SEP-2000; 2000US-0236489P.  
PR 29-SEP-2000; 2000US-0236490P.  
PR 29-SEP-2000; 2000US-0236491P.  
PR 29-SEP-2000; 2000US-0236492P.  
PR 29-SEP-2000; 2000US-0236493P.  
PR 29-SEP-2000; 2000US-0236494P.  
PR 29-SEP-2000; 2000US-0236495P.  
PR 29-SEP-2000; 2000US-0236496P.  
PR 29-SEP-2000; 2000US-0236497P.  
PR 29-SEP-2000; 2000US-0236498P.  
PR 29-SEP-2000; 2000US-0236499P.  
PR 29-SEP-2000; 2000US-0236500P.

PR 17-NOV-2000; 2000US-0249239P.  
PR 17-NOV-2000; 2000US-0249239P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rozen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
PS Disclosure; SEQ ID NO 24976; 3071bp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention  
XX  
SQ Sequence 48204 BP; 15691 A; 10292 C; 9074 G; 13147 T; 0 U; 0 Other;

Query Match 10.4%; Score 36; DB 4; Length 48204;  
Best Local Similarity 55.6%; Pred. No. 1.3;  
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 148 AGAGTTCAGTTACGAGAAAGTGAAGCAACAGTCTTTTGGGCTGAGATTTC 207  
Db 31125 AGAAGTGAATATTAAGAGACTGCTGCAAGCAAGCAAGTATTTTCAGTTGAATTGC 31066

QY 208 CTTAAATGCGCAAGCTTTCTGCGTTACTTACAGCCCTGCCAGTCTTAGAATTGAG 267  
Db 31065 ATTAAATAGAAAGTATTTCTTGCTTGTGAGACACGTGAATTTTAAAGAGCTGCT 31006

QY 268 GGGT 271  
Db 31005 GGGT 31002

Search completed: March 22, 2004, 16:13:09  
Job time : 254.445 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 19:33:04 ; Search time 211.915 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-12

Perfect score: 1 ctgaattccgaattacc.....gagcttgcgaagaattcc 346

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 184957674 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	46.8	13.5	3701	US-10-388-470-6
2	46.8	13.5	5860	US-10-388-470-41
3	37	10.7	667	US-10-027-632-97040
4	37	10.7	667	US-10-027-632-97041
5	37	10.7	667	US-10-027-632-319122
6	37	10.7	667	US-10-027-632-319123
7	36	10.4	1691139	US-10-067-514-1
8	36	10.4	1691139	US-10-419-723-1
9	35.8	10.3	5822	US-10-388-470-4
10	35.8	10.3	5875	US-10-388-470-1
11	34.8	10.1	2364	US-10-260-877-27
12	34.8	10.1	1830121	US-10-329-960-1
13	34.8	10.1	1830121	US-10-329-670-1
14	34.2	9.9	444	US-10-040-739-666
15	34.2	9.9	525	US-10-029-386-5767

16	34	9.8	613	US-10-027-632-243535	Sequence 243535,
17	33.2	9.6	26642	US-10-034-650-25	Sequence 25, Appl
18	32.8	9.5	2910	US-10-104-047-1869	Sequence 1869, Ap
19	32.6	9.4	465237	US-09-933-267A-1	Sequence 1, Appl1
20	32.2	9.3	557	US-10-424-599-117935	Sequence 117935,
21	31.8	9.2	1551	US-10-282-122A-27130	Sequence 27130, A
22	31.4	9.1	527	US-09-854-133-683	Sequence 683, App
23	31.4	9.1	527	US-10-144-649A-683	Sequence 683, App
24	31.4	9.1	1794	US-10-259-165-209	Sequence 209, App
25	31.2	9.0	426	US-10-424-599-64375	Sequence 64375, A
26	31	9.0	954	US-10-424-599-81076	Sequence 81076, A
27	31	9.0	1060	US-10-027-632-30641	Sequence 30641, A
28	31	9.0	1620	US-10-369-493-45119	Sequence 45119, A
29	31	9.0	3090	US-10-654-416-5	Sequence 5, Appl1
30	31	9.0	26197	US-09-764-847-1965	Sequence 1965, Ap
31	31	9.0	26197	US-10-092-154-1965	Sequence 1966, Ap
32	31	9.0	26210	US-09-764-847-1966	Sequence 1966, Ap
33	31	9.0	26210	US-10-092-154-1966	Sequence 1966, Ap
34	31	9.0	158091	US-10-235-192A-38	Sequence 38, Appl
35	30.8	8.9	613	US-10-027-632-281398	Sequence 281398,
36	30.8	8.9	1777	US-10-425-114-27027	Sequence 27027, A
37	30.8	8.9	1691139	US-10-067-514-1	Sequence 1, Appl1
38	30.8	8.9	1691139	US-10-419-723-1	Sequence 12433, A
39	30.6	8.8	292	US-10-425-114-12433	Sequence 11483, A
40	30.6	8.8	466	US-10-198-846-11483	Sequence 136164,
41	30.6	8.8	956	US-10-027-632-136164	Sequence 22518, A
42	30.6	8.8	1641	US-10-425-114-22518	Sequence 3, Appl1
43	30.6	8.8	2836	US-10-003-132-3	Sequence 5, Appl1
44	30.6	8.8	2868	US-10-003-132-5	Sequence 272340,
45	30.4	8.8	536	US-10-027-632-272340	

#### ALIGNMENTS

RESULT 1

US-10-388-470-6

Sequence 6, Application US/10388470

Publication No. US2003022862A1

GENERAL INFORMATION:

APPLICANT: Maxman, Stephen G.

TITLE OR INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/10/388, 470

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/09/354,147C

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072, 990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109, 402

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 3701

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(3699)

OTHER INFORMATION: partial human Nan CDNA sequence

FEATURE:

NAME/KEY: unsure

LOCATION: (922)

OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is

OTHER INFORMATION: Leu.

US-10-388-470-6

Query Match 13.5%; Score 46.8; DB 15; Length 3701;

Best Local Similarity 88.1%; Pred. No. 8.8e-05;



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RESULT 5
US-10-027-632-319122/c
; Sequence 319122, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319122
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-319122

Query Match      10.7%; Score 37; DB 15; Length 667;
Best Local Similarity 59.2%; Pred. No. 0.081;
Matches 61; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

Cy 149 GAAGTTCAAGTTAAGAGAAAGTGAAGACCAACAGTTCTTTTGGGCTGAGATTTC 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 GATATGCTTTGCACAAATGCAAGTGCACAAATGCTTCTTCGCTGATATATTC 382

Cy 209 TTAATTCGCAAGCTTTCTCGGTTACTTACCAAGCTGCCCA 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 ATCAATAGTTAAGATGCCCTGGGTAGTTATTTGCTGACTA 339

RESULT 6
US-10-027-632-319123/c
; Sequence 319123, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319123
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-319123

Query Match      10.7%; Score 37; DB 15; Length 667;
Best Local Similarity 59.2%; Pred. No. 0.081;
Matches 61; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

Cy 149 GAAGTTCAAGTTAAGAGAAAGTGAAGACCAACAGTTCTTTTGGGCTGAGATTTC 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 GATATGCTTTGCACAAATGCAAGTGCACAAATGCTTCTTCGCTGATATATTC 382

Cy 209 TTAATTCGCAAGCTTTCTCGGTTACTTACCAAGCTGCCCA 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 ATCAATAGTTAAGATGCCCTGGGTAGTTATTTGCTGACTA 339

RESULT 7
US-10-067-514-1/c
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gretaardottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

Query Match      10.4%; Score 36; DB 14; Length 1691139;
Best Local Similarity 60.0%; Pred. No. 8.3;
Matches 60; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Cy 184 CAGTTCTTTTGGGCTGAGATTCTTAAATTGCGCAAGCTTTTCTGGGTTACTTACAG 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 810036 CAGCTCAGATGAGGCTCACTTTCTGACTTCAGATGCTTTTATCATTTTCTTACAT 809977

Cy 244 CTGCGCCAGTGCCTTAGAATTGAGGGGTAGAGAAAGCCT 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809976 TCTCTCTATTTTTTTGAAGTTTAGAGAGAAAGCTCCT 809937

RESULT 8
US-10-419-723-1/c
; Sequence 1, Application US/10419723
; Publication No. US20040014099A1
; GENERAL INFORMATION:
; APPLICANT: Gretaardottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-005
; CURRENT APPLICATION NUMBER: US/10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/067,514
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;; PRIOR FILING DATE: 2002-02-04  
;; PRIOR APPLICATION NUMBER: 09/811,352  
;; PRIOR FILING DATE: 2001-03-19  
;; NUMBER OF SEQ ID NOS: 87  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 1691139  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-419-723-1

Query Match 10.4%; Score 36; DB 15; Length 1691139;  
Best Local Similarity 60.0%; Pred. No. 8.3;  
Matches 60; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 184 CAGTCTTTTGGGCTGAGATTCTTAAATGCCAAGCTTTCTGGGTTACTTACGAG 243  
DB 810036 CAGCTCAGATGAGCTCCTTTGCTGAACCTCAGATGCTTTATCATTTCTTACAAAT 809977  
QY 244 CCGGCCAGTGCTTGAATTTGAGGGGTAGGAAGGCT 283  
DB 809976 TCTCTCTAATTTTGAAGTTTAGAGGAAGAACTGCT 809937

RESULT 9  
US-10-388-470-4  
; Sequence 4, Application US/10388470  
; Publication No. US20030228662A1  
; GENERAL INFORMATION:  
; APPLICANT: Dib-Hajj, Sulayman  
; APPLICANT: Waxman, Stephen G.  
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
; FILE REFERENCE: 44574-5004-01-US  
; CURRENT APPLICATION NUMBER: US/10/388,470  
; PRIOR FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: US/09/354,147C  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 60/072,990  
; PRIOR FILING DATE: 1998-01-29  
; PRIOR APPLICATION NUMBER: US 60/109,402  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: PCT/US99/02008  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 5822  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (19)..(5313)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (5804)  
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t  
US-10-388-470-4

Query Match 10.3%; Score 35.8; DB 15; Length 5822;  
Best Local Similarity 80.6%; Pred. No. 0.6;  
Matches 54; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 61 AGAACCTTCCGAGATCTACGAGACTGAGGCTCT-CTGCGCTGTCCAGTTGAAGGA 119  
DB 3386 AGTCCTCCGGAATCTGCGAGCGCTGAGACCTCTGCGGGCACTGCTGAGTTGAAGGA 3445  
QY 120 TGAAGT 126  
DB 3446 TGAAGT 3452

RESULT 10  
US-10-388-470-1

;; Sequence 1, Application US/10388470  
;; Publication No. US20030228662A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dib-Hajj, Sulayman  
;; APPLICANT: Waxman, Stephen G.  
;; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
;; FILE REFERENCE: 44574-5004-01-US  
;; CURRENT APPLICATION NUMBER: US/10/388,470  
;; PRIOR FILING DATE: 2003-03-17  
;; PRIOR APPLICATION NUMBER: US/09/354,147C  
;; PRIOR FILING DATE: 1999-07-16  
;; PRIOR APPLICATION NUMBER: US 60/072,990  
;; PRIOR FILING DATE: 1998-01-29  
;; PRIOR APPLICATION NUMBER: US 60/109,402  
;; PRIOR FILING DATE: 1998-11-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/02008  
;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 44  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 5875  
;; TYPE: DNA  
;; ORGANISM: Rattus norvegicus  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (41)..(5335)  
;; OTHER INFORMATION: cDNA sequence for rat Nan  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (1996)..(4042)  
;; OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position  
;; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn  
US-10-388-470-1

Query Match 10.3%; Score 35.8; DB 15; Length 5875;  
Best Local Similarity 80.6%; Pred. No. 0.6;  
Matches 54; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 61 AGAACCTTCCGAGATCTACGAGACTGAGGCTCT-CTGCGCTGTCCAGTTGAAGGA 119  
DB 3405 AGTCCTCCGGAATCTGCGAGCGCTGAGACCTCTGCGGGCACTGCTGAGTTGAAGGA 3464  
QY 120 TGAAGT 126  
DB 3465 TGAAGT 3471

RESULT 11  
US-10-260-877-27/C  
; Sequence 27, Application US/10260877  
; Publication No. US20030021813A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Chovan, Linda E.  
; APPLICANT: Hessler, Paul E.  
; APPLICANT: Reich, Karl A.  
; TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME  
; TITLE OF INVENTION: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF  
; TITLE OF INVENTION: 'ESSENTIAL GENES'  
; FILE REFERENCE: 6565.US.PI  
; CURRENT APPLICATION NUMBER: US/10/260,877  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/649,145  
; PRIOR FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 2364  
; TYPE: DNA  
; ORGANISM: H. influenzae  
; FEATURE:  
; NAME/KEY: CDS

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LOCATION: (1)...(2364)
OTHER INFORMATION: HI-0061
US-10-260-877-27

Query Match 10.1%, Score 34.8, DB 14, Length 2364;
Best Local Similarity 54.8%, Pred. No. 0.84;
Matches 69, Conservative 0, Mismatches 57, Indels 0, Gaps 0,

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DB 461 TCCGATCAAAACCCAGCAATTTATGTCAGAAAGGAAACCTAAAGAAATTCAGCT 402
QY 67 TTCCGATCTAACGAGCACTGAGGCTCTCCGCGCTGTCAGTTGAGGAATGAGAGT 126
DB 401 TCCGAATTTCCGATTAATGAGGACCTCTTCGCTTCAATTAAAGAAATTCGTTGT 342
QY 127 ACATTTC 132
DB 341 TCTTGC 336

RESULT 12
US-10-329-960-1
Sequence 1, Application US/10329960
Publication No. US20030099277A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
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FEATURE:
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc feature  
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NAME/KEY: misc feature  
LOCATION: (145171) .. (145171)  
OTHER INFORMATION: n equals a, t, g or c  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (145942) .. (145942)  
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NAME/KEY: misc feature  
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Best Local Similarity 54.8%; Pred. No. 22;  
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;  
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Qy 67 TTCCGATCTACGAGCACTGAGCCTCTGTCGCTGTCCAGTTTGAAGAAATGAAAGT 126  
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Qy 127 ACATTC 132  
Db 64631 TCTTGC 64636  
RESULT 13  
US-10-329-670-1  
; Sequence 1, Application US/10329670  
; Publication No. US20040018503A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frasn  
; TITLE OF INVENTION: Thercof. and Uses Thereof  
; FILE REFERENCE: PB186P1  
; CURRENT APPLICATION NUMBER: US/10/329,670  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: US 09/643,990  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: US 08/487,429  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/426,787  
; PRIOR FILING DATE: 1995-04-21  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patencin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1830121  
; TYPE: DNA  
; ORGANISM: Haemophilus influenzae  
; FEATURE:  
NAME/KEY: misc feature  
LOCATION: (4747) .. (4747)  
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NAME/KEY: misc feature  
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FEATURE:
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FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc\_feature  
LOCATION: (152530) .. (152530)

Query Match 10.1%; Score 34.8; DB 15; Length 1830121;  
Best Local Similarity 54.8%; Pred. No. 22;  
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 7 TTCCGAATCTAACCCTGTACGAGAACTCTGAATCTTAATGAATTAAGAAC 66  
DB 64511 TGCCGATCAAAACCCGAAATTTATGTCGAGAAAGCAAGTAAGAAATTCACGT 64570  
QY 67 TTCCGATCTACGACACTGAGGCTCTTCGCGCTGTCACGTTTGAAGAAATTAAGT 126  
DB 64571 TGCCAAATTTCCGAAATTAAGGACCTCTTTCGCTTCAATTAAGAAATTCGTTGT 64630  
QY 127 ACATTC 132  
DB 64631 TCTTGC 64636

## RESULT 14

US-10-040-739-666  
Sequence 666, Application US/10040739  
Publication No. US20020173635A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John  
Lavallie, Edward  
Racie, Lisa  
Merberg, David  
Tresacy, Maurice  
Spaulding, Vikki  
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS  
NUMBER OF SEQUENCES: 1519  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/040,739  
FILING DATE: 07-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/036,520  
FILING DATE: 03-JUN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 666:

SEQUENCE CHARACTERISTICS:  
LENGTH: 444 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 666:  
US-10-040-739-666

Query Match 9.9%; Score 34.2; DB 13; Length 444;

Best Local Similarity 62.1%; Pred. No. 0.59;  
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AGAAGTCAGTTACAGAGAAAGGTGAAAGACCAAGTCTTTGGGCTGAGATTTC 207  
DB 25 AGAAGTCAGTTACAGAGAAAGGTGAAAGACCAAGTCTTTGGGCTGAGATTTC 84  
QY 208 CTTAATGCGCAAGCTTTCTCGGCTT 234  
DB 85 ATTAAATTAAGTAATTTCTTCTT 111

## RESULT 15

US-10-029-386-5767/c  
Sequence 5767, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: ABOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 5767  
LENGTH: 525  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: MAP TO AC009086.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6  
OTHER INFORMATION: NT HIT: g14775898, EVALUE 1.00e-111  
OTHER INFORMATION: SWISSPROT HIT: P07954, EVALUE 1.70e+00  
OTHER INFORMATION: EST\_HUMAN HIT: BF819829.1, EVALUE 0.00e+00  
US-10-029-386-5767

Query Match 9.9%; Score 34.2; DB 14; Length 525;  
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QY 148 AGAAGTCAGTTACAGAGAAAGGTGAAAGACCAAGTCTTTGGGCTGAGATTTC 207  
DB 412 AGAAGTCAGTTACAGAGAAAGGTGAAAGACCAAGTCTTTGGGCTGAGATTTC 353  
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DB 352 ATTAAATTAAGTAATTTCTTCTT 326

Search completed: March 23, 2004, 05:13:32  
Job time : 303.915 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:45:54 ; Search time 2607.25 Seconds

(without alignments)  
4669.435 Million cell updates/sec

Title: US-09-646-224A-12

Sequence: 1 ctgaatccgaatcctaacc.....gagcttgcgaagaatcc 346

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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53: /cgn2\_6/ptodata/2/pna/US106\_COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US107A\_COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US107B\_COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*  
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64: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq.\*  
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75: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*  
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78: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq.\*  
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104: /cgn2\_6/ptodata/2/pna/US6048\_COMB.seq.\*  
105: /cgn2\_6/ptodata/2/pna/US6049\_COMB.seq.\*  
106: /cgn2\_6/ptodata/2/pna/US6050\_COMB.seq.\*  
107: /cgn2\_6/ptodata/2/pna/US6051\_COMB.seq.\*  
108: /cgn2\_6/ptodata/2/pna/US6052\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	100.0	346	27 US-09-646-224A-12	Sequence 12, Appl
2	256	74.0	115159	103 US-60-466-412-84151	Sequence 84151, A
3	255.2	72.8	6925	76 US-60-207-214-72	Sequence 72, Appl
4	197.6	57.1	201	103 US-60-466-412-152344	Sequence 152344, A
5	104	30.1	201	103 US-60-466-412-152284	Sequence 152284, A
6	46.8	13.5	856	77 US-09-195-851-3	Sequence 3, Appl
7	46.8	13.5	3163	77 US-60-213-846-1412	Sequence 1412, Ap
8	46.8	13.5	3701	1 PCT-US00-19342-6	Sequence 6, Appl
9	46.8	13.5	3701	1 PCT-US99-02008-6	Sequence 6, Appl
10	46.8	13.5	3701	50 US-10-388-470-6	Sequence 6, Appl
11	46.8	13.5	5080	46 US-10-170-225-13985	Sequence 13985, A
12	46.8	13.5	5080	102 US-60-453-050-2171	Sequence 2171, Ap
13	46.8	13.5	5080	102 US-60-453-135-2171	Sequence 2171, Ap
14	46.8	13.5	5080	103 US-60-466-412-2171	Sequence 2171, Ap
15	46.8	13.5	5728	47 US-10-219-051B-910	Sequence 910, Ap
16	46.8	13.5	5728	48 US-10-296-130-3	Sequence 3, Appl
17	46.8	13.5	5860	1 PCT-US00-19342-41	Sequence 41, Appl
18	46.8	13.5	5860	1 PCT-US03-08611-3	Sequence 3, Appl
19	46.8	13.5	5860	50 US-10-388-470-41	Sequence 41, Appl
20	46.8	13.5	5860	93 US-60-365-550-3	Sequence 3, Appl
21	46.8	13.5	6237	108 US-60-516-609-317	Sequence 317, Ap
22	46.8	13.5	6499	32 US-09-770-175-8399	Sequence 8399, Ap
23	46.8	13.5	6528	48 US-10-296-130-1	Sequence 1, Appl
24	46.8	13.5	6528	105 US-60-485-101-251	Sequence 251, App
25	37.6	10.9	1108228	103 US-60-466-412-86602	Sequence 86602, A
26	37.6	10.9	1391915	103 US-60-466-412-87958	Sequence 87958, A
27	37.4	10.8	492	23 US-09-540-233D-84582	Sequence 84582, A
28	37	10.7	667	26 US-09-634-306B-97040	Sequence 97040, A
29	37	10.7	667	26 US-09-634-306B-97041	Sequence 97041, A
30	37	10.7	667	26 US-09-634-306B-319122	Sequence 319122, A
31	37	10.7	667	26 US-09-634-306B-319123	Sequence 319123, A
32	37	10.7	667	43 US-10-027-632-97040	Sequence 97040, A
33	37	10.7	667	43 US-10-027-632-97041	Sequence 97041, A
34	37	10.7	667	43 US-10-027-632-319122	Sequence 319122, A
35	37	10.7	667	43 US-10-027-632-319123	Sequence 319123, A
36	36.8	10.6	502	73 US-60-170-912-2118	Sequence 2118, Ap
37	36.8	10.6	593	33 US-09-795-301-410	Sequence 410, Appl
38	36.8	10.6	229549	39 US-09-948-124-93	Sequence 93, Appl
39	36.8	10.6	274739	39 US-09-948-124-94	Sequence 94, Appl
40	36.6	10.6	409	27 US-09-644-873-3634	Sequence 3634, Ap
41	36	10.4	395	20 US-09-489-036-34841	Sequence 34841, A
42	36	10.4	395	39 US-09-943-143-34841	Sequence 34841, A
43	36	10.4	13578	1 PCT-US01-01354-36474	Sequence 36474, A
44	36	10.4	13578	32 US-09-764-905-36474	Sequence 36474, A
45	36	10.4	13578	44 US-10-093-399-36474	Sequence 36474, A

## ALIGNMENTS

RESULT 1  
US-09-646-224A-12  
Sequence 12, Application US/09646224A  
GENERAL INFORMATION:  
APPLICANT: Glaxo Wellcome PLC  
APPLICANT: Tate, Simon N  
APPLICANT: Grose, David T  
APPLICANT: Hicks, Caroline A  
TITLE OF INVENTION: Ion Channels  
FILE REFERENCE: PG3432  
CURRENT APPLICATION NUMBER: US/09/646, 224A  
CURRENT FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: GB 9805793.8  
PRIOR FILING DATE: 1998-03-18  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 346  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-646-224A-12  
Query Match 100.0%; Score 346; DB 27; Length 346;  
Best Local Similarity 100.0%; Pred. No. 5.5e-97;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 TTAGATTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 60  
1 TTAGATTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 60  
1 TTAGATTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 60  
1 TTAGATTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 60  
61 AGAATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 120  
61 AGAATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 120  
61 AGAATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 120  
121 GAAGTATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 180  
121 GAAGTATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 180  
121 GAAGTATCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 180  
181 CAACAGTCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 240  
181 CAACAGTCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 240  
181 CAACAGTCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 240  
241 CAGCTGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 300  
241 CAGCTGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 300  
241 CAGCTGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 300  
301 CTAAAGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 360  
301 CTAAAGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 360  
301 CTAAAGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 360  
301 CTAAAGCTTCGCAATCTAACCGCTGACAGATCCTGATCCTTAATGAATG 360  
RESULT 2  
US-60-466-412-84151  
Sequence 84151, Application US/60466412  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
APPLICANT: IAKUBOVA, Olga  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01466  
CURRENT APPLICATION NUMBER: US/60/466, 412  
CURRENT FILING DATE: 2003-04-30  
NUMBER OF SEQ ID NOS: 429241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84151  
LENGTH: 115159  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: misc feature  
LOCATION: (1)...(115159)  
OTHER INFORMATION: n = A,T,C or G  
US-60-466-412-84151  
Query Match 74.0%; Score 256; DB 103; Length 115159;  
Best Local Similarity 95.9%; Pred. No. 6.9e-68;  
Matches 282; Conservative 2; Mismatches 7; Indels 3; Gaps 2;  
46 TAACCTTAATGAAT-AGAACTTCGATCTACAGACTGAGGCTTC-TGTCGCT 102  
46 TAACCTTAATGAAT-AGAACTTCGATCTACAGACTGAGGCTTC-TGTCGCT 102  
83823 TAACCTTAATGAATGAAGTCTTCGAGCTCTACAGACTGAGGCTTCGTCGCT 83882  
83823 TAACCTTAATGAATGAAGTCTTCGAGCTCTACAGACTGAGGCTTCGTCGCT 83882  
103 GTCCAGTTTGAAGAAAGAGTACATTCGCAAGAAAGAGTGAAGTCACTTAAC 162  
103 GTCCAGTTTGAAGAAAGAGTACATTCGCAAGAAAGAGTGAAGTCACTTAAC 162  
83883 GTCCAGTTTGAAGAAAGAGTACATTCGCAAGAAAGAGTGAAGTCACTTAAC 83942  
163 AGAAGAGTGAAGAAAGAGTCAAGTCTTTGGGCTGAGATTTCTTAATGCAAGC 222  
163 AGAAGAGTGAAGAAAGAGTCAAGTCTTTGGGCTGAGATTTCTTAATGCAAGC 222  
83943 AGAAGAGTGAAGAAAGAGTCAAGTCTTTGGGCTGAGATTTCTTAATGCAAGC 84002  
223 TTTCTGCTTACTTACAGGCTGCAAGTCTTAATGATTTAGGGGTGAGAAAGCC 282  
223 TTTCTGCTTACTTACAGGCTGCAAGTCTTAATGATTTAGGGGTGAGAAAGCC 282

Db 84003 TTTCCTGGTACTTTCAGCAGCTGCGCCAGTGTAGAAATTTGAGGGGTAGAGAAAACC 84062  
QY 283 TAAGATATATCTTTCTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTTAGC 336  
Db 84063 TAAGATATATCTTTCTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTTAGC 84116

## RESULT 3

US-60-207-214-72  
; Sequence 172, Application US/60207214  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000581  
; CURRENT APPLICATION NUMBER: US/60/207,214  
; CURRENT FILING DATE: 2000-05-26  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 72  
; LENGTH: 6925  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-207-214-72

Query Match 73.8%; Score 255.2; DB 76; Length 6925;  
Best Local Similarity 96.3%; Pred. No. 4.2e-68;  
Matches 283; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 46 TAACCTTAATGAGT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TGTGGGCT 102  
Db 2211 TAACCTTAATGAGTGAAGTCTTCGCGACTTACGAGCACTGAGGCTCTGTGGGCT 2270  
QY 103 GTCCAGTTTGAAGAGATGAGTACATCTTCGAGAGATGGTGAAGTTCAGTTAC 162  
Db 2271 GTCCAGTTTGAAGAGATGAGTACATCTTCGAGAGATGGTGAAGTTCAGTTAC 2330  
QY 163 AGAGAAAGGTGAAAGACCAACAGTTTCTTTGGGCTGAGATTTCTTAAATTGCCAAGC 222  
Db 2331 AGAGAAAGGTGAAAGACCAACAGTTTCTTTGGGCTGAGATTTCTTAAATTGCCAAGC 2390  
QY 223 TTTTCTCGGTTACTTACCGAGCTGCGCCAGTCTTAAGATTTGAGGGGTAGAGAAAACC 282  
Db 2391 TTTTCTCGGTTACTTACCGAGCTGCGCCAGTCTTAAGATTTGAGGGGTAGAGAAAACC 2450  
QY 283 TAAGATATATCTTTCTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTTAGC 336  
Db 2451 TAAGATATATCTTTCTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTTAGC 2504

## RESULT 4

US-60-466-412-152344  
; Sequence 1152344, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 152344  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-152344

Query Match 57.1%; Score 197.6; DB 103; Length 201;  
Best Local Similarity 99.5%; Pred. No. 1.1e-50;  
Matches 197; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 139 AGAATGGGTAGAACTTCACTTAACAGAGAAAGGTGAAAGACCAAGTCTTTTGGGC 138  
Db 1 AGAATGGGTAGAACTTCACTTAACAGAGAAAGGTGAAAGACCAAGTCTTTTGGGC 60  
QY 199 TGAGATTTCTTAAATTTGCCAAGCTTTCTGTGGTTACTTACCAAGCTTGCAGTGTTA 258  
Db 61 TGAGATTTCTTAAATTTGCCAAGCTTTCTGTGGTTACTTACCAAGCTTGCAGTGTTA 120  
QY 259 GAATTTGAGGGGTAGAGAAAAGCTTAAGATATCTTTCACTTAAGAGTTCTGTGACA 318  
Db 121 GAATTTGAGGGGTAGAGAAAAGCTTAAGATATCTTTCACTTAAGAGTTCTGTGACA 180  
QY 319 GCCAAGATGAGCTGTAGC 336  
Db 181 GCCAAGATGAGCTGTAGC 198

## RESULT 5

US-60-466-412-152284  
; Sequence 152284, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 152284  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-152284

Query Match 30.1%; Score 104; DB 103; Length 201;  
Best Local Similarity 98.1%; Pred. No. 2.1e-21;  
Matches 104; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 231 GGTACTTACCGAGCTGCGCCAGTCTTAAGATTTGAGGGGTAGAGAAAAGCTTAAGATAT 290  
Db 1 GGTACTTACCGAGCTGCGCCAGTCTTAAGATTTGAGGGGTAGAGAAAAGCTTAAGATAT 60  
QY 291 ACTTTTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTGTAGC 336  
Db 61 ACTTTTACCTTAAAGCTTCTGTGACAGCCAGATGAGCTGTAGC 106

## RESULT 6

US-09-195-851-3  
; Sequence 3, Application US/09195851  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: Fish, Linda M.  
; APPLICANT: Khare, Reena  
; APPLICANT: Rabert, Douglas K.  
; APPLICANT: Sangameswaran, Lakshmi  
; TITLE OF INVENTION: A Voltage-Gated Nervous Tissue Sodium Channel,  
; TITLE OF INVENTION: Polynucleotides Encoding Thereof, and Methods of Use  
; FILE REFERENCE: R0021B-REG  
; CURRENT APPLICATION NUMBER: US/09/195,851  
; CURRENT FILING DATE: 1998-11-19  
; EARLIER APPLICATION NUMBER: 60/066,225  
; EARLIER FILING DATE: 1997-11-20  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 3  
; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-195-851-3

Query Match 13.5%; Score 46.8; DB 15; Length 856;  
Best Local Similarity 88.1%; Pred. No. 0.0027;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGGCGT 102  
DB 214 TAACTTAATGGAATGGAATGATGCTTCCTCCGACTCTACGAGCACTGAGGCTCTTCGTGGCGT 273

QY 103 GTCCCAAGTTTGAAGAAATGAAGT 126  
DB 274 GTCCCAAGTTTGAAGAAATGAAGT 297

RESULT 7

US-60-213-846-1412  
Sequence 1412, Application US/60213846  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
FILE REFERENCE: CLO00703  
CURRENT APPLICATION NUMBER: US/60/213,846  
CURRENT FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1412  
LENGTH: 3163  
TYPE: DNA  
ORGANISM: HUMAN  
US-60-213-846-1412

Query Match 13.5%; Score 46.8; DB 77; Length 3163;  
Best Local Similarity 88.1%; Pred. No. 0.0045;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGGCGT 102  
DB 2251 TAACTTAATGGAATGGAATGATGCTTCCTCCGACTCTACGAGCACTGAGGCTCTTCGTGGCGT 2310

QY 103 GTCCCAAGTTTGAAGAAATGAAGT 126  
DB 2311 GTCCCAAGTTTGAAGAAATGAAGT 2334

RESULT 8

PCT-US00-19342-6  
Sequence 6, Application PC/TUS0019342  
GENERAL INFORMATION:  
APPLICANT: Yale University  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-02-WO  
CURRENT APPLICATION NUMBER: PCT/US00/19342  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/354,147  
PRIOR FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: Y = C or T

PCT-US00-19342-6

Query Match 13.5%; Score 46.8; DB 1; Length 3701;  
Best Local Similarity 88.1%; Pred. No. 0.0048;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGGCGT 102  
DB 2817 TAACTTAATGGAATGGAATGATGCTTCCTCCGACTCTACGAGCACTGAGGCTCTTCGTGGCGT 2876

QY 103 GTCCCAAGTTTGAAGAAATGAAGT 126  
DB 2877 GTCCCAAGTTTGAAGAAATGAAGT 2900

RESULT 9

PCT-US99-02008-6  
Sequence 6, Application PC/TUS9902008D  
GENERAL INFORMATION:  
APPLICANT: Yale University  
TITLE OF INVENTION: Dorsal Root Ganglia-Specific and Tetrodotoxin Resistant  
TITLE OF INVENTION: Voltage-Gated Sodium Channel, S. Dib-Hajj et al.  
FILE REFERENCE: 44574-5004-WO, Yale University  
CURRENT APPLICATION NUMBER: PCT/US99/02008D  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: US 60/072,990  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: US 60/109,402  
EARLIER FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: Y = C or T  
PCT-US99-02008-6

Query Match 13.5%; Score 46.8; DB 1; Length 3701;  
Best Local Similarity 88.1%; Pred. No. 0.0048;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGGAAT--AGAACCTTCGGATCTACGAGCACTGAGGCTC-TCGTGGCGT 102  
DB 2817 TAACTTAATGGAATGGAATGATGCTTCCTCCGACTCTACGAGCACTGAGGCTCTTCGTGGCGT 2876

QY 103 GTCCCAAGTTTGAAGAAATGAAGT 126  
DB 2877 GTCCCAAGTTTGAAGAAATGAAGT 2900

QY 103 GTCCCAAGTTTGAAGAAATGAAGT 126  
DB 2877 GTCCCAAGTTTGAAGAAATGAAGT 2900

RESULT 10

US-10-388-470-6  
Sequence 6, Application US/10388470  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is  
OTHER INFORMATION: Leu.  
US-10-388-470-6

Query Match 13.5%; Score 46.8; DB 50; Length 3701;  
Best Local Similarity 88.1%; Pred. No. 0.0048;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAT--AGAACCTTCGGATCTACGACACTGAGGCTC-TCGTGGCT 102  
DB 2817 TAACTTAATGAATGAAGTCTTCGACTCTACGACACTGAGGCTCTTCGTGGCT 2876  
QY 103 GTCCCACTTGAAGATGAAGT 126  
DB 2877 GTCCCACTTGAAGATGAAGT 2900

RESULT 11  
US-10-170-235-13985  
Sequence 13985, Application US/10170235  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig  
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
FILE REFERENCE: CL001380  
CURRENT APPLICATION NUMBER: US/10/170,235  
CURRENT FILING DATE: 2003-03-17  
NUMBER OF SEQ ID NOS: 42514  
SEQ ID NO 13985  
LENGTH: 5080  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-170-235-13985

Query Match 13.5%; Score 46.8; DB 46; Length 5080;  
Best Local Similarity 88.1%; Pred. No. 0.0054;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAT--AGAACCTTCGGATCTACGACACTGAGGCTC-TCGTGGCT 102  
DB 3568 TAACTTAATGAATGAAGTCTTCGACTCTACGACACTGAGGCTCTTCGTGGCT 3627  
QY 103 GTCCCACTTGAAGATGAAGT 126  
DB 3628 GTCCCACTTGAAGATGAAGT 3651

RESULT 12  
US-60-453-050-2171  
Sequence 2171, Application US/60453050  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001457  
CURRENT APPLICATION NUMBER: US/60/453,050

CURRENT FILING DATE: 2003-03-10  
NUMBER OF SEQ ID NOS: 82762  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2171  
LENGTH: 5080  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-453-050-2171

Query Match 13.5%; Score 46.8; DB 102; Length 5080;  
Best Local Similarity 88.1%; Pred. No. 0.0054;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAT--AGAACCTTCGGATCTACGACACTGAGGCTC-TCGTGGCT 102  
DB 3568 TAACTTAATGAATGAAGTCTTCGACTCTACGACACTGAGGCTCTTCGTGGCT 3627  
QY 103 GTCCCACTTGAAGATGAAGT 126  
DB 3628 GTCCCACTTGAAGATGAAGT 3651

RESULT 13  
US-60-453-135-2171  
Sequence 2171, Application US/60453135  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001456  
CURRENT APPLICATION NUMBER: US/60/453,135  
CURRENT FILING DATE: 2003-03-10  
NUMBER OF SEQ ID NOS: 82762  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2171  
LENGTH: 5080  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-453-135-2171

Query Match 13.5%; Score 46.8; DB 102; Length 5080;  
Best Local Similarity 88.1%; Pred. No. 0.0054;  
Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAT--AGAACCTTCGGATCTACGACACTGAGGCTC-TCGTGGCT 102  
DB 3568 TAACTTAATGAATGAAGTCTTCGACTCTACGACACTGAGGCTCTTCGTGGCT 3627  
QY 103 GTCCCACTTGAAGATGAAGT 126  
DB 3628 GTCCCACTTGAAGATGAAGT 3651

RESULT 14  
US-60-466-412-2171  
Sequence 2171, Application US/60466412  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001466  
CURRENT APPLICATION NUMBER: US/60/466,412  
CURRENT FILING DATE: 2003-04-30  
NUMBER OF SEQ ID NOS: 429241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2171  
LENGTH: 5080  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-466-412-2171

Query Match 13.5%; Score 46.8; DB 103; Length 5080;  
 Best Local Similarity 88.1%; Pred. No. 0.0054;  
 Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAAT--AGAACCTTCCGATCTACGAGCACTGAGGCTC-TCGTGCGCT 102  
 DB 3568 TAACTTAATGAAATGAGTCTTCCGACTCTACGAGCACTGAGGCTCTTCGTGCGCT 3627

QY 103 GTCCAGTTTGAAGATGAAGT 126  
 DB 3628 GTCCAGTTTGAAGATGAAGT 3651

## RESULT 15

US-10-219-051B-910  
 ; Sequence 910, Application US/10219051B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
 ; APPLICANT: Hoospital / Bayer AG  
 ; TITLE OF INVENTION: Nucleotide sequences involved in pain  
 ; FILE REFERENCE: Lea 35693 Foreign Countries  
 ; CURRENT FILING DATE: 2003-05-09  
 ; PRIOR APPLICATION NUMBER: US/10/219,051B  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/346,382  
 ; PRIOR FILING DATE: 2001-11-01  
 ; PRIOR APPLICATION NUMBER: US 60/333,347  
 ; PRIOR FILING DATE: 2001-11-26  
 ; NUMBER OF SEQ ID NOS: 14715  
 ; SOFTWARE: Perl script  
 ; SEQ ID NO 910  
 ; LENGTH: 5728  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(5728)  
 ; OTHER INFORMATION: n=a, c, g or t  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: EMBL / AF150882  
 ; DATABASE ENTRY DATE: 2000-01-16  
 ; US-10-219-051B-910

Query Match 13.5%; Score 46.8; DB 47; Length 5728;  
 Best Local Similarity 88.1%; Pred. No. 0.0057;  
 Matches 74; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 46 TAACTTAATGAAAT--AGAACCTTCCGATCTACGAGCACTGAGGCTC-TCGTGCGCT 102  
 DB 3613 TAACTTAATGAAATGAGTCTTCCGACTCTACGAGCACTGAGGCTCTTCGTGCGCT 3672

QY 103 GTCCAGTTTGAAGATGAAGT 126  
 DB 3673 GTCCAGTTTGAAGATGAAGT 3696

Search completed: March 23, 2004, 04:00:14  
 Job time : 2619.4 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: March 22, 2004, 16:13:34 ; Search time 438.472 Seconds  
(without alignments)  
414.412 Million cell updates/sec

Title: US-09-646-224A-12

Perfect score: 346 US-09-646-224A-12

Sequence: 1 ttagaattccgaattcaacc.....gagctgtagcgaagaattc 346

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1155024 seqs, 262583689 residues

Total number of hits satisfying chosen parameters: 2310048

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Pending Patents NA New:  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34.8	10.1	659	US-10-474-495-208	Sequence 208, App
C 2	33.8	9.8	62555	US-60-548-091-5623	Sequence 5623, Ap
C 3	33	9.5	732	US-10-767-701-1073	Sequence 1073, Ap
C 4	31.2	9.0	304123	US-10-796-280-12363	Sequence 12363, A
C 5	31	9.0	149000	US-60-548-091-5666	Sequence 5666, Ap
C 6	30.8	8.9	1647	US-10-767-701-12785	Sequence 12785, A
C 7	30.8	8.9	21872	US-10-796-280-12516	Sequence 12516, A
C 8	30.6	8.8	1126118	US-10-767-471-10615	Sequence 10615, A
C 9	30.6	8.8	1126118	US-10-796-280-12479	Sequence 12479, A
C 10	30.4	8.8	8517	US-10-021-698A-760	Sequence 760, App
C 11	30.2	8.7	663098	US-10-796-280-12289	Sequence 12289, A
C 12	29.8	8.6	175737	US-10-783-271-34	Sequence 34, Appl
C 13	29.2	8.4	726	US-10-767-701-4116	Sequence 4116, Ap
C 14	29.2	8.4	7684	US-10-100-683-11693	Sequence 11693, A
C 15	29.2	8.4	104403	US-10-796-280-12430	Sequence 12430, A
C 16	29.2	8.4	380963	US-10-765-790-5	Sequence 5, Appl
C 17	29.2	8.4	383432	US-10-765-790-34	Sequence 34, Appl
C 18	29.2	8.4	803755	US-10-767-471-10700	Sequence 10700, A
C 19	29	8.4	487	US-10-778-543-20049	Sequence 20049, A
C 20	29	8.4	558	US-10-779-543-21989	Sequence 21989, A
C 21	29	8.4	572	US-10-779-543-21706	Sequence 21706, A
C 22	29	8.4	435302	US-10-767-471-10552	Sequence 10552, A
C 23	28.8	8.3	1116	US-10-767-795-927	Sequence 927, App
C 24	28.8	8.3	1117	US-10-767-701-6319	Sequence 6319, Ap
C 25	28.8	8.3	13578	US-10-767-471-10563	Sequence 10563, A
C 26	28.8	8.3	24990	US-10-767-471-10903	Sequence 10903, A

C 27	28.6	8.3	600	US-60-545-213-2438	Sequence 2438, Ap
C 28	28.6	8.3	600	US-60-545-213-6710	Sequence 6710, Ap
C 29	28.6	8.3	91000	PCT-US03-35876-1	Sequence 1, Appl
C 30	28.6	8.3	183334	US-10-796-280-12260	Sequence 12260, A
C 31	28.4	8.2	631	US-10-767-701-24323	Sequence 24323, A
C 32	28.2	8.2	1232	US-10-767-701-14040	Sequence 14040, A
C 33	28.2	8.2	27227	US-10-796-280-12482	Sequence 12482, A
C 34	28.2	8.2	261922	US-10-767-471-10653	Sequence 10653, A
C 35	28.2	8.2	261922	US-10-796-280-12284	Sequence 12284, A
C 36	28.2	8.2	444922	US-60-550-051-3005	Sequence 3005, Ap
C 37	28.2	8.2	645179	US-10-796-280-12317	Sequence 12317, A
C 38	28	8.1	201	US-60-548-091-12015	Sequence 12015, A
C 39	28	8.1	76064	US-60-548-091-5566	Sequence 5566, Ap
C 40	28	8.1	91571	US-10-796-280-12166	Sequence 12166, A
C 41	28	8.1	228854	US-60-548-091-5633	Sequence 5633, Ap
C 42	28	8.1	309849	US-60-550-051-2977	Sequence 2977, Ap
C 43	28	8.1	361121	US-60-550-051-2997	Sequence 2997, Ap
C 44	28	8.1	388939	US-10-417-375A-4	Sequence 4, Appl
C 45	28	8.1	519599	US-10-765-790-73	Sequence 73, Appl

## ALIGNMENTS

RESULT 1  
US-10-474-495-208/c  
; Sequence 208, Application US/10474495  
; GENERAL INFORMATION:  
; APPLICANT: YOSHIKAWA, Yoshie et al.  
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES  
; FILE REFERENCE: 1422-0606P  
; CURRENT APPLICATION NUMBER: US/10/474,495  
; PRIOR FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: JP 2001-112039  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: JP 2001-290193  
; PRIOR FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 264  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 208  
; LENGTH: 659  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: 6, 648  
; OTHER INFORMATION: n is a or c or g or t.  
US-10-474-495-208  
  
Query Match 10.1%; Score 34.8; DB 6; Length 659;  
Best Local Similarity 53.7%; Pred. No. 0.045;  
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
  
QY 199 TGAGATTCTTAATTCAGAGCTTTCTGGTTACTTACAGAGCTGCCAGTCTTA 258  
DB 162 TGGAGCTAACCTTAATGAGACAGCTTCTTCTGCTGAATGCTTCTTAAGCTGA 103  
QY 259 GAATTGAGGGGTAGAGAAAGCTTAATATCTTCAACCTTAAGAGCTTCTGTGACA 318  
DB 102 AACCTGACAGGCTTAGAGAAAGAGAGAGCTGCTGCTCCATTCATCTTCATACCA 43  
QY 319 GCCAAGTGAAGCTG 332  
DB 42 ACCAGATGACATG 29  
  
RESULT 2  
US-60-548-091-5623/c  
; Sequence 5623, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARDILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF

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/ FILE REFERENCE: CL001506
/ CURRENT APPLICATION NUMBER: US/60/548,091
/ CURRENT FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 24433
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 5623
/ LENGTH: 62555
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-548-091-5623

Query Match          9.8%; Score 33.8; DB 7; Length 62555;
Best Local Similarity 62.4%; Pred. No. 0.93;
Matches 53; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 80 AGCACTGAGGCTCTGTCGCGCTGCCAGTTTGAAGAGATGATGATTCATTCGACAGA 139
DB 22481 AGCACTGATGCCGCTGAGAGACAGCTCCATGTGAAGAAATGACAGTCTGTTCTTGT 22422
QY 140 GAATGGGTAGAAGTTCAGTTACAG 164
DB 22421 GCTGGGAAACAAGACAGAAACAG 22397

RESULT 3
US-10-767-701-1073
/ Sequence 1073, Application US/10767701
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(5353)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 1073
/ LENGTH: 732
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS14784_1
US-10-767-701-1073

Query Match          9.5%; Score 33; DB 6; Length 732;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 81 GCACGTGAGGCTCTGTCGCGCTGCCAGTTTGAAGAGATGATGATTCATTCGACAGA 140
DB 129 GTAAAGAGTCATTTGCTGAGCCACCGAGATGAGCAATGAAAGTATTATCATCAAAAG 188
QY 141 AATGGGTAGAAGTTCAGTTACAGAAAGGTGAGAA 177
DB 189 AATGTTTGGACGATGAGACAGTGAAGATCAAA 225

RESULT 4
US-10-796-280-12363
/ Sequence 12363, Application US/10796280
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001510
/ CURRENT APPLICATION NUMBER: US/10/796,280
/ CURRENT FILING DATE: 2004-03-10
/ NUMBER OF SEQ ID NOS: 68533
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 12363
/ LENGTH: 304123
/ TYPE: DNA
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/ ORGANISM: Homo sapiens
US-10-796-280-12363

Query Match          9.0%; Score 31.2; DB 6; Length 304123;
Best Local Similarity 54.3%; Pred. No. 16;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 145 GGTAGAAGTTCAGTTACAGAGAAAGGTGAAACCAACCAAGTTCCTTTGGGCTGAGAT 204
DB 157318 GTGCAAGCTTCTGAAACAGACACGACCTGCAATTAACACCTCTGGGGGTGACAT 157377
QY 205 TTCCTTAATTGCCAAGCTTTTCCTGGGTAATTACCAAGCTGCCAGTGGCTTGA 260
DB 157378 TGCCGGGATTTGTAATCTTTTCATGTGTCAATTCACATGAACCAATCTGCTGAGA 157433

RESULT 5
US-60-548-091-5666
/ Sequence 5666, Application US/60548091
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001506
/ CURRENT APPLICATION NUMBER: US/60/548,091
/ CURRENT FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 24433
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 5666
/ LENGTH: 149000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-548-091-5666

Query Match          9.0%; Score 31; DB 7; Length 149000;
Best Local Similarity 51.0%; Pred. No. 13;
Matches 73; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 177 AGACCAAGTTCCTTTTGGGCTGAGATTCCTTAATTCGACGCTTCTGCGGTAC 236
DB 84316 ATAAAGAGGCTCTTAAGCTGCATCGCTTCAGTGCATTCGCTTTTGAGTGGCAG 84375
QY 237 TTACAGGCTGCCAGTCTTAGAATTTGAGGGGTAGAGAAAGCTTAATATCTTTC 296
DB 84376 TGCAATGCTTGAAGTTAATTTTCATTCGAAAGTTTTTGAAGACTAATCATATTG 84435
QY 297 TACCTAAAGCTTCTGTGACAG 319
DB 84436 CACATTAAGGACACAGACAG 84458

RESULT 6
US-10-767-701-12785
/ Sequence 12785, Application US/10767701
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(5353)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 12785
/ LENGTH: 1647
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS19950_1
US-10-767-701-12785

Query Match          8.9%; Score 30.8; DB 6; Length 1647;
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RESULT 8
US-10-767-471-10615/c
/ Sequence 10615, Application US/10767471
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001505
/ CURRENT APPLICATION NUMBER: US/10/767,471
/ CURRENT FILING DATE: 2004-01-30
/ NUMBER OF SEQ ID NOS: 50231
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 10615
/ LENGTH: 1126118
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) --(1126118)
/ OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-767-471-10615

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RESULT 10
US-10-021-698A-760/C
/ Sequence 760, Application US/10021698A
/ GENERAL INFORMATION:
/ APPLICANT: KEITH, TIM
/ APPLICANT: LITTLE, RANDALL
/ APPLICANT: VAN EERDEMEGH, PAUL
/ APPLICANT: DUPUIS, JOSEB
/ APPLICANT: DEL MASTRO, RICHARD
/ APPLICANT: SIMON, JASON
/ APPLICANT: ALLEN, KRISTINA
/ APPLICANT: PANUIT, SUNDI
/ TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO
/ TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
/ FILE REFERENCE: 2976-404US1
/ CURRENT APPLICATION NUMBER: US/10/021, 698A
/ CURRENT FILING DATE: 2001-10-22

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PRIOR APPLICATION NUMBER: 60/211,749  
PRIOR FILING DATE: 2000-06-14  
NUMBER OF SEQ ID NOS: 6160  
SOFTWARE: PatentIn 2.1  
SEQ ID NO 760  
LENGTH: 8517  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-021-698A-760

Query Match  
Best Local Similarity 55.8%; Pred. No. 5.2;  
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 220 AGCTTTCTGGGTACTTACCAAGCTGCGCCAGTGTGAGATTTGAGGGTGAAGAAA 279  
DB 1226 ACCCTTTATGCTGGAAATACATCAACCAAGAACTTCCCTTTGACTTAACATTA 1167  
QY 280 GCGTAAGATATCTTCTACCTTAAAGCTTGTGACAGCCAA 323  
DB 1166 GCCAGAGATTCACCTTTAAATTAACCTTTGTGCAAAAGAAA 1123

RESULT 11  
US-10-796-280-12289  
Sequence 12289, Application US/10796280  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001510  
CURRENT APPLICATION NUMBER: US/10/796,280  
CURRENT FILING DATE: 2004-03-10  
NUMBER OF SEQ ID NOS: 6853  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12289  
LENGTH: 663098  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(663098)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-796-280-12289

Query Match  
Best Local Similarity 58.2%; Pred. No. 50;  
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 125 GTACATTCGCAAGAAATGGGTAGAGTTCAGTTAAGAGAAAGTGAAGAACCAAC 184  
DB 639246 GGACTCCCTGGAGAAAGTATGTCTGAGTCCCTTTGAGGAAAGATTAAAGTTAAAC 639305

QY 185 AGTTCTTTTGGGCTGAGATTTCTTAAAT 215  
DB 639306 GATTAGTTCAGTGTGATGATGATTAAC 639336

RESULT 12  
US-10-783-271-34/C  
Sequence 34, Application US/10783271  
GENERAL INFORMATION:  
APPLICANT: Veridex, LLC  
APPLICANT: Wang, Yixin  
TITLE OF INVENTION: BREAST CANCER PROGNOSTICS  
FILE REFERENCE: VDX-5003 USNP  
CURRENT APPLICATION NUMBER: US/10/783,271  
CURRENT FILING DATE: 2004-02-20  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34  
LENGTH: 175737  
TYPE: DNA

ORGANISM: human  
US-10-783-271-34

Query Match  
Best Local Similarity 58.4%; Pred. No. 37;  
Matches 52; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 224 TTTCCTGGGTACTTACCAAGCTGCGCCAGTGTGAGATTTGAGGGTGAAGAAAGCT 283  
DB 162670 TGTGCTAGATTTGCTGCGCATTAACGCGCCATGCTAAGACATTTACCCCTAGCAAAATGGCT 162611

QY 284 AAGATATCTTTTACCTTAAAGCTTCT 312  
DB 162610 CTGTTACTTCCGAACCTTAATCCCT 162582

RESULT 13  
US-10-767-701-4116/C  
Sequence 4116, Application US/10767701  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Tongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(5353)B  
CURRENT APPLICATION NUMBER: US/10/767,701  
CURRENT FILING DATE: 2004-01-29  
NUMBER OF SEQ ID NOS: 63128  
SEQ ID NO 4116  
LENGTH: 726  
TYPE: DNA  
ORGANISM: Sorghum bicolor  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(726)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: SORBI-28WAY03-CLUS71888\_1  
US-10-767-701-4116

Query Match  
Best Local Similarity 50.0%; Pred. No. 4;  
Matches 73; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 90 CCTTCGCGCGTGTCCAGTTTGAAGATGAGTACATTTCCAAAGATGGTAG 149  
DB 582 CCTCCATGCTGGTTCCAAATGAGAGAGTGAAGCTTACATACGCAATTAAGTTTGG 523

QY 150 AAGTCAGTTAAGAGAAAGTGAAGCAACAGTTCTTTTGGCTGAGATTTCT 209  
DB 522 CAGGTTCTTTCAGAGATGAGATTAATTAATGAGATCACTGTCTTTGAGATGTAT 463

QY 210 TAAATGCCAAGCTTTCTGAGTTA 235  
DB 462 TGATTTGAAAACCTTTCTGTGTGTA 437

RESULT 14  
US-10-100-683-11693  
Sequence 11693, Application US/10100683  
GENERAL INFORMATION:  
APPLICANT: Rosen, et al.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS900  
CURRENT APPLICATION NUMBER: US/10/100,683  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US 60/040,162  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: US 60/043,576  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: US 60/047,601  
PRIOR FILING DATE: 1997-05-23



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 2030.07 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-12

Sequence: 346  
1 ttagaattccgaattacc.....gagcttgcgaagaattcc 346

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

EST:\*

1: em\_estba:\*  
2: em\_estbun:\*  
3: em\_estcin:\*  
4: em\_estcun:\*  
5: em\_estcov:\*  
6: em\_estdpl:\*  
7: em\_estcro:\*  
8: em\_estc1:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241.4	69.8	658	29	AG128206 Pan trogl
2	108.2	31.3	496	28	AG0605323 HS 2119 B
3	83.2	24.0	385	28	AO876800 HS_2114_B
4	46.8	13.5	4614	29	AY404475 Homo sapi

Result No.	Score	Query Match	Length	ID	Description
5	39.2	11.3	3772	29	AY404476 Pan trogl
6	37.8	10.9	817	28	CC124756 NDL 70A13
7	37.6	10.9	569	28	AQ487752 RCEI-11-2
8	36.8	10.6	363	12	BU255463 BU255463
9	36.8	10.6	395	12	BU220478 BU220478
10	36.8	10.6	405	14	CA629583 w1eln.pko
11	36.8	10.6	427	14	CA642524 w1eln.pko
12	36.8	10.6	435	12	BU240877 BU240877
13	36.8	10.6	448	28	AQ931925 RCEI-23-2
14	36.8	10.6	452	14	CA683546 w1m96.pko
15	36.8	10.6	455	14	BE443872 WHE1124_E
16	36.8	10.6	467	12	BU235660 BU235660
17	36.8	10.6	466	14	CD916884 G608.103F
18	36.8	10.6	565	14	CD917696 G608.106F
19	36.8	10.6	573	12	BU284707 BU284707
20	36.8	10.6	573	14	CD880790 F1.075014
21	36.8	10.6	596	14	CD919301 G608.1120
22	36.8	10.6	624	13	BO237410 TAE050178
23	36.8	10.6	625	14	CA730068 w1d1c.pko
24	36.8	10.6	630	29	CC770951 CH240.6A9
25	36.8	10.6	650	12	BU219937 BU219937
26	36.8	10.6	687	14	CD452535 WHE1110_B
27	36.8	10.6	697	12	BU265353 BU265353
28	36.8	10.6	715	14	CD917423 G608.105E
29	36.8	10.6	774	13	BO802652 WHE2828_D
30	36.8	10.6	886	14	CK154639 FGA030334
31	36.8	10.6	1101	29	CNS00852 AL052363 Drosoph11
32	36.8	10.6	583	10	BF648975 NP05404E
33	36.6	10.6	831	14	CB894180 EST646972
34	36.6	10.6	1107	28	CC190579 CH261-152
35	36.6	10.4	590	28	AZ441646 IM0233P11
36	35.8	10.3	258	10	BB328002 BB328002
37	35.8	10.3	498	14	H76844 H76844
38	35.8	10.3	700	9	AV782699 AV782699
39	35.8	10.3	851	12	BI830346 603073082
40	35.8	10.3	4556	29	AY404477 RICE muscu
41	35.6	10.3	386	14	D46977 RICE11978A
42	35.6	10.3	451	13	C74678 C74678
43	35.6	10.3	1033	28	CC232410 CH261-48N
44	35.4	10.2	646	12	BU238970 BU238970
45	35.2	10.2	812	14	CF410545 CH3#067_G

#### ALIGNMENTS

RESULT 1  
AG128206/c 658 bp DNA linear GSS 04-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-139E19.R, genomic survey sequence.  
DEFINITION AG128206  
ACCESSION AG128206.1 GI:16657371  
VERSION  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 658)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan 1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of

clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. 658  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-139E19.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC library"

ORIGIN  
Query Match 69.8%; Score 241.4; DB 29; Length 658;  
Best Local Similarity 95.6%; Pred. No. 1.1e-66;  
Matches 259; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 67 TTCGAGATCTACGACGCTGAGGCTTC-TGTCGCTGTCCAGTTTGAGGAATGAGC 125  
DB TCCGAGGCTCTACGACGCTGAGGCTTCGTGCGCTGTGCGAGTTGGAAGATGAGA 440  
QY 126 TCACATTCGACAAAGAAATGGGTGAAGTTCAGTTAAAGAGAAAGGTGAAGACCAACA 185  
DB TACATTCGACAAAGAAATGGGTGAAGTTCAGTTAAAGAGAAAGGTGAAGACCAACA 380  
QY 186 GTTCTTTTGGGCTGAGATTTCTTAAATTGGCCAAAGCTTTTCTGGGTTACTTACCAAGC 245  
DB GTTCTTTTGGGCTGAGATTTCTTAAATTGGCCAAAGCTTTTCTGGGTTACTTACCAAGC 320  
QY 246 TGCCAGATGCTTGAATTTGAGGGGTGAAGAAAGCTTAAGATATCTTTCTACCTTAA 305  
DB TCACACAGTCTTGAATTTGAGGAGTGAAGAAAGCTTAAGATATCTTTCTACCTTAA 260  
QY 306 AGCTTCTGTGACAGCCAAAGATGAGCTGTAGC 336  
DB AGCTTCTGTGACAGCCAAAGATGAGCTGTAGC 229

RESULT 2  
LOCUS A0605323 496 bp DNA linear GSS 10-JUN-1999  
DEFINITION HS\_2119\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2119 Col=5 Row=N, genomic survey sequence.  
ACCESSION A0605323  
VERSION A0605323.1 GI:5065317  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 496)  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
JOURNAL CONTACT: Mahairas GG, Wallace JC, Hood L  
MEDLINE 10449764  
PUBMED 99380589  
COMMENT High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 2119 row: N column: 5  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 496.  
Location/Qualifiers  
1. 496  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2119 Col=5 Row=N"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN  
Query Match 31.3%; Score 108.2; DB 28; Length 496;  
Best Local Similarity 97.3%; Pred. No. 1.1e-23;  
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 TTTCCTGGCTTACTTACGAGCTGCGCCAGTGTGAATTTGAGGCGTGAAGAAAGCT 283  
DB TTTCCTGGCTTACTTACGAGCTGCGCCAGTGTGAATTTGAGGCGTGAAGAAAGCT 61  
QY 284 AAGATATCTTTTACCTTAAAGCTTGTGACAGCCAAAGATGAGCTGTAGC 336  
DB AAGATATCTTTTACCTTAAAGCTTGTGACAGCCAAAGATGAGCTGTAGC 114

RESULT 3  
LOCUS A0876800 385 bp DNA linear GSS 09-NOV-1999  
DEFINITION HS\_2114\_B2\_G08\_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2114 Col=16 Row=N, genomic survey sequence.  
ACCESSION A0876800  
VERSION A0876800.1 GI:6308280  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 385)  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
JOURNAL CONTACT: Mahairas GG, Wallace JC, Hood L  
MEDLINE 10449764  
PUBMED 99380589  
COMMENT High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 2114 row: N column: 16  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 385.  
Location/Qualifiers  
1. 385  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2114 Col=16 Row=N"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"

Department of Eukaryotic Genomics  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: entae@ligr.org  
Library was provided by David Severson  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
Source

Location/Qualifiers  
1..817  
/organism="Aedes aegypti"  
/mol\_type="genomic DNA"  
/strain="liverpool"  
/db\_xref="taxon:7159"  
/clone="NHL-70A13"  
/clone\_lib="Notre Dame Liverpool"  
/note="Vector: pECBAC1, Site\_1: Hind III, The library was prepared from whole body tissue of newly hatched 1d larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 10.9%; Score 37.8; DB 28; Length 817;  
Best Local Similarity 55.8%; Pred. No. 0.74;  
Matches 72; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 16 TAACCGTGTAGAGAAATCCTGATCCTTAACCTTATGGAATGAAACCTCCGATC 75  
DB 496 TGACCTGGACCTGTAATCCAGTACGCTCGAATCTGATGATGGTGGCCGCTTGGAAC 437  
OY 76 TACGAGCACTAGAGCGCTCGTGCCTGCCAGTTTGAAGATGAAAGTACATCTGCG 135  
DB 436 GAAGAAATACCAACCGCTGTGATGAGATATCTTGTTGTTGATGAGAAACACTCGG 377  
OY 136 AGAAGATG 144  
DB 376 AAAAGAGG 368

RESULT 7  
AQ487752/c 569 bp DNA linear GSS 24-APR-1999  
LOCUS  
DEFINITION  
RPCI-11-262E15.TU RPCI-11 Homo sapiens genomic clone  
ACCESSION  
AQ487752  
VERSION  
AQ487752.1 GI:4673626  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 569)  
Zhao,S., Adams,W.D., Nieman,W., Malek,J., de Jong,P. and  
Venter,J.C.  
Title  
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building (1997)  
Unpublished (1997)  
Other GSSes: RPCI-11-262E15.TV  
Contact: Shaying Zhao, William Nieman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@ligr.org

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Piere de Jong  
(piere@ligr.med.bufo.edu). Clones may be purchased from  
BACRAC Resources (http://bacpac.med.bufo.edu/ordering) or from  
Research Genet cs (http://resgen.com). BAC end search page:  
http://www.ligr.org/cdb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers

FEATURES

source

1..569  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="GDB:7600334"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-262E15"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPCI-11"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
RPCI11 Human Male BAC library"

ORIGIN

Query Match 10.9%; Score 37.6; DB 28; Length 569;  
Best Local Similarity 57.8%; Pred. No. 0.75;  
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 138 AAGATGGGTAGAGATTGACGTTAAGAGAAAGGTGAAAGCAACAGTTCTTTGGG 197  
DB 263 AAGAAAGCTTGAAGGTTTATTAATGATGATGATCAAAACAAATTTCTTCATGA 204  
OY 198 CTGAGATTCTTAAATTCGCAAGCTTTCTCGGTACTTACAGCGCTGCCAGT 253  
DB 203 CTGATGGTTGTTCAAAATATCCAGCATTTGATCCCTTAGTACTTCTGACCAAT 148

RESULT 8  
BUT55463 363 bp mRNA linear EST 17-SEP-2002  
LOCUS  
DEFINITION  
BUT55463 Y. Ogihara unpublished cDNA library, wh\_f Triticum  
aestivum cDNA clone wh23n18 3', mRNA sequence.  
ACCESSION  
BUT55463  
VERSION  
BUT55463.1 GI:23089032  
KEYWORDS  
EST.  
SOURCE  
Triticum aestivum (bread wheat)  
ORGANISM  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 363)  
Ogihara,Y. and Murai,K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tehin@genes.nig.ac.jp.

FEATURES  
Source

Location/Qualifiers  
1..363  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="wh23n18"  
/tissue\_type="spike at flowering date"  
/dev\_stage="feekes" scale 10.5.1"  
/clone\_lib="Y. Ogihara unpublished cDNA library, wh\_f"

ORIGIN

Query Match 10.6%; Score 36.8; DB 12; Length 363;  
Best Local Similarity 59.6%; Pred. No. 1.1;  
Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 89 GCCTCTGCGCGCTGCTCCAGTTTGAAGAAATGAGTACATTTGCAAGAAATGGGTA 148  
DB 2 GCATGTGCTGACATCTTTATGATGAGGGGCAATGACATTTCCAAAGAGGCGATGATA 61  
OY 149 GAAGTTCAAGTTAAGAGAGAAAGGTGAAAGCAACCAAGTTCTTT 192  
DB 62 GAAGTACACTTAATTTACAGGGGAAAGCAACCAACTGAGTTT 105



RESULT 9	
LOCUS	BJ220478
DEFINITION	BJ220478 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
ACCESSION	CJ220478
VERSION	BJ220478
KEYWORDS	EST.
SOURCE	BJ220478.1 GI:23073310
ORGANISM	Triticum aestivum (bread wheat)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 395) Ogihara, Y. and Murai, K. Expressed genes in Triticum aestivum Unpublished (2002) Contact: Tadasu Shin-1 Center For Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp. Location/Qualifiers 1..395 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="wh2oe23" /tissue.type="spike at meiosis" /dev stage="Peekes" scale 9" /clone_idb="Y. Ogihara unpublished cDNA library, wh"
FEATURES	
source	
Query Match	10.6%; Score 36.8; DB 12; Length 395;
Best Local Similarity	54.6%; Pred. No. 1.2;
Matches	71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
OY	63 AACCTCCGGAATCTGCAGACATGAGCGCTCTCGGCGCCTGCCAGTTTGAGAAGTA 122
DB	3 AAGAGTCAGCTAAACAGAGCACAGCATCTGCTGCACTGTGTAGTAGGGGACATGA 62
OY	123 AGTACATTCTGCAGAGAAATGGGTAGAGTTCACTTAACAAGAGAGTAAGCA 182
DB	63 CACTTCTTCCAACAGACGGCATGATGATAGTACACTTAATTACAGGGGAAGAACCA 122
OY	183 ACAGTTCTTT 192
DB	123 ATTGAGTTT 132
RESULT 10	
LOCUS	CA629583
DEFINITION	wleln.pk0019.g6 wleln Triticum aestivum cDNA clone wleln.pk0019.g6
ACCESSION	CA629583
VERSION	CA629583
KEYWORDS	EST.
SOURCE	CA629583.1 GI:25207879
ORGANISM	Triticum aestivum (bread wheat)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 405) Timney, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K. Dufent Wheat cDNA Sequence Unpublished (2002)
TITLE	
JOURNAL	

```

COMMENT
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com

FEATURES
source
Location/Qualifiers
1..405
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wleln.pk0019.g6"
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/notes="Vector: pBluescript SK+, Site 1: EcoRI, Site 2:
XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
etiolated seedling (normalized)"

ORIGIN
Query Match 10.6%; Score 36.8; DB 14; Length 405;
Best Local Similarity 59.6%; Pred. No. 1.2;
Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Oy 89 GCCTTCGTGCGCTGTCCAGATTGAAGATGAGTACTTTCGACGAGAAATGGTA 148
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 45 GCATCTCTGTCACACTGTGTAGTTGGGGGCGATGACACTTCTTCCACAGACGGCATGATA 104
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 149 GAATTCAGTTAAACAGAGAAAGGGAAGCAACAGTCTTT 192
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 105 GTAGTACACTTAATTATTCAGGGGAGAACACCACTGAGTTT 148
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
LOCUS CA642524 427 bp mRNA linear EST 23-NOV-2002
DEFINITION wleln.pk0058.b8 wleln Triticum aestivum cDNA clone wleln.pk0058.b8
5' end, mRNA sequence.
ACCESSION CA642524
VERSION CA642524.1 GI:25220820
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 427)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
Dupont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
1..427
/organism="Triticum aestivum"
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/db_xref="taxon:4565"
/clone="wleln.pk0058.b8"
/tissue_type="root"
/clone_id="wleln"
/notes="Vector: pBluescript SK+, Site 1: EcoRI, Site 2:
XhoI; Wheat (Triticum aestivum L.) root, normalized
wlel library"

ORIGIN

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Query Match 10.6%; Score 36.8; DB 14; Length 427;  
 Best Local Similarity 59.6%; Pred. No. 1.2; Mismatches 42; Indels 0; Gaps 0;  
 Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 89 GCCTCTCGTGGCTGTCCAGTTTGAAGAAATGAAGTACATTTGCGAAGAAATGGGTA 148  
 DB 360 GCATCTGCTGCACTGTGTAGTTAGGGGCGCATGACATCTTCCAAACAGACGCGATGATA 301

QY 149 GAAGTTCAGTTAACAGAGAAGGTGGAAGACCAACAGTTCCTT 192  
 DB 300 GTAGTACACTTAATTATTAACAGGGAAGAACCAACCACTAGTTT 257

RESULT 12  
 LOCUS BJ240877 435 bp mRNA linear EST 17-SEP-2002  
 DEFINITION BJ240877 Y. Ogihara unpublished cDNA library, wh\_e Triticum aestivum cDNA clone whel108 3', mRNA sequence.  
 ACCESSION BJ240877  
 VERSION BJ240877.1 GI:23083160  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 435)  
 Ogihara, Y. and Murai, K.  
 Expressed genes in Triticum aestivum  
 Unpublished (2002)  
 Contact: Tadao Shin-1  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp.  
 Location/Qualifiers  
 source 1..435  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="whel108"  
 /tissue\_type="seed, DPA10"  
 /dev\_stage="Fekkes" scale 11.2"  
 /clone\_lib="Y. Ogihara unpublished cDNA library, wh\_e"

ORIGIN  
 Query Match 10.6%; Score 36.8; DB 12; Length 435;  
 Best Local Similarity 59.6%; Pred. No. 1.2; Mismatches 42; Indels 0; Gaps 0;  
 Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 89 GCCTCTCGTGGCTGTCCAGTTTGAAGAAATGAAGTACATTTGCGAAGAAATGGGTA 148  
 DB 50 GCATCTGCTGCACTGTGTAGTTAGGGGCGCATGACATCTTCCAAACAGACGCGATGATA 109

QY 149 GAAGTTCAGTTAACAGAGAAGGTGGAAGACCAACAGTTCCTT 192  
 DB 110 GTAGTACACTTAATTATTAACAGGGAAGAACCAACCACTAGTTT 153

RESULT 13  
 LOCUS AO931925 448 bp DNA linear GSS 21-DEC-1999  
 DEFINITION RPCI-23-282F23.TU RPCI-23 Mus musculus genomic clone  
 ACCESSION AO931925  
 VERSION AO931925.1 GI:6620939  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 448)  
 Zhao, S., Niernan, W., Feldblum, T., Malek, D., Shatsman, S., Akintest, B., Levins, M., Mogann, S., Tesgeye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.K.  
 Mouse BAC End Sequences from Library RPCI-23  
 Unpublished (1999)  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org, med.bufileo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tcb/bac\_ends/mouse/bac\_end\_intro.html  
 Plate: 282 row: F column: 23  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 source 1..448  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-282F23"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1: EcoRI, Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN  
 Query Match 10.6%; Score 36.8; DB 28; Length 448;  
 Best Local Similarity 66.2%; Pred. No. 1.2; Mismatches 53; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 126 TACATTCGCGAAGATGGGTAGAGTTCAGTTAACAGAGAAGGTGGAAGACCAACA 185  
 DB 169 TAGTATTTGGAATGAAATGAACTTCAAAATCCGGCAAGATGAAGTGAAGACCAACA 110

QY 186 GTTCTTTTGGGCTGAGATT 205  
 DB 109 GAATCTGTGAATGTCAATT 90

RESULT 14  
 LOCUS CA683546 452 bp mRNA linear EST 25-NOV-2002  
 DEFINITION wlm96.pk0018.a12 wlm96 Triticum aestivum cDNA clone  
 ACCESSION CA683546  
 VERSION CA683546.1 GI:25269571  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 452)  
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hatney, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, W.K.  
 Dupont Wheat cDNA Sequence  
 Unpublished (2002)

## COMMENT

Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13

## FEATURES

## Source

Location/Qualifiers  
1. .452  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Strepens"  
/db\_xref="taxon:4565"  
/clone="wlm96.pk0018.a12"  
/tissue\_type="leaf"  
/clone\_id="wlm96"  
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after inoculation w/ E. graminis"

## ORIGIN

Query Match 10.6%; Score 36.8; DB 14; Length 452;  
Best Local Similarity 59.6%; Pred. No. 1.2;  
Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 89 GCCTTCGTGCGCTGTCCTCCAGTTGAAGAAAGTACATTCTGCAGAAAGTGGTA 148  
379 GCATCTGCTGCACGTGTGATGTTAGGGGGCATGACACTTCTCCACAGACGGCATGATA 320  
DB 149 GAAGTTGAGTTAACAGAGAAAGTGGAAAGCCCAACAGTTCTTT 192  
QY 319 GTAGTACACTTAATTTCACAGGGGAAACCAACCACTGAGTTT 276

RESULT 15  
BE443872/c 455 bp mRNA linear EST 25-JUL-2000  
LOCUS  
DEFINITION  
Library Triticum aestivum cDNA clone WHE1124\_E10\_J20, mRNA  
sequence.  
BE443872  
BE443872.1 GI:9443412

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Triticum aestivum (bread wheat)

REFERENCE  
AUTHORS  
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.  
The structure and function of the expressed portion of the wheat genomes Normalized root cDNA library

TITLE  
Unpublished (2000)

## JOURNAL

COMMENT  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

Email: oanderson@pw.usda.gov  
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20  
Seq primer: Stragene SK primer.

## FEATURES

## Source

Location/Qualifiers  
1. .455  
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/clone="WHE1124\_E10\_J20"

## ORIGIN

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Best Local Similarity 59.6%; Pred. No. 1.2;  
Matches 62; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 89 GCCTTCGTGCGCTGTCCTCCAGTTGAAGAAAGTACATTCTGCAGAAAGTGGTA 148  
398 GCATCTGCTGCACGTGTGATGTTAGGGGGCATGACACTTCTCCACAGACGGCATGATA 339  
DB 149 GAAGTTGAGTTAACAGAGAAAGTGGAAAGCCCAACAGTTCTTT 192  
QY 338 GTAGTACACTTAATTTCACAGGGGAAACCAACCACTGAGTTT 295

Search completed: March 22, 2004, 23:12:35  
Job time : 2045.07 secs

/tissue\_type="Root"  
/dev\_stage="Five day old etiolated seedling"  
/lab\_host="E. coli DH10B"  
/clone\_id="wheat etiolated seedling root normalized cDNA library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and ceftotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 1186.12 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-13

Perfect score: 223  
Sequence: 1 gggcaccctaccatccatct.....aggaattccagagatctct 223

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: \*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_ov:\*
- 5: gb\_ov:\*
- 6: gb\_ov:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pl:\*
- 10: gb\_ro:\*
- 11: gb\_ro:\*
- 12: gb\_ro:\*
- 13: gb\_ro:\*
- 14: gb\_ro:\*
- 15: gb\_ro:\*
- 16: gb\_ro:\*
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- 34: gb\_ro:\*
- 35: gb\_ro:\*
- 36: gb\_ro:\*
- 37: gb\_ro:\*
- 38: gb\_ro:\*
- 39: gb\_ro:\*
- 40: gb\_ro:\*
- 41: gb\_ro:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	223	100.0	223	6	AX017229	AX017229 Sequence
2	223	100.0	223	6	BD138451	BD138451 Mammalian
3	123.8	55.5	167476	9	AC116038	AC116038 Homo sapi
4	107.8	48.3	856	6	E36123	E36123 Nucleic aci
5	107.8	48.3	3701	6	AR340648	AR340648 Sequence
6	107.8	48.3	3701	6	BD217793	BD217793 Regulatio
7	107.8	48.3	5728	6	BD012083	BD012083 Human bod
8	107.8	48.3	5728	6	BD082952	BD082952 Human bod
9	107.8	48.3	5728	6	AF150882	AF150882 Homo sapi
10	107.8	48.3	5860	6	AR340678	AR340678 Sequence
11	107.8	48.3	6237	9	AF188679	AF188679 Homo sapi
12	107.8	48.3	6528	6	BD012082	BD012082 Human bod
13	107.8	48.3	6528	6	BD082951	BD082951 Human bod
14	107.8	48.3	6528	6	AF109737	AF109737 Homo sapi
15	106.2	47.6	5419	9	HSAA17790	AJ417790 Homo sapi
16	89.2	40.0	241289	2	AC124662	AC124662 Mus muscu
17	83.6	37.5	5822	6	AR340647	AR340647 Sequence
18	83.6	37.5	5822	6	BD217792	BD217792 Regulatio
19	83.6	37.5	5858	10	AF118044	AF118044 Mus muscu
20	83.6	37.5	5921	10	AB031389	AB031389 Mus muscu
21	76.8	34.4	210800	2	AC127824	AC127824 Rattus no
22	76.8	34.4	243048	2	AC127215	AC127215 Rattus no
23	72.8	32.6	5334	6	E36125	E36125 Nucleic aci
24	72.8	32.6	5849	10	RN0237852	AJ237852 Rattus no
25	72.8	32.6	5875	6	AR340646	AR340646 Sequence
26	72.8	32.6	5875	6	BD217791	BD217791 Regulatio
27	72.8	32.6	5897	6	AX017217	AX017217 Sequence
28	72.8	32.6	5897	6	BD138440	BD138440 Mammalian
29	72.8	32.6	5905	10	AF059030	AF059030 Rattus no
30	72.8	32.6	5908	6	E36122	E36122 Nucleic aci
31	61	27.4	1466	5	AY204535	AY204535 Ictalurus
32	59.8	26.8	139245	2	AC137540	AC137540 Fells cat
33	59.8	26.8	142025	2	AC137541	AC137541 Fells cat
34	59.8	26.8	207679	2	BX511272	BX511272 Danilo rer
35	59.6	26.7	133311	2	AC134403	AC134403 Mus muscu
36	57.8	25.9	1466	5	AY204538	AY204538 Ictalurus
37	57.6	25.8	156655	2	AC144605	AC144605 Canis fam
38	57.2	25.7	150515	10	AL928726	AL928726 Mouse DNA
39	57.2	25.7	157981	2	AC144693	AC144693 Sus scrofa
40	56.6	25.4	112944	9	AC107082	AC107082 Homo sapi
41	56.6	25.4	112944	9	AC137587	AC137587 Homo sapi
42	56.6	25.4	169755	2	AP001199	AP001199 Homo sapi
43	56.6	25.4	171287	9	AP006241	AP006241 Homo sapi
44	56.6	25.4	171366	9	AC130303	AC130303 Homo sapi
45	56.4	25.3	8530	6	AX552195	AX552195 Sequence

## ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	bp	DNA	PAT	07-SEP-2000
AX017229	AX017229	Sequence 13 from Patent WO947670.	223	linear		
DEFINITION	AX017229	Sequence 13 from Patent WO947670.				
ACCESSION	AX017229	Sequence 13 from Patent WO947670.				
VERSION	AX017229.1	GI:10042149				
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE						
AUTHORS	1	Tate, S.N., Grose, D.T. and Hick, C.A.				
TITLE		Mammalian sodium channel proteins				
JOURNAL		Patent: WO 947670-A 13 23-SEP-1999;				

Pred. No. is the number of results predicted by chance to have a

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS (GB) ; HICK CAROLINE ANNE (GB)

## FEATURES

source

1..223  
/organism="Homo sapiens"  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6,4e-51;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCCCTACCCCATCTGTATGTTTCCCTTTGTTTGTTCATTAAGGTGTG 60  
DB 1 GGTGATCCCTACCCCATCTGTATGTTTCCCTTTGTTTGTTCATTAAGGTGTG 60

QY 61 GTCAATGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGTCTGCTCAT 120  
DB 61 GTCAATGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGTCTGCTCAT 120

QY 121 TTTCTGGCTCGTATTTTGTATCTGGAGTACTCTTTTCTCGAATAATTGGGAAA 180  
DB 121 TTTCTGGCTCGTATTTTGTATCTGGAGTACTCTTTTCTCGAATAATTGGGAAA 180

QY 181 TGCATTCAATGGAACAGACTTTTAGAATTTCAGGCAATTCCT 223  
DB 181 TGCATTCAATGGAACAGACTTTTAGAATTTCAGGCAATTCCT 223

RESULT 2  
LOCUS BD138451 223 bp DNA linear PAT 18-SEP-2002  
DEFINITION Mammalian sodium channel protein.  
ACCESSION BD138451  
VERSION BD138451.1 GI:23233396  
KEYWORDS JP 2002508941-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 223)  
AUTHORS Grose,D.T., Hick,C.A. and Tate,S.N.  
TITLE Mammalian sodium channel protein  
JOURNAL Patent: JP 2002508941-A 12 26-MAR-2002;  
COMMENT GLAXO GROUP LTD  
OS Homo sapiens (human)  
PN JP 2002508941-A/12  
PD 26-MAR-2002

PF 18-MAR-1999 JP 2000536853  
PI 18-MAR-1998 GB 9805793.8  
PR DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N15/09,A61K45/00,A61P17/04,A61P25/02,C07K14/705,C07K16/28, PC  
C12N1/15, PC  
PC C12N1/19,C12N1/21,C12N5/10,C12Q1/02,G01N33/15,G01N33/50,G01N33/ PC  
68, C12N15/00,C12N5/00  
CC Mammalian sodium channel protein  
FH Key Location/Qualifiers  
FT source 1..223  
FT Location/Qualifiers  
1..223  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 223; DB 6; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6,4e-51;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCCCTACCCCATCTGTATGTTTCCCTTTGTTTGTTCATTAAGGTGTG 60  
DB 1 GGTGATCCCTACCCCATCTGTATGTTTCCCTTTGTTTGTTCATTAAGGTGTG 60

QY 61 GTCAATGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGTCTGCTCAT 120  
DB 61 GTCAATGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGTCTGCTCAT 120

QY 121 TTTCTGGCTCGTATTTTGTATCTGGAGTACTCTTTTCTCGAATAATTGGGAAA 180  
DB 121 TTTCTGGCTCGTATTTTGTATCTGGAGTACTCTTTTCTCGAATAATTGGGAAA 180

QY 181 TGCATTCAATGGAACAGACTTTTAGAATTTCAGGCAATTCCT 223  
DB 181 TGCATTCAATGGAACAGACTTTTAGAATTTCAGGCAATTCCT 223

RESULT 3  
LOCUS AC116038/c 167476 bp DNA linear PRI 07-OCT-2003  
DEFINITION Homo sapiens chromosome 3 clone RP11-134J21, complete sequence.  
ACCESSION AC116038  
VERSION AC116038.3 GI:37537604  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Unpublished  
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
3 (bases 1 to 167476)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
4 (bases 1 to 167476)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
On Oct 7, 2003 this sequence version replaced gi:21622736.

COMMENT  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgchgs@u.washington.edu  
Project Information  
Center project name: chr-3  
Center clone name: RP11-134J21 (bc0780)  
----- Summary Statistics  
Sequencing vector: plasmid; 100% of reads  
Chemistry: Dye-terminator ET; 45% of reads  
Chemistry: Dye-terminator Big Dye; 55% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 167467 bases at least Q40  
Consensus quality: 167476 bases at least Q30  
Consensus quality: 167476 bases at least Q20  
Insert size: 167476; sum-of-contigs  
Quality coverage: 18.9x in Q20 bases; sum-of-contigs

## Overlapping Sequences:

5' : RP11-1114A3 AC137625, 2001-bp overlap  
 3' : RP11-182A24 (UMGC:bc0782) AC123903, 41341-bp overlap

## Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
 all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI

HindIII

BglII

SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt

8696	8629	2732	2741	2234	2259
6	<800	6382	6514	2067	2008
2248	2299	512	<800	5097	5007
9345	9792	449	<800	2317	2259
2016	2003	2707	2741	2813	2744
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3455	3447	184	<800	1923	2008
245	<800	5818	5899	2486	2550
72	<800	1364	1346	4036	3992
4175	4167	999	990	2583	2550
72	<800	3014	3028	8136	8039
6640	6560	4721	4667	2738	2744
4710	4771	727	745	4704	4629
3468	3447	179	<800	2649	2744
687	<800	7123	7158	2550	2550
3049	3091	2078	2040	5020	4862
762	<800	1891	1888	6949	6960
553	<800	8072	8171	4636	4629

5080	5088	92	<800	3588	3544
6613	6560	3674	3639	604	<800
8963	9211	5478	5397	5748	6106
331	<800	240	<800	953	943
2328	2299	5050	4878	4728	4629
2038	2003	1053	1068	178	<800
712	<800	3231	3264	1222	1220
1368	1370	86	<800	604	<800
182	<800	5444	5397	3022	3007
1620	1560	1265	1228	4079	3992
775	<800	438	<800	1294	1220
2583	2686	1436	1408	2044	2008
2709	2686	5528	5397	3725	3544
1984	19753	475	<800	790	<800
8729	8629	2310	2371	4232	4223
2264	2299	5177	5089	396	<800
651	<800	391	<800	4714	4629
7181	7213	166	<800	2486	2550
6166	6159	3594	3639	14	<800
500	<800	1172	1188	4240	4223
8764	8629	316	<800	879	917
57	<800	4023	4039	317	<800
3737	3718	1975	2040	161	<800
3711	3718	324	<800	1198	1220
9961	9792	1341	1346	1967	2008
560	<800	4463	4430	344	<800
8662	8629	3569	3639	6314	6531
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309	<800	7414	7557	3335	3339
835	822	511	<800	253	<800
1568	1560	602	<800	1242	1220
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		6843	6824	3630	3727
		2033	2040	252	<800
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Matches	143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;			
OY	52 AAGGTGTCATCATCTCTCATAGTGGCCACTCCTCCATTCTGAATGTTTGCTTGT	111		
DB	2896 AAGGTGTCATCATCTCTCATAGTGGCCACTCCTCCATTCTGAATGTTTGCTTGT	2954		
OY	112 CTGCCTCAATTTTCGCGCTGTAATTTTGATTTCTGGAGTATACCTCTTCCCTGAAAA	171		
DB	2955 CTGCCTCAATTTTCGCGCTGTAATTTTGATTTCTGGAGTATACCTCTTCCCTGAAAA	3012		
OY	172 TTGGGAATGATTCATTCATGGAGAAGACT	200		
DB	3013 TTGGGAATGATTCATTCATGGAGAAGACT	3040		
RESULT 7				
LOCUS	BD012083	5728 bp	DNA	linear PAT 02-AUG-2002
DEFINITION	Human sodium channel SCN12A and SCN8A.			
ACCSSION	BD012083			
VERSION	BD012083.1 GI:22092272			
KEYWORDS	WO 0190355-A/2.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 5728) Kanazawa,I., Goto,U.J. and Jeong,S.Y. Humana sodium channel SCN12A and SCN8A Patent: WO 0190355-A 2 29-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP,ICHIRO KANAZAWA,JUN GOTO, EON YONG JEONG			
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
	OS Homo sapiens (human)			
	PN WO 0190355-A/2			
	PD 29-NOV-2001			
	PF 11-JUL-2000 WO 2000JP004629			
	PR 23-MAY-2000 JP 00P 152085			
	PI ICHIRO KANAZAWA,JUN GOTO,SEON YONG JEONG			
	PC C12N15/12,C07K14/47,C07K16/18			
	CC			
	FH Key			
	CDS Location/Qualifiers			
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Best Local Similarity	96.0%; Pred. No. 3.5e-19;			
Matches	143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;			
OY	52 AAGGTGTCATCATCTCTCATAGTGGCCACTCCTCCATTCTGAATGTTTGCTTGT	111		
DB	3692 AAGGTGTCATCATCTCTCATAGTGGCCACTCCTCCATTCTGAATGTTTGCTTGT	3750		
OY	112 CTGCCTCAATTTTCGCGCTGTAATTTTGATTTCTGGAGTATACCTCTTCCCTGAAAA	171		
DB	3751 CTGCCTCAATTTTCGCGCTGTAATTTTGATTTCTGGAGTATACCTCTTCCCTGAAAA	3808		

QY	172	TTTGGGAATGCATTCCATGAGACAGACT	200
Db	3809	TTTGGGAATGCATT-AATGGAACAGACT	3836
RESULT 8	BD082952		
LOCUS	BD082952	Human sodium channel SCN12A.	
DEFINITION	BD082952		
ACCESSION	BD082952.1	GI:22628562	
VERSION	JP 2001327294-A/2.		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1 (bases 1 to 5728)		
TITLE	Kanazawa, I., Goto, J. and Tei, Y.		
JOURNAL	Human sodium channel SCN12A Patent: JP 2001327294-A 2 27-NOV-2001;		
COMMENT	JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2001327294-A/2 PD 27-NOV-2001 PF 23-MAY-2000 JP 2000152085 PI ICHIRO KANAZAWA, JUN GOTO, YOSHIMIRO TEI PC 12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00 CC FT Key Location/Qualifiers		
FEATURES	source		
ORIGIN	1..5728 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
Query Match	48.3%; Score 107.8; DB 6; Length 5728;		
Best Local Similarity	96.0%; Pred. No. 3.5e-19;		
Matches	143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;		
QY	52	AAGGTGTCGTCATGCTCTGCATAGTGCCATACCTCCCATTCCTGAATGTTTGCCTTG	111
Db	3692	AAGGTGTCGTCATGCTCTGCATAGTGCCATACCTCCCATTCCTGAATGTTTGCCTTG	3750
QY	112	CTGCTCATTTTCGCTGCTGCTGATTTTGTATTCGCGAGTATPACTCTCTTTCCTGAGAAA	171
Db	3751	CTGCTCATTTTCGCTGCTGCTGATTTTGTATTCGCGAGTATPACTCTCTTTCCTGAGAAA	3808
QY	172	TTTGGGAATGCATTCCATGAGACAGACT	200
Db	3809	TTTGGGAATGCATT-AATGGAACAGACT	3836
RESULT 9	AF150882		
LOCUS	AF150882	5728 bp mRNA linear PRI 15-JAN-2000	
DEFINITION	Homo sapiens voltage-gated sodium channel alpha subunit, alternate splice variant SCN12A-s (SCN12A) mRNA, complete cds.		
ACCESSION	AF150882		
VERSION	AF150882.1	GI:6693704	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1 (bases 1 to 5728)		
TITLE	Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isehara, K., Uchiyama, Y. and Kanazawa, I.		
JOURNAL	Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A		
BIOCHEM. BIOPHYS. RES. COMMUN.	267 (1), 262-270 (2000)		
MEDLINE	20090626		

PUBMED 10623608  
REFERENCE 2 (bases 1 to 5728)  
AUTHORS Jeong,S.-Y., Suzuki,T., Hashida,H., Ogata,K., Masuda,M., Goto,J.  
and Kanazawa,I.  
TITLE Direct Submision  
JOURNAL Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,  
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan  
FEATURES location/Qualifiers  
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200..4534  
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ORIGIN

Query Match 48.3%; Score 107.8; DB 9; Length 5728;  
Best Local Similarity 96.0%; Pred. No.3.5e-19;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGTGTCAAGTCTCTCAGTGCATCTCCCATTCCTGAATGTTTGTCTGT 111  
Db 3692 AAGGTGTGTCAATCTCTCAGTGCATCTCCCATTCCTGAATGTTTGTCTGT 3750

QY 112 CTGCTCATTTTCTGCTGCTGATTTGTATTCCTGGAGTAACTCTTTCCTGAAAA 171  
Db 3751 CTGCTCATTTTCTGCTGCTGATTTGTATTCCTGGAGTAACTCTTTCCTGAAAA 3808

QY 172 TTGGGAATGATTCATGAGAACAGACT 200  
Db 3809 TTGGGAATGATTCATGAGAACAGACT 3836

RESULT 10  
AR340678 5860 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340678  
DEFINITION Sequence 41 from patent US 6573067.  
ACCESSION AR340678

VERSION AR340678.1 GI:33732410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5860)  
AUTHORS Dib-Hajj,S. and Waxman,S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 41 03-JUN-2003;  
FEATURES location/Qualifiers  
source 1..5860  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 48.3%; Score 107.8; DB 6; Length 5860;  
Best Local Similarity 96.0%; Pred. No.3.5e-19;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGTGTCAAGTCTCTCAGTGCATCTCCCATTCCTGAATGTTTGTCTGT 111  
Db 3523 AAGGTGTGTCAATCTCTCAGTGCATCTCCCATTCCTGAATGTTTGTCTGT 3581

QY 112 CTGCTCATTTTCTGCTGCTGATTTGTATTCCTGGAGTAACTCTTTCCTGAAAA 171  
Db 3582 CTGCTCATTTTCTGCTGCTGATTTGTATTCCTGGAGTAACTCTTTCCTGAAAA 3639

QY 172 TTGGGAATGATTCATGAGAACAGACT 200  
Db 3640 TTGGGAATGATTCATGAGAACAGACT 3667

RESULT 11  
AR188679 6237 bp mRNA linear PRI 14-DEC-1999  
LOCUS AR188679  
DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit  
(SCN11A) mRNA, complete cds.  
ACCESSION AF188679  
VERSION AF188679.1 GI:6572949  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 6237)  
AUTHORS Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A., Wood,P.M. and  
Waxman,S.G.  
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root  
ganglion neurons  
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)  
MEDLINE 20047838  
PUBMED 10580103  
REFERENCE 2 (bases 1 to 6237)  
AUTHORS Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman,S.G.  
TITLE Direct Submission  
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VMMC, 127A,  
Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA  
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VLISVSTMISTLENOHIIPPPLTFVIRIARIGRIILVRARIGRIILFALMML  
PSLENTGLILFLMFIYAILGMMFVKYNPESGDDIENKTRPSSMLCFOISTSG  
WDSLSPLMKSKESCNSSSENCPLGATISFVSIIISPLIVNMVIAVILEFNFA  
TEESBDFGEEDFDIFYEWEKFPDEATQIKYSALDFADALPEVRVAKPNKYQFL  
VMDLPMYSEDLICMDILFAFARVAVLGGSDLDMSKAMEKMEANPLKLYPIYT  
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ORIGIN

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Best Local Similarity 96.0%; Pred. No. 3.5e-19;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGTCATAGTCTTCATAGTGCATACCTCCCATCTCGATGTTTGGCTTGT 111  
DB 3523 AAGGTGTCATAGTCTTCATAGTGCATACCTCCCATCTCGATGTTTGGCTTGT 3581  
QY 112 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGTAACTCTTTTCTGGA 171  
DB 3582 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGTAACTCTTTTCTGGA 3639  
QY 172 TTGGGAATGCAATTCATGGAACAGACT 200  
DB 3640 TTGGGAATGCAATTCATGGAACAGACT 3667

RESULT 12

BD012082 6528 bp DNA linear PAT 02-AUG-2002

LOCUS Human sodium channel SCN12A and SCN8A.

DEFINITION BD012082

ACCESSION BD012082.1 GI:22092271

VERSION WO 0190355-A/1.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 6528)  
AUTHORS Kanazawa, I., Goto, J. and Jeong, S. Y.  
TITLE Human sodium channel SCN12A and SCN8A  
JOURNAL Patent: WO 0190355-A 1 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON YONG JEONG  
COMMENT OS Homo sapiens (human)  
FN WO 0190355-A/1  
PD 29-NOV-2001  
PF 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085  
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
PC C12N15/12, C07K14/47, C07K16/18  
CC  
FH Key Location/Qualifiers  
FT CDS (200)..(5575).

FEATURES

source 1..6528  
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ORIGIN

Query Match 48.3%; Score 107.8; DB 6; Length 6528;  
Best Local Similarity 96.0%; Pred. No. 3.5e-19;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGTCATAGTCTTCATAGTGCATACCTCCCATCTCGATGTTTGGCTTGT 111  
DB 3592 AAGGTGTCATAGTCTTCATAGTGCATACCTCCCATCTCGATGTTTGGCTTGT 3750  
QY 112 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGTAACTCTTTTCTGGA 171  
DB 3751 CTGCTCATTTTCTGCTGCTGATTTTGTATCTGGAGTAACTCTTTTCTGGA 3808  
QY 172 TTGGGAATGCAATTCATGGAACAGACT 200  
DB 3809 TTGGGAATGCAATTCATGGAACAGACT 3836

RESULT 13

BD082951 6528 bp DNA linear PAT 27-AUG-2002

LOCUS Human sodium channel SCN12A.

DEFINITION BD082951

ACCESSION BD082951.1 GI:22628561

VERSION JP 2001327294-A/1.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 6528)  
AUTHORS Kanazawa, I., Goto, J. and Tei, Y.  
TITLE Human sodium channel SCN12A  
JOURNAL Patent: JP 2001327294-A 1 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
FN JP 2001327294-A/1  
PD 27-NOV-2001  
PF 23-MAY-2000 JP 2000152085  
PI ICHIRO KANAZAWA, JUN GOTO, YOSHIIRO TEI  
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
CC  
FH Key Location/Qualifiers  
FT CDS (200)..(5575).

FEATURES

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ORIGIN

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QY 52 AAGGTGATGTCATGCTCTCTAGTGGCTCCATTCCTGAAATGTTTCTTGT 111  
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 DB 3692 AAGGTGATGTCATGCTCTCTAGTGGCTCCATTCCTGAAATGTTTCTTGT 3750  
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QY 112 CTGCTCATTTTCTGGCTGATTTTGTATTTCTGGAGATATCTTCTTCTGAAAA 171  
 |||||  
 DB 3751 CTGCTCATTTTCTGGCTGATTTTGTATTTCTGGAGATATCTTCTTCTGAAAA 3808  
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QY 172 TTTGGGAATGCATTCATGAACAGACT 260  
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 DB 3809 TTTGGGAATGCATTCATGAACAGACT 3836  
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RESULT 14  
 AF109737 6528 bp mRNA linear PRI 15-JAN-2000  
 LOCUS Homo sapiens voltage-gated sodium channel alpha subunit SCN12A  
 DEFINITION (SCN12A) mRNA, complete cds.  
 ACCESSION AF109737  
 VERSION AF109737.1 GI:6693696  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 QY 1 (bases 1 to 6528)  
 |||||  
 DB Jeong,S.Y., Goto,J., Suzuki,T., Ogata,K., Masuda,N.,  
 Hirai,M., Ishihara,K., Uchiyama,Y. and Kanazawa,I.  
 Identification of a novel human voltage-gated sodium channel alpha  
 subunit gene, SCN12A  
 Biochem. Biophys. Commun. 267 (1), 262-270 (2000)  
 10623608  
 2 (bases 1 to 6528)  
 |||||  
 DB Jeong,S.Y., Suzuki,T., Hashida,H., Masuda,N., Goto,J. and  
 Kanazawa,I.  
 Direct Submision  
 Submitted (27-NOV-1998) Neurology, Graduate School of Medicine,  
 Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan  
 Location/Qualifiers  
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 IAECPVTGIYEALIKILARGLIDFSLRDPNMWLDISVIAISVIGITIKL  
 LPLRTFRPALKAISVSRKLVIVGALISYKLVNVILTFPCISIALVGOQLFM  
 GSINLKCSIRDCKNISNPAYDHCPEKENSPEFKMGIGIMGNSACSIQECKHTYIN  
 PVTYNPNFPGMSFLAMPRLMTQDSWELYOQLRTTGLVSPFPIVIVIFGSPYLI  
 NLTAVVTVAYEQRQNVAAIEIAKEMKQEOALKEKEKALVAMGIDRSLSLST  
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 KVLRTVMTDPTETALITICIIINTVFLMEHKMAEFKEMNTGNLVTGSIPLAEM  
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ORIGIN

Query Match 48.3%; Score 107.8; DB 9; Length 6528;  
 Best Local Similarity 96.0%; Pred. No. 3.5e-19;  
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QY 52 AAGGTGATGTCATGCTCTCTAGTGGCTCCATTCCTGAAATGTTTCTTGT 111  
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 DB 3692 AAGGTGATGTCATGCTCTCTAGTGGCTCCATTCCTGAAATGTTTCTTGT 3750  
 |||||

QY 112 CTGCTCATTTTCTGGCTGATTTTGTATTTCTGGAGATATCTTCTTCTGAAAA 171  
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 DB 3751 CTGCTCATTTTCTGGCTGATTTTGTATTTCTGGAGATATCTTCTTCTGAAAA 3808  
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QY 172 TTTGGGAATGCATTCATGAACAGACT 200  
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 DB 3809 TTTGGGAATGCATTCATGAACAGACT 3836  
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RESULT 15  
 HSA417790 5419 bp mRNA linear PRI 09-OCT-2002  
 LOCUS Homo sapiens mRNA for voltage-gated sodium channel (NAVL.9 gene).  
 DEFINITION AJ417790  
 ACCESSION AJ417790.1 GI:22796539  
 VERSION NAVL.9 gene; voltage-gated sodium channel.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 QY 1  
 |||||  
 DB Blum,R., Kafitz,K.W. and Kornertb,A.  
 Neurotrophin-evoked depolarization requires the sodium channel  
 Na(V)1.9  
 Nature 419 (6908), 687-693 (2002)  
 22272672  
 12384689  
 2 (bases 1 to 5419)  
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 DB Blum,R.  
 Direct Submision  
 Submitted (25-OCT-2001) Blum R., Institut fuer Physiologie,  
 Ludwig-Maximilians-Universitaet, Biedersteiner Strasse 29, Geb.  
 608, 80802 Muenchen, GERMANY  
 Location/Qualifiers  
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/function="mediates neurotrophin-evoked neuronal  
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KVLRYVTGPFTELATITCIINTVFLAMEHHMEASFEKMLNIGLVFTSIFIAEM  
CLKIILADPYHFRGWNIPDSIVALSLPADVANCVLQKRSWPLRSGFRVLRVFKLAK  
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## ORIGIN

Query Match 47.6%; Score 106.2; DB 9; Length 5419;  
Best Local Similarity 95.3%; Pred. No. 9.8e-19;  
Matches 142; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

QY	52	AAGTGTGTCATGCTCTCATAGTGCATACCTCCCATTCCTGAATGTTTGTCTGT	111
DB	3493	AAGGTGGTGTCAATGCTCTCATAGTGCATACCTGCATT-CTGAATGTTTGTCTGT	3551
QY	112	CTGCTCATTTTTCGGCTCGTATTGTAATCTGGAGTATACCTCTTTCCTGAAAA	171
DB	3552	CTGCTTAATTTTCGGCTCGTATTGTAATCTGGAGTATACCTC--TTTTCGAAAA	3609
QY	172	TTTGGAAATGCATTCAATGAGACAGACT	200
DB	3610	TTTGGAAATGCATT-AATGAGACAGACT	3637

Search completed: March 22, 2004, 19:32:33  
Job time : 1190.12 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:33:04 ; Search time 161.414 Seconds

(without alignments)  
5869.049 Million cell updates/sec

Title: US-09-646-224A-13

Perfect score: 223 ggcgcacccctaccaccatcct.....aggcaattccagcagctcct 223

Sequence: 1 ggcgcacccctaccaccatcct.....aggcaattccagcagctcct 223

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N\_Geneseq\_29Jan04:\*

1: geneeqn19808:\*

2: geneeqn19908:\*

3: geneeqn20008:\*

4: geneeqn20018:\*

5: geneeqn20028:\*

6: geneeqn20038:\*

7: geneeqn20048:\*

8: geneeqn20058:\*

9: geneeqn20068:\*

10: geneeqn20078:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223	100.0	223	2	AAZ21491 Human sen
2	107.8	48.3	856	2	AAZ60242 CDNA enc
3	107.8	48.3	3638	2	AAZ87602 Human sod
4	107.8	48.3	3701	4	AAZ30104 Human sod
5	107.8	48.3	5728	6	AAZ42750 Human sod
6	107.8	48.3	5860	4	AAZ30101 Human sod
7	107.8	48.3	5860	9	AAZ32193 Human Na
8	107.8	48.3	6528	6	AAZ42749 Human sod
9	83.6	37.5	5822	2	AAZ87601 Mouse sod
10	83.6	37.5	5822	4	AAZ30103 Mouse sod
11	83.6	37.5	5822	4	AAZ32195 Mouse Na
12	72.8	32.6	5298	9	AAZ32209 Rat Na v
13	72.8	32.6	5334	2	AAZ60244 Stab11se
14	72.8	32.6	5875	2	AAZ87600 Rat sodu
15	72.8	32.6	5875	4	AAZ30102 Rat sodu
16	72.8	32.6	5897	2	AAZ21480 Rat senso
17	72.8	32.6	5905	9	AAZ52929 Primary r
18	72.8	32.6	5905	9	AAZ32191 Rat Na v
19	72.8	32.6	5908	2	AAZ60241 CDNA enc
20	56.4	25.1	8530	4	AAZ31089 Human dia
21	56.4	25.1	6048	2	AAZ09029 Human htl
22	56.4	25.1	6048	4	AAZ30825 Human SCN
23	56.4	25.1	8490	6	AAZ35506 Human gen

24	56	25.1	8509	7	ACC46433 Human dit
25	54.6	24.5	297	4	AAI25358 Probe #15
26	54.6	24.5	297	4	AAI71346 Human toe
27	54.6	24.5	297	4	AAI51597 Probe #20
28	54.6	24.5	297	4	AAI37601 Probe #16
29	54.6	24.5	297	4	AAI45671 Human bon
30	54.6	24.5	297	4	AAI19655 Human bra
31	54.6	24.5	297	4	ABZ45358 Human liv
32	54.6	24.5	297	6	ABZ19943 Human gen
33	52.2	23.4	6606	2	AAZ60872 NaNG poly
34	52.2	23.4	465	4	AAZ30203 Human bon
35	52.2	23.4	465	4	AAZ04690 Human bra
36	52.2	23.4	487	6	ABZ05191 Human gen
37	52.2	23.4	606	5	ABZ58235 Human pro
38	52.2	23.4	677	5	AAH55787 Human SCN
39	52.2	23.4	6348	10	AAZ77201 Human cdn
40	52.2	23.4	6371	2	AAZ30194 Periphera
41	52.2	23.4	6371	7	ADA19379 Human ins
42	52.2	23.4	6371	7	ADA19333 Human ins
43	52.2	23.4	6404	2	AAZ30195 Periphera
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## ALIGNMENTS

RESULT 1  
ID AAZ21491 standard; CDNA; 223 BP.

XX AC AAZ21491;  
XX DT 03-DEC-1999 (first entry)  
XX DE Human sensory neurone specific 2a nucleotide sequence fragment #11.  
XX KW Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;  
XX KM voltage gated; hypersensitivity; ss.  
XX OS Homo sapiens.  
XX PN W09947670-A1.  
XX PD 23-SEP-1999.  
XX PF 18-MAR-1999; 99WC-GB000838.  
XX PR 18-MAR-1998; 98GB-00005793.  
XX PA (GLAX ) GLAXO GROUP LTD.  
XX PI Grose DT, Hick CA, Tate SN;  
XX DR WPI; 1999-562112/47.  
XX PT Mammalian sodium channel protein for treating pain and hypersensitivity.  
XX PS Claim 6; Page 67; 73pp; English.

CC AAZ21481 to AAZ21495 represent fragments of the human sensory neurone  
CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel  
CC protein. SNS-2a can be used in a method for the identification of a  
CC modulator of a sodium channel, and for assaying for compounds which  
CC modulate sodium flux. The sodium channel modulators can be used in a  
CC medicament for the treatment of pain or hypersensitivity

XX SQ Sequence 223 BP; 41 A; 50 C; 44 G; 88 T; 0 U; 0 Other;

Query Match 100.0%; Score 223; DB 2; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6; 1e-54;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCCCTACCCCATCTGTATGTTTCTTGGTTTTCCTTCCATTAAGGTGATG 60  
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 QY 61 GTCAATGCTCTCAATAGTGCCATACCTCCATTCCTGAATGTTTGTCTGCTCAT 120  
 DB 61 GTCAATGCTCTCAATAGTGCCATACCTCCATTCCTGAATGTTTGTCTGCTCAT 120  
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 DB 121 TTTCTGCTCGTATTTTGTATTTCTGAGATATCTTCTTTCCTGAAAAATTTGGAAA 180  
 QY 181 TGCATTCAATGAGACACTTTAGGAATTTCCAGCAATTCCT 223  
 DB 181 TGCATTCAATGAGACACTTTAGGAATTTCCAGCAATTCCT 223

## RESULT 2

AAK60242  
 ID AAK60242 standard; cDNA; 856 BP.

AC AAK60242;  
 XX

DT 11-AUG-1999 (first entry)  
 XX

DE cDNA encoding type 5 sodium channel protein designated PNS.  
 XX

KM Type 5 sodium channel; PNS; nervous system; plexiform;  
 KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
 KM diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
 XX neuropathic pain; migraine; headache; ss.

XX Homo sapiens.  
 OS

XX FR2771103-A1.  
 PN

XX 21-MAY-1999.  
 PD

XX 19-NOV-1998; 98FR-00014551.  
 PF

XX 20-NOV-1997; 97US-0066225P.  
 PR

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA

XX Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;  
 PI

XX WPI; 1999-315739/27.  
 DR

XX P-PSDB; AAY16577.  
 DR

XX Isolated DNA encoding sodium channel of the nervous system.  
 PT

XX Claim 1; Fig 3A; 90pp; French.  
 PS

XX The present sequence encodes a type 5 sodium channel protein designated  
 CC PNS. The protein is a sodium ion channel of the nervous system, and is  
 CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
 CC used to identify inhibitors of sodium channel proteins that are resistant  
 CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
 CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
 CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
 XX

XX Sequence 856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 2; Length 856;  
 Best Local Similarity 96.0%; Pred. No. 6.9e-21;  
 Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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 DB 293 AAGGTGCTGCTCAATGCTCTCATAGGTGCAATCTCCATTCCTGAATGTTTGTCTGT 351  
 QY 112 CTGGCTCATTTTCTGGCTCGATTTTGTATTTCTGGAGATATCTCTTCTCTGAAAA 171  
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DB 352 CTGGCTCATTTTCTGGCTCGATTTTGTATTTCTGGAGATATCTCTCTTCTGAAAA 409  
 QY 172 TTTGGAAATGCTATTCATTAAGACAGACT 200  
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## RESULT 3

AAK87602  
 ID AAK87602 standard; cDNA; 3638 BP.

AC AAK87602;  
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DT 26-OCT-1999 (first entry)  
 XX

DE Human sodium channel NAN partial cDNA.  
 XX

KM NaN; sodium channel; ion transport; human; dorsal root ganglia; pain;  
 KW paresthesia; hyperexcitability; therapy; SCN11a gene; ss.

XX Homo sapiens.  
 OS

XX WO938889-A2.  
 PN

XX 05-AUG-1999.  
 PD

XX 29-JAN-1999; 99WO-US002008.  
 PF

XX 29-JAN-1998; 98US-0072990P.  
 PR

XX 20-NOV-1998; 98US-0109402P.  
 PR

XX (UYVA) UNIV YALE.  
 PA

XX Dib-Hajj S, Waxman S;  
 PI

XX WPI; 1999-479168/40.  
 DR

XX P-PSDB; AAY06598.  
 DR

XX New isolated nucleic acids encoding sodium channels, used to develop  
 PT products for treating acute or chronic pain or hyperexcitability  
 PT phenomena.  
 PT

XX Claim 1; Fig 8A1-2; 91pp; English.  
 PS

XX This is the nucleotide sequence of a partial cDNA clone which codes for a  
 CC portion (see AAY06596) of human NaN, a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The NaN channel cDNA was obtained from human DRG tissue  
 CC cDNA by PCR amplification (see also AAK87620-22). Rat, mouse and human  
 CC NaN nucleic acids (see AAK87600-02) and polypeptides (see AAY06596-98)  
 CC are provided. The invention also includes expression vectors and  
 CC transformed host cells, methods for identifying tissues and cells that  
 CC express NaN, methods for identifying agents that modulate NaN channel  
 CC activity or NaN channel mRNA transcription or translation, and a method  
 CC for using such agents to treat acute or chronic pain, paresthesia and  
 CC hyperexcitability phenomena. The preferential expression of NaN in  
 CC sensory DRG and trigeminal neurons provides a target for selectively  
 CC modifying the behaviour of these nerve cells while not affecting other  
 CC nerve cells in the brain and spinal cord. The gene is named SCN11a  
 XX

XX Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 2; Length 3638;  
 Best Local Similarity 96.0%; Pred. No. 1e-20;  
 Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGCTGCTCAATGCTCTCATAGGTGCAATCTCCATTCCTGAATGTTTGTCTGT 111  
 DB 2833 AAGGTGCTGCTCAATGCTCTCATAGGTGCAATCTCCATTCCTGAATGTTTGTCTGT 2891  
 QY 112 CTGGCTCATTTTCTGGCTCGATTTTGTATTTCTGGAGATATCTCTTCTCTGAAAA 171  
 |||



Db 2892 CTGCGCATTTTCGCTCGATTTTGATTCGAGATATCTC--TTTCTGAAAA 2949

Qy 172 TTGGGAAATGCATTCATGGAACAGACT 200  
 |||||  
 Db 2950 TTGGGAAATGCATT-AATGGAACAGACT 2977

RESULT 4  
 AAF30104 standard; cDNA; 3701 BP.

XX AAF30104;  
 XX AAF30104;  
 AC AAF30104;  
 XX AAF30104;  
 DT 30-APR-2001 (first entry)

XX Human sodium channel NAN partial cDNA.  
 XX Sodium channel; NAN; human; tetrodotoxin resistant; pain; paraesthesia;  
 XX hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; se.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..3699  
 FT CDS /\*tag= a  
 FT /partial

XX WO200105831-A1.  
 XX 25-JAN-2001.  
 XX 14-JUL-2000; 2000WO-US019342.  
 XX 16-JUL-1999; 99US-00354147.  
 XX (UYVA ) UNIV YALE.  
 XX Db-Hajj S, Waxman SG;  
 XX WPI; 2001-103147/11.  
 XX P-PSDB; AAB20125.

XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 PT channels, useful for preventing, diagnosing and treating pain,  
 PT paraesthesia and/or hyperexcitability phenomena.  
 XX Example 4; Fig 8A; 162pp; English.

XX The present sequence is that of a partial cDNA for a novel human  
 CC tetrodotoxin resistant sodium channel, termed NAN (see AAB20125). The  
 CC cDNA was isolated from a human dorsal root ganglia tissue library by  
 CC PCR amplification (see also AAF30122-23). A full-length sequence is given  
 CC in AAF30101. Human NAN belongs to the a-subunit voltage-gated sodium  
 CC channel protein family and produces a TTX-R sodium current. Such channels  
 CC underlie the generation and propagation of impulses in excitable cells  
 CC such as neurons and muscle fibres. Preferential expression of NAN on  
 CC sensory neurons innervating the body (dorsal root ganglia) and the face  
 CC (trigeminal ganglia), but not on other neurons, makes it a very useful  
 CC target for diagnostic and/or therapeutic uses in relation to acute and/or  
 CC chronic pain pathologies. A claimed method of treating pain, paraesthesia  
 CC and/or hyperexcitability phenomena in a human or animal subject involves  
 CC administering an agent that alters sodium current flow through NAN  
 CC channels, or which modulates transcription or translation of NAN mRNA, in  
 CC dorsal root ganglia or trigeminal neurons. NAN nucleic acids are used in  
 CC gene therapy to correct disorders associated with decreased sodium  
 CC channel expression or (antisense) to down-regulate NAN expression, in the  
 CC diagnosis of disease, and in the recombinant production of NAN  
 CC polypeptides

XX Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 4; Length 3701;  
 Best Local Similarity 96.0%; Pred. No. 1e-20;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGTGGTGGTCAATGCTTCATAGCGCATACCTCCCTTCCTGAGATTTTGGCTGT 111  
 |||||  
 Db 2896 AAGTGGTGGTCAATGCTTCATAGCGCATACCTCCCTTCCTGAGATTTTGGCTGT 2954

Qy 112 CTGCGCATTTTCGCTCGATTTTGATTCGAGATATCTCCTTTCCCTGAAAA 171  
 |||||  
 Db 2955 CTGCGCATTTTCGCTCGATTTTGATTCGAGATATCTC--TTTCTGAAAA 3012

Qy 172 TTGGGAAATGCATTCATGGAACAGACT 200  
 |||||  
 Db 3013 TTGGGAAATGCATT-AATGGAACAGACT 3040

RESULT 5  
 AAL42750 standard; cDNA; 5728 BP.

XX AAL42750;  
 AC AAL42750;  
 XX AAL42750;  
 DT 19-JUL-2002 (first entry)

XX Human sodium channel subunit SCN12A-s coding sequence.  
 XX Human sodium channel subunit SCN12A-s coding sequence.  
 XX Human gene; se; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
 XX human nervous system; chromosome 3p23-21.3; excitatory cell;  
 XX drug development; familial hyperglycaemia; QT extending syndrome type 3;  
 XX motor endplate disease.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 200..4534  
 FT CDS /\*tag= a  
 FT /product= "Human sodium channel subunit SCN12A-s"

XX WO200190355-A1.  
 XX 29-NOV-2001.  
 XX 11-JUL-2000; 2000WO-JP004629.  
 XX P-PSDB; AAO14926.

XX 23-MAY-2000; 2000JP-00152085.  
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX PA  
 XX PI Kanazawa I, Goto J, Jeong S;  
 XX WPI; 2002-393394/42.  
 XX P-PSDB; AAO14926.

XX Sodium channel alpha subunit SCN12A and SCN8A of human nervous system  
 PT together with splicing variants, useful in studying physiological  
 PT mechanism relating to excitatory cells and in drug development.  
 XX Claim 7; Page 55-70; 118pp; Japanese.

XX The invention comprises the amino acid and coding sequence of three  
 CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s  
 CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and  
 CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
 CC subunit proteins are useful in studying physiological mechanisms relating  
 CC to excitatory cells and in drug development. The sodium ion channel  
 CC subunit proteins are useful for treating diseases such as familial  
 CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.  
 CC The present cDNA sequence encodes the human SCN12A-s sodium channel  
 CC subunit

XX Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 6; Length 5728;  
 Best Local Similarity 96.0%; Pred. No. 1.2e-20;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGGTGGCAATGCTCTCATAGTGTCCATCTCCATTCCTGATGTTTCTTGT 111  
DB 3692 AAGGTGGTGGCAATGCTCTCATAGTGTCCATCTCCATTCCTGATGTTTCTTGT 3750  
QY 112 CTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGTATACCTCTTTCTCGAAAA 171  
DB 3751 CTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGTATACCTCTTTCTCGAAAA 3808  
QY 172 TTGGGAAATGCATTCATGGAACGACT 200  
DB 3809 TTGGGAAATGCATTCATGGAACGACT 3836

RESULT 6  
AAF30101  
ID AAF30101 standard; cDNA, 5860 BP.  
AC AAF30101;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Human sodium channel NaV cDNA.  
XX  
XX Sodium channel; NaV; human; tetrodotoxin resistant; pain; paraesthesia;  
XX hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT 31..5406  
XX CDS /\*tag= a  
XX  
XX WO200105831-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 14-JUL-2000; 2000WO-US019342.  
XX  
XX 16-JUL-1999; 99US-00354147.  
XX  
XX (UYVA ) UNIV YALE.  
XX  
XX DiB-Hajj S, Waxman SG;  
XX  
XX WPI; 2001-103147/11.  
XX  
XX P-PSDB; AAB20121.  
XX  
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
XX channels, useful for preventing, diagnosing and treating pain,  
XX paraesthesia and/or hyperexcitability phenomena.  
XX  
XX Claim 1; Fig 11A; 1622p; English.

The present sequence is that of cDNA encoding a novel human tetrodotoxin  
resistant sodium channel, termed NaV (see AAB20121). The cDNA was  
isolated from a human dorsal root ganglia tissue cDNA library by PCR  
amplification (see also AAF30122-23). NaV belongs to the a-subunit  
voltage-gated sodium channel protein family and produces a TTX-R sodium  
current. Such channels underlie the generation and propagation of  
impulses in excitable cells such as neurons and muscle fibres.  
Preferential expression of NaV on sensory neurons innervating the body  
(dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
neurons, makes it a very useful target for diagnostic and/or therapeutic  
uses in relation to acute and/or chronic pain pathologies. A claimed  
method of treating pain, paraesthesia and/or hyperexcitability phenomena  
in a human or animal subject involves administering an agent that alters  
sodium current flow through NaV channels, or which modulates  
transcription or translation of NaV mRNA, in dorsal root ganglia or  
trigeminal neurons. NaV nucleic acids are used in gene therapy to correct  
disorders associated with decreased sodium channel expression or  
(antisense) to down-regulate NaV expression, in the diagnosis of disease,

CC and in the recombinant production of NaV polypeptides  
XX  
XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
SQ  
Query Match 48.3%; Score 107.8; DB 4; Length 5860;  
Best Local Similarity 96.0%; Pred. No. 1.2e-20;  
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGGTGGCAATGCTCTCATAGTGTCCATCTCCATTCCTGATGTTTCTTGT 111  
DB 3523 AAGGTGGTGGCAATGCTCTCATAGTGTCCATCTCCATTCCTGATGTTTCTTGT 3581  
QY 112 CTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGTATACCTCTTTCTCGAAAA 171  
DB 3582 CTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGTATACCTCTTTCTCGAAAA 3639  
QY 172 TTGGGAAATGCATTCATGGAACGACT 200  
DB 3640 TTGGGAAATGCATTCATGGAACGACT 3667

RESULT 7  
ADD32193  
ID ADD32193 standard; cDNA, 5860 BP.  
XX  
XX AC ADD32193;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
XX Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
XX  
XX expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT 31..5406  
XX CDS /\*tag= a  
XX FT /product= "Na v 1.9 sodium channel protein"  
XX  
XX WO2003080570-A2.  
XX  
XX 02-OCT-2003.  
XX  
XX 20-MAR-2003; 2003WO-US008611.  
XX  
XX 20-MAR-2002; 2002US-0365550P.  
XX  
XX (TRAN-) TRANSMOLECULAR INC.  
XX  
XX Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
XX  
XX P-PSDB; ADD32194.  
XX  
XX Expression vector useful for stable cloning and expression of Nav1.9  
XX sodium channel at the mRNA and protein levels comprises a nucleic acid  
XX sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
XX fragment.  
XX  
XX Disclosure; SEQ ID NO 3; 125p; English.

The present invention describes an expression vector comprising a nucleic  
acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
its fragment, and producing a sodium current when transfected in a cell.  
Also described: (1) a recombinant cell comprising the plasmid selected  
from pNaV, pCMV-rNaV-GFP, pEG338XN-rNaV and the plasmid described above;  
(2) a method of making a cell or cell line that produces a Na v 1.9  
sodium channel-dependent sodium current by: (a) providing a cell that has  
been transfected with the expression vector; and (b) culturing the cell  
under conditions that allow expression of Na v 1.9 sodium channel protein  
to produce a sodium current into the transfected cell; (3) a method of

CC screening for an agent that modulates sodium current in a cell by: (a)  
 CC exposing the cell or cell line produced by the method to the agent; and  
 CC (b) measuring sodium current following exposure to the agent, where an  
 CC alteration in the level of sodium current is indicative of an agent  
 CC capable of modulating sodium current in a cell; and (4) a recombinant  
 CC cell comprising the expression vector. The expression vectors are useful  
 CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
 CC the mRNA and protein levels, and for producing sodium channel currents  
 CC characteristic of native currents in dorsal root ganglion neurons. The  
 CC present sequence encodes a human Na v 1.9 sodium channel protein, which  
 CC is used in the exemplification of the present invention.

XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 9; Length 5860;  
 Best Local Similarity 96.0%; Pred. No. 1.2e-20;  
 Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGGTGCATAGCTCTCATAGGTCATACCTCCATTCCTGATGTTTGGCTTGT 111  
 DB 3523 AAGGTGGTGCATAGCTCTCATAGGTCATACCTCCATTCCTGATGTTTGGCTTGT 3581  
 QY 112 CTGCTCATTTTCTGCTCGTATTTTGTATTTCTGGAGTATACCTCTTCTCGAAAA 171  
 DB 3582 CTGCTCATTTTCTGCTCGTATTTTGTATTTCTGGAGTATACCTC--TTTCTGAAAA 3639  
 QY 172 TTTGGGAAATGCATTCATGAGACGACT 200  
 DB 3640 TTTGGGAAATGCATTCATGAGACGACT 3667

RESULT 8  
 AAL42749  
 ID AAL42749 standard; cDNA; 6528 BP.  
 XX  
 AC AAL42749;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human sodium channel subunit SCN12A coding sequence.  
 XX  
 KW Human; Gene; ss; sodium channel subunit; SCN12A; SCN12A-B; SCN8A;  
 KW human nervous system; chromosome 3p23-21.3; excitatory cell;  
 KW drug development; familial hyperglycaemia; QT extending syndrome type 3;  
 KW motor endplate disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 200..5575  
 FT /\*tag= a  
 FT /product= "Human sodium channel subunit SCN12A"  
 XX  
 PN WO200190355-A1.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 11-JUL-2000; 2000WO-JP004629.  
 XX  
 PR 23-MAY-2000; 2000JP-00152085.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Kanazawa I, Goto J, Jeong S;  
 XX  
 DR WPI: 2002-393394/42.  
 DR P-PSDB; AAO14925.  
 XX  
 XX Sodium channel alpha subunits SCN12A and SCN8A of human nervous system  
 PT together with splicing variants, useful in studying physiological  
 PT mechanism relating to excitatory cells and in drug development.  
 XX  
 PS Claim 6; Page 23-46; 118pp; Japanese.

XX  
 CC The invention comprises the amino acid and coding sequence of three  
 CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s  
 CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and  
 CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
 CC subunit proteins are useful in studying physiological mechanisms relating  
 CC to excitatory cells and in drug development. The sodium ion channel  
 CC subunit proteins are useful for treating diseases such as familial  
 CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.  
 CC The present cDNA sequence encodes the human SCN12A sodium channel subunit  
 XX

XX Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;  
 SQ

Query Match 48.3%; Score 107.8; DB 6; Length 6528;  
 Best Local Similarity 96.0%; Pred. No. 1.2e-20;  
 Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 52 AAGGTGGTGCATAGCTCTCATAGGTCATACCTCCATTCCTGATGTTTGGCTTGT 111  
 DB 3692 AAGGTGGTGCATAGCTCTCATAGGTCATACCTCCATTCCTGATGTTTGGCTTGT 3750  
 QY 112 CTGCTCATTTTCTGCTCGTATTTTGTATTTCTGGAGTATACCTC--TTTCTGAAAA 171  
 DB 3751 CTGCTCATTTTCTGCTCGTATTTTGTATTTCTGGAGTATACCTC--TTTCTGAAAA 3808  
 QY 172 TTTGGGAAATGCATTCATGAGACGACT 200  
 DB 3809 TTTGGGAAATGCATTCATGAGACGACT 3836

RESULT 9  
 AAX87601  
 ID AAX87601 standard; cDNA; 5822 BP.  
 XX  
 AC AAX87601;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Mouse sodium channel Nan cDNA.  
 XX  
 KW NAN; sodium channel; ion transport; mouse; dorsal root ganglia; pain;  
 KW paraesthesia; hyperexcitability; therapy; Scnla gene; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 19..5316  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /note= "these bases represent nucleotides missing from  
 FT the sequence given in Fig 7 of the specification. The  
 FT nucleotides are included to maintain the nucleotide  
 FT numbering given in the specification for this DNA  
 FT sequence"  
 FT polyA\_signal 5789..5794  
 FT /\*tag= c  
 XX  
 PN WO9938889-A2.  
 XX  
 PD 05-AUG-1999.  
 XX  
 PF 29-JAN-1999; 99WO-US002008.  
 XX  
 PR 29-JAN-1998; 98US-0072990P.  
 XX  
 PA 20-NOV-1998; 98US-0109402P.  
 XX  
 DR (UYVA ) UNIV YALE.  
 DR Dlb-Hajj S, Waxman S;  
 DR WPI: 1999-479168/40.  
 DR P-PSDB; AAY06597.





Db 3544 TTTGGAAGCTCATTAACGGGA 3565

RESULT 13  
AAx60244  
ID AAx60244 standard; cDNA; 5334 BP.

XX AAx60244;

DT 11-AUG-1999 (first entry)

DE Stabilised cDNA encoding type 5 sodium channel protein designated PNS.

XX Type 5 sodium channel; PNS; nervous system; plexiform;  
KM dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
KM diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
KM neuropathic pain; migraine; headache; ss.

OS Synthetic.  
OS Rattus sp.

PN FR2771103-A1.

PD 21-MAY-1999.

PF 19-NOV-1998; 98FR-00014551.

PR 20-NOV-1997; 97US-0066225P.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;

DR WPI, 1999-315739/27.

PT Isolated DNA encoding sodium channel of the nervous system.

PS Example 7; Fig 5A-E; 90pp; French.

CC The present sequence encodes a type 5 sodium channel protein designated  
CC PNS. The protein is a sodium ion channel of the nervous system, and is  
CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
CC used to identify inhibitors of sodium channel proteins that are resistant  
CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
CC  
SQ Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;

Query Match 32.6%; Score 72.8; DB 2; Length 5334;  
Best Local Similarity 78.9%; Pred. No. 1.1e-10;  
Matches 112; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 52 AAGGTGATGTCATAGTCTCTAGTGCATACCTCCCATTCGTAATGTTTCTGT 111

DB 3450 AAGGTGATGTCATAGTCTCTAGTGCATACCTCCCATTCGTAATGTTTCTGT 3508

QY 112 CTGCTCATTTTCTGCTGATTTTGTATTTCTGGAGATACCTCTTTCTGGAAAA 171

DB 3509 CTGCTCATTTTCTGCTGATTTTGTATTTCTGGAGATACCTCTTTCTGGAAAA 3566

QY 172 TTTGGAAATGCATTCATGGA 193

DB 3567 TTTGGAAATGCATTCATGGA 3588

RESULT 14

AAx87600  
ID AAx87600 standard; cDNA; 5875 BP.

XX AAx87600;

DT 26-OCT-1999 (first entry)  
XX Rat sodium channel NAN cDNA.

DE NAN; sodium channel; ion transport; rat; dorsal root ganglia; pain;  
KM paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

OS Rattus sp.

Key location/Qualifiers

FT CDS 41..5338

FT misc\_feature 5551..5600

FT /tag= a

FT /tag= b

/note= "these bases represent nucleotides missing from the sequence given in Fig 1 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

MO9938889-A2.

PD 05-AUG-1999.

PF 29-JAN-1999; 99WO-US002008.

PR 29-JAN-1998; 98US-0072990P.

PR 20-NOV-1998; 98US-0109402P.

PA (UYVA) UNIV YALE.

PI DiB-Hajj S, Waxman S;

DR WPI, 1999-479168/40.

DR P-ESDB; AAY06596.

PT New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability phenomena.

PS Claim 1; Fig 1A-D; 91pp; English.

CC This is the nucleotide sequence of an isolated nucleic acid which encodes  
CC the rat NAN channel (see AAY06596), a previously unidentified voltage  
CC gated sodium channel protein that is preferentially expressed in dorsal  
CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
CC sodium current. The NAN channel cDNA was obtained from Sprague-Dawley rat  
CC DRG cDNA by PCR and RACE amplification (see also AAx87603-17). Rat, mouse  
CC and human NAN nucleic acids (see AAx87600-02) and polypeptides (see  
CC AAY06596-98) are provided. The invention also includes expression vectors  
CC and transformed host cells, methods for identifying tissues and cells  
CC that express NAN, methods for identifying agents that modulate NAN  
CC channel activity or NAN channel mRNA transcription or translation, and a  
CC method for using such agents to treat acute or chronic pain, paraesthesia  
CC and hyperexcitability phenomena. The preferential expression of NAN in  
CC sensory DRG and trigeminal neurons provides a target for selectively  
CC modifying the behaviour of these nerve cells while not affecting other  
CC nerve cells in the brain and spinal cord. The NAN gene has been named  
CC Scn1a

SQ Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;

Query Match 32.6%; Score 72.8; DB 2; Length 5875;  
Best Local Similarity 78.9%; Pred. No. 1.2e-10;  
Matches 112; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 52 AAGGTGATGTCATAGTCTCTAGTGCATACCTCCCATTCGTAATGTTTCTGT 111

DB 3467 AAGGTGATGTCATAGTCTCTAGTGCATACCTCCCATTCGTAATGTTTCTGT 3525

QY 112 CTGCTCATTTTCTGCTGATTTTGTATTTCTGGAGATACCTCTTTCTGGAAAA 171

DB 3526 CTGCTCATTTTCTGCTGATTTTGTATTTCTGGAGATACCTCTTTCTGGAAAA 3583

OY	172 TTTGGGAATGCATTCAATGGA	193
Db	3584 TTGTGAAGGTGCATTAAACGGA	3605

RESULT 15	
AAAF30102	
ID	AAAF30102 standard; cDNA; 5875 BP.

AC	AAF30102;
XX	
DT	30-APR-2001 (first entry)

KM Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia;  
KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.

*Rattus norvegicus.*

	Key	Location/Qualifiers
PH		41. .5338
FT		/*tag= a
FT	CDS	
....		

PN WO200105831-A1.

PD 25-JAN-2001.

PF 14-JUL-2000; 2000WO-US019342.

PR 16-JUL-1999; 99US-00354147.

PA (UYYA ) UNIV YALE.

PI Dib-Hajj S, Waxman SG;

WPI; 2001-103147/11

2000

PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.

PS Example 1; Fig 1; 162pp; English.

The present sequence is that of DNA encoding an novel rat tetrodotoxin resistant sodium channel, termed NAN (see AAB20122). The cDNA was isolated from a dorsal root ganglia tissue cDNA library by PCR amplification using generic primers (from conserved regions of a subunit sodium channel proteins) and NAN-specific primers (see also AAF30105-19), and RACE amplification. The open reading frame shows 73% similarity to the human NAN sequence (see AAF30101). NAN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NAN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NAN channels, or which modulates transcription or translation of NAN mRNA, in dorsal root ganglia or trigeminal neurons. NAN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NAN expression, in the diagnosis of disease, and in the recombinant production of NAN polypeptides.

Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;

Query Match	32.6%;	Score 72.8;	DB 4;	Length 5875;
Best Local Similarity	78.9%;	Pred. No. 1.2e-10;		

[illegible]

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Search completed: March 22, 2004, 16:13:13
Job time : 165.414 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 19:33:04 ; Search time 136.581 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-13

Perfect score: 223  
1 ggtgcattccctaccatccatc.....aggaattccagcagatccct 223

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

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5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

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9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107.8	48.3	3701	15	US-10-388-470-6 Sequence 6, Appl1
2	107.8	48.3	5860	15	US-10-388-470-41 Sequence 41, Appl1
3	83.6	37.5	5822	15	US-10-388-470-4 Sequence 4, Appl1
4	72.8	32.6	5875	15	US-10-388-470-1 Sequence 1, Appl1
5	56.4	25.3	8530	12	US-10-220-120-104 Sequence 104, App
6	56.4	25.1	6048	9	US-09-840-125-3 Sequence 3, Appl1
7	56.4	25.1	6048	10	US-09-896-994-1 Sequence 1, Appl1
8	56.4	25.1	6091	14	US-10-077-054-1 Sequence 1, Appl1
9	56.4	25.1	8490	14	US-10-101-510-617 Sequence 617, App
10	56.4	25.1	8491	15	US-10-333-191-1 Sequence 1, Appl1
11	56.4	25.1	8491	15	US-10-333-191-3 Sequence 1, Appl1
12	54.6	24.5	297	9	US-09-864-761-22921 Sequence 22921, A
13	52.2	23.4	465	9	US-09-864-761-10437 Sequence 10437, A
14	52.2	23.4	487	9	US-09-864-761-15573 Sequence 15573, A
15	52.2	23.4	6348	10	US-09-919-039-366 Sequence 366, App

16	52.2	23.4	6361	14	US-10-161-803-61 Sequence 61, Appl1
17	52.2	23.4	6371	10	US-09-457-571-13 Sequence 13, Appl1
18	52.2	23.4	6404	10	US-09-457-571-14 Sequence 14, Appl1
19	50.6	22.7	3033	10	US-09-457-571-9 Sequence 9, Appl1
20	50.6	22.7	6452	10	US-09-457-571-9 Sequence 9, Appl1
21	50.2	22.5	6344	14	US-10-209-776-1 Sequence 1, Appl1
22	50.2	22.5	6524	14	US-10-202-824-1 Sequence 1, Appl1
23	50.2	22.5	6527	14	US-10-202-824-7 Sequence 7, Appl1
24	50.2	22.5	7032	14	US-10-202-824-5 Sequence 5, Appl1
25	46.6	20.9	6822	9	US-09-917-800A-1604 Sequence 1604, Ap
26	45.4	20.4	6328	14	US-10-161-803-60 Sequence 60, Appl
27	45.4	20.4	7028	14	US-10-101-510-630 Sequence 630, App
28	44.2	19.8	4146	9	US-09-930-871-7 Sequence 7, Appl1
29	44.2	19.8	4179	9	US-09-930-871-17 Sequence 17, Appl
30	44.2	19.8	4329	9	US-09-930-871-5 Sequence 5, Appl1
31	44.2	19.8	4362	9	US-09-930-871-15 Sequence 15, Appl
32	44.2	19.8	5889	9	US-09-930-871-3 Sequence 3, Appl1
33	44.2	19.8	5922	9	US-09-930-871-13 Sequence 13, Appl
34	44.2	19.8	5997	9	US-09-930-871-11 Sequence 11, Appl
35	44.2	19.8	6030	9	US-09-930-871-11 Sequence 11, Appl
36	43.8	19.6	4164	9	US-09-930-871-9 Sequence 9, Appl1
37	43.8	19.6	4197	9	US-09-930-871-19 Sequence 19, Appl
38	42.6	19.1	6027	15	US-10-297-022-40 Sequence 40, Appl
39	39.4	17.7	472	9	US-09-864-761-6181 Sequence 6181, Ap
40	38.6	17.3	6315	10	US-09-428-371-2 Sequence 2, Appl1
41	38.6	17.3	6318	10	US-09-428-371-1 Sequence 1, Appl1
42	37.4	16.8	611	15	US-10-027-632-238204 Sequence 238204,
43	35.6	16.0	341	9	US-09-867-701-10175 Sequence 10175, A
44	35.6	16.0	9646	14	US-10-111-455-1662 Sequence 1662, Ap
45	34.6	15.5	5051	16	US-10-389-566-330 Sequence 330, App

## ALIGNMENTS

RESULT 1

US-10-388-470-6

Sequence 6, Application US/10388470

Publication No. US2003028662A1

GENERAL INFORMATION:

APPLICANT: Dab-Hajj, Sulayman

TITLE OR INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/09/354, 147C

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/702, 990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109, 402

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 3701

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS (3699)

LOCATION: (1)..(3699)

OTHER INFORMATION: partial human Nan cDNA sequence

FEATURE:

NAME/KEY: unsure

LOCATION: (922)

OTHER INFORMATION: Y = C or T. Xaa at amino acid position 308 is

OTHER INFORMATION: Leu.

US-10-388-470-6

Query Match 48.3%; Score 107.8; DB 15; Length 3701;

Best Local Similarity 96.0%; Pred. No. 2.0e-22;

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Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;
QY 52 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 111
Db 2896 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 2954
QY 112 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 171
Db 2955 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 3012
QY 172 TTTGGAAATGCATTCATGGAACAGACT 200
Db 3013 TTTGGAAATGCATTCATGGAACAGACT 3040

RESULT 2
US-10-388-470-41
; Sequence 41, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human Nan
US-10-388-470-41

Query Match 48.3%; Score 107.8; DB 15; Length 5860;
Best Local Similarity 96.0%; Pred. No. 3.4e-22;
Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;
QY 52 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 111
Db 3523 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 3581
QY 112 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 171
Db 3582 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 3639
QY 172 TTTGGAAATGCATTCATGGAACAGACT 200
Db 3640 TTTGGAAATGCATTCATGGAACAGACT 3667

RESULT 3
US-10-388-470-4
; Sequence 4, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
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; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; NAME/KEY: unsure
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-10-388-470-4

Query Match 37.5%; Score 83.6; DB 15; Length 5822;
Best Local Similarity 82.5%; Pred. No. 7.8e-15;
Matches 132; Conservative 0; Mismatches 24; Indels 4; Gaps 3;
QY 52 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 111
Db 3448 AAGGTGGTGCATGCTCTCATAGTGCCTACCTCCCATTCCTGGAATGTTTGCTGT 3506
QY 112 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 171
Db 3507 CTGCTCATTTTCTGGCTCGTATTTTGTATTTCTGGAGATATACCTCTTTCTGGAATA 3564
QY 172 TTTGGAAATGCATTCATGGAACAGACTTTTGAATAT 211
Db 3565 TTTGGAAATGCATTCATGGAACAGACTTAATATAT 3603

RESULT 4
US-10-388-470-1
; Sequence 1, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; NAME/KEY: unsure
; LOCATION: (1996)..(4042)
```

OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position  
; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn  
; OTHER INFORMATION: or Lys.  
US-10-386-470-1

Query Match	32.6%	Score	72.2	DB	15	Length	5875
Best Local Similarity	78.9%	Pred.	No	1.5e-11			
Matches	112	Conservative	0	Mismatches	27	Indels	3
						Gaps	2

QY	52	AAGGTGGTGGTCATAGCTCTCATAGAGTGCACCTCCCATTCCTGAAAGTTTGCTGT	111
Db	3467	AAGGTGGTGGTCATAGCTCTCATAGAGTGCACCTCCCATTCCTGAAAGTTTGCTGT	3525
QY	112	CTGCTCATTTTCTGGCTGCTGATTTTGATTTCTGGAGTATACCTCTTTCCTGGAAA	171
Db	3526	CTGCTCATTTTCTGGCTGCTGATTTTGATTTCTGGAGTATATTT -ATTTTCTGGAG	3583
QY	172	TTTGGGAATGTCATTCATGGA	193
Db	3584	TTTGGGAATGTCATTCATGGA	3605

US-10-220-120-104  
RESULT 5

Sequence 104, Application US/10220120  
Publication No. US20040048253A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.  
APPLICANT: PANZER, Scott R.  
APPLICANT: BANVILLE, Steven C.  
APPLICANT: SHAH, Purni  
APPLICANT: CHALUP, Michael S.  
APPLICANT: CHANG, Simon C.  
APPLICANT: CHEN, Alice  
APPLICANT: D'SA, Steven A.  
APPLICANT: AMSHEY, Stefan  
APPLICANT: DAHL, Christopher R.  
APPLICANT: DAM, Tam C.  
APPLICANT: DANIELS, Susan E.  
APPLICANT: DUFOUR, Gerard E.  
APPLICANT: FLORES, Vincent  
APPLICANT: FONG, Willy T.  
APPLICANT: GREENWALT, Lila B.  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: JONES, Antissa L.  
APPLICANT: LIU, Tommy F.  
APPLICANT: ROSEBERRY, Ann M.  
APPLICANT: ROSEN, Bruce H.  
APPLICANT: RUSSO, Frank D.  
APPLICANT: STOCKREHER, Theresa K.  
APPLICANT: DAFRO, Abel  
APPLICANT: WRIGHT, Rachel J.  
APPLICANT: YAP, Pierre E.  
APPLICANT: YU, Jimmy Y.  
APPLICANT: BRADLEY, Diana L.  
APPLICANT: BRATCHER, Shawn R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: COHEN, Howard J.  
APPLICANT: HODGSON, David M.  
APPLICANT: LINCOLN, Stephen E.  
APPLICANT: JACKSON, Stuart  
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: PT-1113 PCT  
CURRENT APPLICATION NUMBER: US/10/220,120  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 60/184,777; 60/184,777; 60/184,797; 60/184,698; 60/184,770; 60/184,774  
60/184,693; 60/184,771; 60/184,813; 60/184,773; 60/184,776;  
60/184,769; 60/184,768; 60/184,837; 60/184,697; 60/184,841;  
60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/205,221;  
60/204,815; 60/203,785; 60/204,821; 60/204,908; 60/204,226;  
60/204,525; 60/205,285; 60/205,232; 60/205,323; 60/205,287;  
60/205,324; 60/205,286

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PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-05-17; 2000-05-12; 2000-05-16; 2000-05-15;
2000-05-16; 2000-05-17; 2000-05-16; 2000-05-17;
2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17;
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PERL Program
SEQ ID NO 104
LENGTH: 8530
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:410188.1:2000MAY01
FEATURE:
NAME/KEY: unsure
LOCATION: 6797, 7046, 7252, 7311, 7325, 7326, 7502-7503, 7563
OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-104

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Query Match	25.3%	Score 56.4	DB 12	Length 8530
Best Local Similarity	68.6%	Pred. No. 1.7e-06		
Matches 107, Conservative	0	Mismatches 46	Indels 3	Gaps 2

Qy	40	TTTTCTTTTCATAGGTGGTGGTCAAGTCTCTAAGAGGTGCATACCTCCCATCTCGAA	99
Db	4108	TTTTAGGGGCATGAGGGTGGTGGTAAATGCCCTGGTGGGGCCGCAATCCCTCCA-TCATGAA	4166
Qy	100	TGTTTGCTGTCTGCGCCATTTTCTGGCTGGTATTTGTATTCGGAGATATACTTCT	159
Db	4167	CGTCTCTCTGCTGCGCCATCTTCTGGCTATCTTCAGCATCATGGGCGTGAACTTC-	4224
Qy	160	TTTCTGGAATAATTGGGAAATGCATTCATGGAAC	195
Db	4225	TTTTCGGGGAAAGTTTGGAGGTGCATCACTATATCC	4260

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RESULT 6
US-09-840-125-3
; Sequence 3, Application US/09840125
; Patent No. US20020061524A1
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME
; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/840.125
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/634,920
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6048)
US-09-840-125-3

Query Match      25.1%, Score 56; DB 9; Length 6048;
Best Local Similarity 68.8%; Pred. NO. 1.9e-06;
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2.

09      40      TTGTTTTCATAGGTGGTGGTCATAGCTCTCATAGATGTCATACCTCCATTCCTGAA 99
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db       3449  TTATAGGCGCATGAGGGTGGTGGTCATATCCCTGGTGGGCGCCATTCCTCCA-TATATGA 4007

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QY 100 TGTGTTGCTGTCGCCCTCATTTCTGGCTGTAATTTGTAATTCGGAGTAATCTTCT 159  
DB 4008 CGTCTCTCTGCTGCTCATCTTCTGGCTCATTCAGCATCAGGCGGAACTTC-- 4065  
QY 160 TTTCCTGGAATAATTGGGAATGCAATTCATGGA 193  
DB 4066 TTTCGGGGAGATTGGAGAGTGATCAACACAGA 4099

## RESULT 7

US-09-896-994-1

; Sequence 1, Application US/09896994

; Publication No. US20030074024A1

; GENERAL INFORMATION:

; APPLICANT: Ken Stokes

; J. e. Morissette

; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC

; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM

; CORRESPONDENCE ADDRESSES:

; ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/896,994

; FILING DATE: 02-Jul-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/514,907

; FILING DATE: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul K. Legaard

; REGISTRATION NUMBER: 38,534

; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6048 bases

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

; US-09-896-994-1

Query Match 25.1%; Score 56; DB 10; Length 6048;  
Best Local Similarity 68.8%; Pred. No. 1.9e-06;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 40 TTTGTTTTCATAGTGTGTCATAGTCTCATAGTGCATACCTCCATTCCTGAA 99  
DB 3949 TTTGAGGAGATAGAGGTGTGTGTCATAGTCCCTGTGGGCGCATCCCGCCA-TATGAA 4007  
QY 100 TGTGTTGCTGTCGCTCATTTTCTGGCTCGATTTTGTATTTCTGGAGATATCTTCT 159  
DB 4008 CGTCTCTCTGCTGCTCATCTTCTGGCTCATCTTCAGCATCAGGCGGAACTTC-- 4065  
QY 160 TTTCCTGGAATAATTGGGAATGCAATTCATGGA 193  
DB 4066 TTTCGGGGAGATTGGAGAGTGATCAACACAGA 4099

## RESULT 8

US-10-077-054-1  
; Sequence 1, Application US/10077054  
; Publication No. US20030157600A1  
; GENERAL INFORMATION:  
; APPLICANT: Makieski, Jonathan C  
; APPLICANT: Ye, Bin  
; TITLE OF INVENTION: Sodium Channel Alpha Subunits  
; FILE REFERENCE: 960296,98032  
; CURRENT APPLICATION NUMBER: US/10/077,054  
; CURRENT FILING DATE: 2002-02-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 6091  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(6054)  
US-10-077-054-1

Query Match 25.1%; Score 56; DB 14; Length 6091;  
Best Local Similarity 68.8%; Pred. No. 1.9e-06;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 40 TTTGTTTTCATAGTGTGTCATAGTCTCATAGTGCATACCTCCATTCCTGAA 99  
DB 3955 TTTGAGGAGATAGAGGTGTGTGTCATAGTCCCTGTGGGCGCATCCCGCCA-TATGAA 4013  
QY 100 TGTGTTGCTGTCGCTCATTTTCTGGCTCGATTTTGTATTTCTGGAGATATCTTCT 159  
DB 4014 CGTCTCTCTGCTGCTCATCTTCTGGCTCATCTTCAGCATCAGGCGGAACTTC-- 4071  
QY 160 TTTCCTGGAATAATTGGGAATGCAATTCATGGA 193  
DB 4072 TTTCGGGGAGATTGGAGAGTGATCAACACAGA 4105

## RESULT 9

US-10-101-510-617

; Sequence 617, Application US/10101510

; Publication No. US20030148295A1

; GENERAL INFORMATION:

; APPLICANT: WAN, JACKSON

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

; FILE REFERENCE: 15117,0012

; CURRENT APPLICATION NUMBER: US/10/101,510

; CURRENT FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: 60/276,947

; PRIOR FILING DATE: 2001-03-20

; NUMBER OF SEQ ID NOS: 805

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 617

; LENGTH: 8490

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (6774)

; OTHER INFORMATION: a, t, c, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7021)

; OTHER INFORMATION: a, t, c, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7227)

; OTHER INFORMATION: a, t, c, g, other or unknown

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7286)

; OTHER INFORMATION: a, t, c, g, other or unknown

FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7300)..(7301)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7477)..(7478)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7538)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8167)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-101-510-617

Query Match 25.1%; Score 56; DB 14; Length 8490;  
Best Local Similarity 68.8%; Pred. No. 2.2e-06;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

Qy 40 TTTGTTTCCATAGAGTGAGTGATGCTCTCATAGAGTGCCATACCTCCATTCTGAA 99  
Db 4099 TTTGAGGCGATGAGGAGTGATGCTCAATGCCCTGAGGCGCCATCCGTCA-TCATGAA 4157  
Qy 100 TGTTCCTGCTGCTGCTCATTTTCTGCTGATTTTGTATTCCTGGAGTAACTTCT 159  
Db 4158 CGTCTCCTCGTCTGCTCATCTTCTGCTCATCTTCAGCATCAATGGGCGGAACTTC-- 4215  
Qy 160 TTTCCGTGAAATTTGGGAATGCATTCATGCA 193  
Db 4216 TTGCGGGGAAGTTTGGAGGTGATCAACCA 4249

RESULT 10  
US-10-333-191-1  
Sequence 1, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
FILE OF INVENTION: Arrhythmia  
FILE REFERENCE: 2323-154-11  
CURRENT APPLICATION NUMBER: US/10/333,191  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 8491  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 25.1%; Score 56; DB 15; Length 8491;  
Best Local Similarity 68.8%; Pred. No. 2.2e-06;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;  
Qy 40 TTTGTTTCCATAGAGTGAGTGATGCTCTCATAGAGTGCCATACCTCCATTCTGAA 99  
Db 4099 TTTGAGGCGATGAGGAGTGATGCTCAATGCCCTGAGGCGCCATCCGTCA-TCATGAA 4157

Qy 100 TGTTCCTGCTGCTGCTCATTTTCTGCTGATTTTGTATTCCTGGAGTAACTTCT 159  
Db 4158 CGTCTCCTCGTCTGCTCATCTTCTGCTCATCTTCAGCATCAATGGGCGGAACTTC-- 4215  
Qy 160 TTTCCGTGAAATTTGGGAATGCATTCATGCA 193  
Db 4216 TTGCGGGGAAGTTTGGAGGTGATCAACCA 4249

RESULT 11  
US-10-333-191-3  
Sequence 3, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
FILE OF INVENTION: Arrhythmia  
FILE REFERENCE: 2323-154-11  
CURRENT APPLICATION NUMBER: US/10/333,191  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 8491  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-3

Query Match 25.1%; Score 56; DB 15; Length 8491;  
Best Local Similarity 68.8%; Pred. No. 2.2e-06;  
Matches 106; Conservative 0; Mismatches 45; Indels 3; Gaps 2;  
Qy 40 TTTGTTTCCATAGAGTGAGTGATGCTCTCATAGAGTGCCATACCTCCATTCTGAA 99  
Db 4099 TTTGAGGCGATGAGGAGTGATGCTCAATGCCCTGAGGCGCCATCCGTCA-TCATGAA 4157  
Qy 100 TGTTCCTGCTGCTGCTCATTTTCTGCTGATTTTGTATTCCTGGAGTAACTTCT 159  
Db 4158 CGTCTCCTCGTCTGCTCATCTTCTGCTCATCTTCAGCATCAATGGGCGGAACTTC-- 4215  
Qy 160 TTTCCGTGAAATTTGGGAATGCATTCATGCA 193  
Db 4216 TTGCGGGGAAGTTTGGAGGTGATCAACCA 4249

RESULT 12  
US-09-864-761-22921/C  
Sequence 22921, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 22921  
LENGTH: 297  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005803.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.5  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3  
OTHER INFORMATION: SWISSPROT HIT: P35439, EVALUATE 1.00e-48  
OTHER INFORMATION: EST HUMAN HIT: A1016157.1, EVALUATE 9.00e-26  
OTHER INFORMATION: NT HIT: L01978.1, EVALUATE 0.00e+00  
US-09-864-761-22921

Query Match 24.5%; Score 54.6; DB 9; Length 297;  
Best Local Similarity 73.5%; Pred. No. 1.4e-06;  
Matches 83; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 48 CCATAGGAGTGTGATGCTCTCATAGTGCATATCCCATCTCGAATGTTTGC 107  
DB 286 CCCCCAGGTGGTGAAGCCCTCTTAGGCGCCATCCCTCCA-TCATGAATGCTGC 228  
QY 108 TTGTGCTCATATTTCTGCTCGATATTTGATTTGGAGATATCTTCTT 160  
DB 227 TTGTGCTCATATTTCTGCTCGATATTTGATTTGGAGATATCTTCTT 175

RESULT 13  
US-09-864-761-10437  
Sequence 10437, Application US/09864761  
Patent No. US20020048763A1

GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecomica-X-1  
CURRENT FILING DATE: 2001-05-23  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
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PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 10437  
LENGTH: 465  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC010127.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
US-09-864-761-10437

Query Match 23.4%; Score 52.2; DB 9; Length 465;  
Best Local Similarity 66.9%; Pred. No. 9.3e-06;  
Matches 89; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

QY 28 TTTCCTTCTGTTTTCATAGGAGTGTGATGCTCTCATAGTGTGCTACTACT 87  
DB 208 TTTCCTTCTGTTTTCATAGGAGTGTGATGCTCTCATAGTGTGCTACTACT 267  
QY 88 CCAATTCGATATGTTTCTGCTGCTCATATTTCTGCTCGATATTTGATTTGCGG 147  
DB 268 TCCA-TCATGAATGCTTCTGCTGCTCATATTTCTGCTCGATATTTGATTTGCGG 326  
QY 148 AGTATCTTCTTCTT 160  
DB 327 CATAATTTGTTT 339

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RESULT 14
US-09-864-761-15573
Sequence 15573, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
  APPLICANT: Penn, Sharon G.
  APPLICANT: Rank, David R.
  APPLICANT: Hanzel, David K.
  APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aemica-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2001-05-23
PRIORITY FILING DATE: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY FILING DATE: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY FILING DATE: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
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PRIORITY APPLICATION NUMBER: US 60/234,687
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PRIORITY APPLICATION NUMBER: US 09/608,408
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PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15573
LENGTH: 487
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010127.2
US-09-864-761-15573
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 12

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	Query Match	Similarity	Score	DB	Length
Best Local	89	66.9%	52.2	DB 9	487
Matches	89	Conservative	0	Mismatches	43
				Indels	1
				Gaps	1
Qy	28	TTTTCCCTTGGCTTTGTTTCATAGGTGGTGCATAGCTCATAGTCCATACCT	87		
Db	200	TTTTCTTTTTCATATTGTATAGGTGGTGGAAAGCCCTTTTAGGACAAATTCGA	259		
Qy	88	CCCATCTCGAATGTTTGGCTGTCTGCTCAATTTTCGCTCGATTTTGAATCTGGG	147		

Db	260	TCCA-TCATGATGTCCTTCGGTTTGTCTATATCTGGCTAATTTCAAGATCATGGG	318
Qy	148	AGTATCTTCTT	160
Db	319	CGTAATTTGTTT	331

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RESULT 15
US-09-919-039-366
: Sequence 366, Application US/09919039
: Publication No. US20030108871A1
: GENERAL INFORMATION:
: APPLICANT: Kaeser, Matthew R.
: TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
: FILE REFERENCE: PA-0035 US
: CURRENT APPLICATION NUMBER: US/09/919,039
: CURRENT FILING DATE: 2002-09-09
: PRIOR APPLICATION NUMBER: 60/222,113
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 401
: SOFTWARE: PERL Program
: SEQ ID NO 366
: LENGTH: 6348
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: incyte ID No. US20030108871A1 1719478C81
US-09-919-039-366

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Query Match	23.4%	Score 52.2;	DB 10;	Length 6348;
Best Local Similarity	73.4%	Pred. No. 2.8e-05;		
Matches	80;	Conservative	0;	Mismatches 28; Indels 1; Gaps 1.

  

QY	52	AAGGTGGTGCATGCTCTCATAGAGGCATACCTCCCATTCCTGATGTTTGGTGT	111
Db	3937	AGGGTCCTTGGATGACATCATAGGAGCAATTCCTTCCA-TCAATGATGTCGTACTTGT	3999
QY	112	CTGCCTATTTTCTGCCTCGATATTTTATCTGGAGATACTTCCCT	160
Db	3996	GTCGCTTAATTCCTGCCTGATATTCACAGCATATGGAGATAAATTTGTTT	4044

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OM nucleic - nucleic search, using sw model

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Title: US-09-646-224A-13

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Gapop 10.0 , Gapext 1.0

Searched: 3757730 seqs, 17593059518 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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54: /cgn2\_6/ptodata/2/pna/US107A\_COMB.seq.\*  
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56: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*  
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66: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*  
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84: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223	100.0	223	US-09-646-224A-13	Sequence 11, Appl
2	123.8	55.5	3194	US-60-213-846-1109	Sequence 1109, Ap
3	123.8	55.5	6925	US-60-207-214-72	Sequence 72, Appl
4	123.8	55.5	115159	US-60-466-412-84151	Sequence 84151, A
5	107.8	48.3	856	US-09-195-851-3	Sequence 3, Appl
6	107.8	48.3	3163	US-60-213-846-1412	Sequence 1412, Ap
7	107.8	48.3	3701	PCT-US00-19342-6	Sequence 6, Appl
8	107.8	48.3	3701	PCT-US99-02008-6	Sequence 6, Appl
9	107.8	48.3	3701	US-10-388-470-6	Sequence 6, Appl
10	107.8	48.3	5080	US-10-170-235-13985	Sequence 13985, A
11	107.8	48.3	5080	US-60-453-050-2171	Sequence 2171, Ap
12	107.8	48.3	5080	US-60-453-135-2171	Sequence 2171, Ap
13	107.8	48.3	5080	US-60-466-412-2171	Sequence 2171, Ap
14	107.8	48.3	5728	US-10-219-051B-910	Sequence 910, App
15	107.8	48.3	5728	US-10-296-130-3	Sequence 3, Appl
16	107.8	48.3	5860	PCT-US00-19342-41	Sequence 41, Appl
17	107.8	48.3	5860	PCT-US03-08611-3	Sequence 3, Appl
18	107.8	48.3	5860	US-10-388-470-41	Sequence 41, Appl
19	107.8	48.3	5860	US-60-365-550-3	Sequence 317, App
20	107.8	48.3	6237	US-60-516-609-317	Sequence 317, App
21	107.8	48.3	6499	US-09-770-175-8399	Sequence 8399, Ap
22	107.8	48.3	6528	US-10-296-130-1	Sequence 1, Appl
23	107.8	48.3	6528	US-60-485-101-251	Sequence 251, App
24	83.6	37.5	5822	PCT-US00-19342-4	Sequence 4, Appl
25	83.6	37.5	5822	PCT-US03-08611-5	Sequence 5, Appl
26	83.6	37.5	5822	PCT-US99-02008-4	Sequence 4, Appl
27	83.6	37.5	5822	US-10-388-470-4	Sequence 4, Appl
28	83.6	37.5	5822	US-60-365-550-5	Sequence 5, Appl
29	83.6	37.5	5833	US-10-144-771-19000	Sequence 19000, A
30	83.6	37.5	5833	US-60-360-207-19000	Sequence 19000, A
31	83.6	37.5	5858	US-10-180-934-1	Sequence 1, Appl
32	83.6	37.5	5858	US-10-377-139-15	Sequence 15, Appl
33	83.6	37.5	5858	US-60-485-101-345	Sequence 345, App
34	72.8	32.6	5298	PCT-US03-08611-19	Sequence 19, Appl
35	72.8	32.6	5298	US-60-365-550-19	Sequence 19, Appl
36	72.8	32.6	5334	US-09-195-851-4	Sequence 4, Appl
37	72.8	32.6	5875	PCT-US00-19342-1	Sequence 1, Appl
38	72.8	32.6	5875	PCT-US99-02008-1	Sequence 1, Appl
39	72.8	32.6	5875	US-10-388-470-1	Sequence 1, Appl
40	72.8	32.6	5897	US-09-646-224A-1	Sequence 1, Appl
41	72.8	32.6	5905	PCT-US03-03482-3471	Sequence 3471, Ap
42	72.8	32.6	5905	PCT-US03-08611-1	Sequence 1, Appl
43	72.8	32.6	5905	US-10-219-051B-908	Sequence 908, App
44	72.8	32.6	5905	US-10-357-507-3471	Sequence 3471, Ap
45	72.8	32.6	5905	US-10-377-139-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-09-646-224A-13  
; Sequence 13, Application US/09646224A  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Wellcome PLC  
; APPLICANT: Tate, Simon N  
; APPLICANT: Grose, David T  
; APPLICANT: Hicks, Caroline A  
; TITLE OF INVENTION: Ion Channels  
; FILE REFERENCE: PG3432  
; CURRENT APPLICATION NUMBER: US/09/646,224A  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: GB 9805793.8  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 223  
; TYPE: DNA

ORGANISM: Homo sapiens  
US-09-646-224A-13  
Query Match 100.0%; Score 223; DB 27; Length 223;  
Best Local Similarity 100.0%; Pred. No. 3,1e-48;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATCATCCCAACCCCACTGTATAGTTTCTTCTTGTGTTTCATTAAGTGTG 60  
DB 1 GGTGATCCCAACCCCACTGTATAGTTTCTTCTTGTGTTTCATTAAGTGTG 60  
QY 61 GTCAATGCTCATAGTGCATACCTTCCATCTGAATTTTGTCTGCTTCAT 120  
DB 61 GTCAATGCTCATAGTGCATACCTTCCATCTGAATTTTGTCTGCTTCAT 120  
QY 121 TTTCTGCTCATATTTTGTATCTTGAGAGTATCTTCTTCTGGAATTTGGGAA 180  
DB 121 TTTCTGCTCATATTTTGTATCTTGAGAGTATCTTCTTCTGGAATTTGGGAA 180  
QY 181 TGCAATCATGAACAGACTTTTAGAATTTCCAGCATTCCT 223  
DB 181 TGCAATCATGAACAGACTTTTAGAATTTCCAGCATTCCT 223  
RESULT 2  
US-60-213-846-1109  
; Sequence 1109, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CLO00703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1109  
; LENGTH: 3194  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-213-846-1109  
Query Match 55.5%; Score 123.8; DB 77; Length 3194;  
Best Local Similarity 93.0%; Pred. No. 8e-22;  
Matches 174; Conservative 0; Mismatches 7; Indels 6; Gaps 4;  
QY 14 CCCATCTGTATAGTTTCTTCTTGTGTTTCATTAAGTGTGTCATGCTTCA 73  
DB 2617 CCCATCTGTATAGTTTCTTCTTGTGTTTCATTAAGTGTGTCATGCTTCA 2674  
QY 74 TAGTGCCATACCTCCCATCTCTGAATGTTTGTCTGTCTGCTTATTTTGGCTCGTA 133  
DB 2675 TAGTGCCATACCTCCCATCTCTGAATGTTTGTCTGTCTGCTTATTTTGGCTCGTA 2733  
QY 134 TTTGTATTTGGAGTATCTTCTTCTGGAATTTGGAAATGATTCATGGA 193  
DB 2734 TTTGTATTTGGAGTATCTTCTTCTGGAATTTGGAAATGATTCATGGA 2790  
QY 194 ACAGACT 200  
DB 2791 ACAGACT 2797  
RESULT 3  
US-60-207-214-72  
; Sequence 72, Application US/60207214  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CLO00581



Db 2389 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 2446

Qy 172 TTGGGAAATGCATTCAATGGAACAGACT 200

Db 2447 TTGGGAAATGCATT--AATGGAACAGACT 2474

RESULT 7

PCT-US00-19342-6

; Sequence 6, Application PC/TUS0019342

; GENERAL INFORMATION:

; APPLICANT: Yale University

; APPLICANT: Dib-Hajj, Sulayman

; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

; FILE REFERENCE: 44574-5004-02-WO

; CURRENT APPLICATION NUMBER: PCT/US00/19342

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/354,147

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6

; LENGTH: 3701

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3699)

; OTHER INFORMATION: partial human Nan cDNA sequence

; NAME/KEY: unsure

; LOCATION: (922)

; OTHER INFORMATION: y = c or t

; PCT-US00-19342-6

Query Match 48.3%; Score 107.8; DB 1; Length 3701;

Best Local Similarity 96.0%; Pred. No. 1.4e-17;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 111

Db 2896 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 2954

Qy 112 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 171

Db 2955 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 3012

Qy 172 TTGGGAAATGCATTCAATGGAACAGACT 200

Db 3013 TTGGGAAATGCATT--AATGGAACAGACT 3040

RESULT 8

PCT-US99-02008-6

; Sequence 6, Application PC/TUS9902008D

; GENERAL INFORMATION:

; APPLICANT: Yale University

; TITLE OF INVENTION: Dorsal Root Ganglia-Specific and Tetradotoxin Resistant

; FILE REFERENCE: 44574-5004-WO, Yale University

; CURRENT APPLICATION NUMBER: PCT/US99/02008D

; PRIOR FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: US 60/072,990

; EARLIER FILING DATE: 1998-01-29

; EARLIER APPLICATION NUMBER: US 60/109,402

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 6

; LENGTH: 3701

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3699)

; OTHER INFORMATION: partial human Nan cDNA sequence

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (922)

; OTHER INFORMATION: y = c or t

; PCT-US99-02008-6

Query Match 48.3%; Score 107.8; DB 1; Length 3701;

Best Local Similarity 96.0%; Pred. No. 1.4e-17;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 111

Db 2896 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 2954

Qy 112 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 171

Db 2955 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 3012

Qy 172 TTGGGAAATGCATTCAATGGAACAGACT 200

Db 3013 TTGGGAAATGCATT--AATGGAACAGACT 3040

RESULT 9

US-10-388-470-6

; Sequence 6, Application US/10388470

; GENERAL INFORMATION:

; APPLICANT: Dib-Hajj, Sulayman

; APPLICANT: Maxman, Stephen G.

; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

; FILE REFERENCE: 44574-5004-01-US

; CURRENT APPLICATION NUMBER: US/10/388,470

; PRIOR FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: US/09/354,147C

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: US 60/072,990

; PRIOR FILING DATE: 1998-01-29

; PRIOR APPLICATION NUMBER: US 60/109,402

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: PCT/US99/02008

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6

; LENGTH: 3701

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3699)

; OTHER INFORMATION: partial human Nan cDNA sequence

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (922)

; OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is

; US-10-388-470-6

Query Match 48.3%; Score 107.8; DB 50; Length 3701;

Best Local Similarity 96.0%; Pred. No. 1.4e-17;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 111

Db 2896 AAGGTGTGTCATGCTCTCATAGTGCATACCTCCCATCTGGAATGTTTGGCTTGT 2954

Qy 112 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 171

Db 2955 CTGCTCATTTTCTGGCTCGATTTTGTATCTGGAGTATACCTTC--TTTCTGGAAAA 3012

Qy 172 TTGGGAATGCATTCATGAGACACT 200  
Db 3013 TTGGGAATGCATT-AATGGAACAGACT 3040

## RESULT 10

US-10-170-235-13985  
; Sequence 113985, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; FILE REFERENCE: CI001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; NUMBER OF SEQ ID NOS: 2003-03-17  
; SEQ ID NO 13985  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-13985

Query Match 48.3%; Score 107.8; DB 46; Length 5080;

Best Local Similarity 96.0%; Pred. No. 1.5e-17; Mismatches 2; Indels 4; Gaps 3;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 111

Db 3647 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 3705

Qy 112 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 171

Db 3706 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 3763

Qy 172 TTGGGAATGCATTCATGAGACACT 200

Db 3764 TTGGGAATGCATT-AATGGAACAGACT 3791

## RESULT 11

US-60-453-050-2171  
; Sequence 2171, Application US/60453050  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: LUKE, May  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CI001457  
; CURRENT APPLICATION NUMBER: US/60/453,050  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-050-2171

Query Match 48.3%; Score 107.8; DB 102; Length 5080;

Best Local Similarity 96.0%; Pred. No. 1.5e-17; Mismatches 2; Indels 4; Gaps 3;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 111

Db 3647 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 3705

Qy 112 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 171

Db 3706 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 3763

Qy 172 TTGGGAATGCATTCATGAGACACT 200

Db 3764 TTGGGAATGCATT-AATGGAACAGACT 3791

RESULT 12  
US-60-453-135-2171  
; Sequence 2171, Application US/60453135  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CI001456  
; CURRENT APPLICATION NUMBER: US/60/453,135  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-2171

## RESULT 12

US-60-453-135-2171  
; Sequence 2171, Application US/60453135  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CI001456  
; CURRENT APPLICATION NUMBER: US/60/453,135  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-2171

Query Match 48.3%; Score 107.8; DB 102; Length 5080;

Best Local Similarity 96.0%; Pred. No. 1.5e-17; Mismatches 2; Indels 4; Gaps 3;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 111

Db 3647 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 3705

Qy 112 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 171

Db 3706 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 3763

Qy 172 TTGGGAATGCATTCATGAGACACT 200

Db 3764 TTGGGAATGCATT-AATGGAACAGACT 3791

## RESULT 13

US-60-466-412-2171  
; Sequence 2171, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CI001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-2171

Query Match 48.3%; Score 107.8; DB 103; Length 5080;

Best Local Similarity 96.0%; Pred. No. 1.5e-17; Mismatches 2; Indels 4; Gaps 3;

Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

Qy 52 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 111

Db 3647 AAGGTGTGTCATAGCTCTCATAGTGCATACCTCCCATCTCGAATGTTTGGCTTGT 3705

Qy 112 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 171

Db 3706 CTGCTCATTTTCGGCTCGATTTTGTATCTGGAGTAACTTCTTTCCGAGAAA 3763

Qy 172 TTGGGAATGCATTCATGAGACACT 200

Db 3764 TTGGGAATGCATT-AATGGAACAGACT 3791

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RESULT 14
US-10-219-051B-910
/ Sequence 910, Application US/10219051B
/ GENERAL INFORMATION:
/ APPLICANT: The General Hospital Corporation doing business as Massachusetts General
/ APPLICANT: Hospital / Bayer AG
/ TITLE OF INVENTION: Nucleotide sequences involved in pain
/ FILE REFERENCE: Lea 35693 Foreign Countries
/ CURRENT APPLICATION NUMBER: US/10/219,051B
/ PRIOR FILING DATE: 2003-05-09
/ PRIOR APPLICATION NUMBER: US 60/312,147
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: US 60/346,382
/ PRIOR FILING DATE: 2001-11-01
/ PRIOR APPLICATION NUMBER: US 60/333,347
/ PRIOR FILING DATE: 2001-11-26
/ NUMBER OF SEQ ID NOS: 14715
/ SOFTWARE: Perl script
/ SEQ ID NO 910
/ LENGTH: 5728
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)-(5728)
/ OTHER INFORMATION: n=a, c, g or t
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: EMBL / AF150882
/ DATABASE ENTRY DATE: 2000-01-16
US-10-219-051B-910
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Query Match 48.3%; Score 107.8; DB 47; Length 5728;

Best Local Similarity 96.0%; Pred.No. 1.5e-17; Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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QY 52 AAGTGTGTGTCATGCTCTCATAGTGTGCTACCTCCATTCCTGAATGTTTGTCTGT 111
    |||
DB 3692 AAGTGTGTGTCATGCTCTCATAGTGTGCTACCTCCATTCCTGAATGTTTGTCTGT 3750
QY 112 CTGCTCATTTTCTGCTCTGCTGTAATTTTGTATTTCTGGAGATATACCTTTCTCGAAAA 171
    |||
DB 3751 CTGCTCATTTTCTGCTCTGCTGTAATTTTGTATTTCTGGAGATATACCTTTCTCGAAAA 3808
QY 172 TTGGGAATGTCATTCATGGAACGACT 200
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DB 3809 TTGGGAATGTCATTCATGGAACGACT 3836
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RESULT 15

US-10-296-130-3

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/ Sequence 3, Application US/10296130
/ GENERAL INFORMATION:
/ APPLICANT: KANAZAWA, Ichiro
/ APPLICANT: GOTO, Jun
/ APPLICANT: JEONG, Seon-Yong
/ TITLE OF INVENTION: Human Sodium Channel SCN12A and SCN8A
/ FILE REFERENCE: 2002-1512A/WPC/00653
/ CURRENT APPLICATION NUMBER: US/10/296,130
/ CURRENT FILING DATE: 2003-07-30
/ PRIOR APPLICATION NUMBER: PCT/JP00/04629
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: JP2000-152085
/ PRIOR FILING DATE: 2000-05-23
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 5728
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (200)..(4534)
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/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: 5632
/ OTHER INFORMATION: n = a, g, c or t
/ PUBLICATION INFORMATION:
/ AUTHORS: Seon-Yong Jeong et al.
/ TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel a Subunit
/ JOURNAL: Biochem. Biophys. Res. Commun.
/ VOLUME: 267
/ ISSUE: 1
/ PAGES: 262-270
/ DATE: 2000-01-15
/ DATABASE ACCESSION NUMBER: Genbank AF150882
/ DATABASE ENTRY DATE: 2000-01-15
US-10-296-130-3
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Query Match 48.3%; Score 107.8; DB 48; Length 5728;

Best Local Similarity 96.0%; Pred.No. 1.5e-17; Matches 143; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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QY 52 AAGTGTGTGTCATGCTCTCATAGTGTGCTACCTCCATTCCTGAATGTTTGTCTGT 111
    |||
DB 3692 AAGTGTGTGTCATGCTCTCATAGTGTGCTACCTCCATTCCTGAATGTTTGTCTGT 3750
QY 112 CTGCTCATTTTCTGCTCTGCTGTAATTTTGTATTTCTGGAGATATACCTTTCTCGAAAA 171
    |||
DB 3751 CTGCTCATTTTCTGCTCTGCTGTAATTTTGTATTTCTGGAGATATACCTTTCTCGAAAA 3808
QY 172 TTGGGAATGTCATTCATGGAACGACT 200
    |||
DB 3809 TTGGGAATGTCATTCATGGAACGACT 3836
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Search completed: March 23, 2004, 04:00:18  
Job time : 1684.54 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 16:13:34 ; Search time 282.599 Seconds  
(without alignments)  
414.412 Million cell updates/sec

Title: US-09-646-224A-13

Perfect score: 223 1 ggcgcacccaccaccatc.....aggaattccagcattcct 223

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1155024 seqs, 262583689 residues

Total number of hits satisfying chosen parameters: 2310048

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	56.2	25.2 100374	US-60-548-091-5675	Sequence 5675, App
2	56	25.1 4852	US-60-548-091-267	Sequence 267, App
3	56	25.1 4855	US-60-548-091-266	Sequence 266, App
4	55.6	24.9 4855	US-60-548-091-268	Sequence 268, App
5	54.4	24.4 201	US-60-548-091-5534	Sequence 5534, App
6	53.2	23.9 201	US-60-548-091-19210	Sequence 19210, A
7	50.6	22.7 201	US-60-548-091-5523	Sequence 5523, App
8	50.4	22.6 5874	US-10-487-337-5	Sequence 5, App11
9	50.2	22.5 201	US-60-548-091-5578	Sequence 5578, App
10	50.2	22.5 6524	US-10-487-337-1	Sequence 1, App11
11	44.2	19.8 600	US-60-545-213-3899	Sequence 3899, App
12	44.2	19.8 600	US-60-545-213-8171	Sequence 8171, App
13	36.6	16.4 519599	US-10-765-790-73	Sequence 73, App1
14	35.2	15.8 32100	US-10-100-683-13405	Sequence 13405, A
15	34.6	15.5 201	US-60-548-091-5539	Sequence 5539, App
16	32.2	14.4 149591	US-10-767-471-10601	Sequence 10601, A
17	32	14.3 165502	US-10-796-280-12318	Sequence 12318, A
18	32	14.3 234309	US-10-796-280-12378	Sequence 12378, A
19	32	14.3 394468	US-60-548-091-5725	Sequence 5725, App
20	31.8	14.3 590	US-10-779-543-20169	Sequence 20169, App
21	31.8	14.3 1790242	US-10-767-471-10805	Sequence 10805, A
22	31.6	14.2 728	US-10-779-543-3471	Sequence 3471, App
23	31.6	14.2 1413	US-10-417-884A-1465	Sequence 1465, App
24	31.6	14.2 37544	US-09-889-874A-52	Sequence 52, App1
25	31.4	14.1 184	US-10-770-021-392	Sequence 392, App
26	31.2	14.0 321019	US-60-548-091-5604	Sequence 5604, App

27	31.2	14.0 1790242	US-10-767-471-10805	Sequence 10805, A
28	31	13.9 255	US-10-767-795-6395	Sequence 6395, App
29	31	13.9 185248	US-10-796-280-12228	Sequence 12228, A
30	30.8	13.8 300	US-10-779-543-1428	Sequence 1428, App
31	30.8	13.8 681	US-10-779-543-8139	Sequence 8139, App
32	30.8	13.8 765	US-10-779-543-1466	Sequence 1466, App
33	30.8	13.8 876	US-10-779-543-4539	Sequence 4539, App
34	30.8	13.8 876	US-10-779-543-4540	Sequence 4540, App
35	30.8	13.8 141646	US-60-550-051-3063	Sequence 3063, App
36	30.8	13.8 303523	US-10-796-280-12202	Sequence 12202, A
37	30.8	13.8 645179	US-10-796-280-12317	Sequence 12317, A
38	30.6	13.7 201	US-60-550-051-22567	Sequence 22567, A
39	30.6	13.7 99100	PCT-US03-35879-1	Sequence 1, App11
40	30.6	13.7 324272	US-60-550-051-1109	Sequence 1109, App
41	30.4	13.6 585	US-09-969-034-2496	Sequence 2496, App
42	30.4	13.6 1049	US-10-767-795-6515	Sequence 6515, App
43	30.4	13.6 22372	US-10-796-280-12462	Sequence 12462, A
44	30.4	13.6 32572	US-10-796-280-12422	Sequence 12422, A
45	30.4	13.6 65558	US-10-765-790-103	Sequence 103, App

#### ALIGNMENTS

```

RESULT 1
US-60-548-091-5675
; Sequence 5675, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001506
; CURRENT APPLICATION NUMBER: US/60/548, 091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5675
; LENGTH: 100374
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(100374)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7)
US-60-548-091-5675

Query Match      25.2%: Score 56.2; DB 7; Length 100374;
Best Local Similarity 70.3%; Pred. No. 6.6e-07;
Matches 102; Conservative 1; Mismatches 39; Indels 3; Gaps 2;

QY      49 CATAGGTGTGTGTCATAGCTCTCATAGTGCATACCTCCATTCCTGAATGTTTGGCT
DB      81960 CTTGAGGGTGTGTCATAGCTCTCATAGTGCATACCTCCATTCCTGAATGTTTGGCT 82018
QY      109 TGTTCGCTCATTTTTCGCGCTGATTTTGTATTCGTGGAGTATACCTCTTTTCCTGGA
DB      81960 CTTGAGGGTGTGTCATAGCTCTCATAGTGCATACCTCCATTCCTGAATGTTTGGCT 82018
QY      82019 CGTTCGCTCATTTTTCGCGCTGATTTTGTATTCGTGGAGTATACCTCTTTTCCTGGA
DB      82019 CGTTCGCTCATTTTTCGCGCTGATTTTGTATTCGTGGAGTATACCTCTTTTCCTGGA 82076
QY      169 AAATTTGGAGAAATGATTCATGGA 193
DB      82077 AAATTTGGAGAAATGATTCATGGA 82101

RESULT 2
US-60-548-091-267
; Sequence 267, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001506
; CURRENT APPLICATION NUMBER: US/60/548, 091
; CURRENT FILING DATE: 2004-02-27

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 1308.4 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-13

Perfect score: 223  
Sequence: 1 ggcgcacccctaccacccatc.....aggaaattccagcagcattcct 223

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_eeetba:\*  
2: em\_eeetbhum:\*  
3: em\_eeetbhum:\*  
4: em\_eeetbhum:\*  
5: em\_eeetbhum:\*  
6: em\_eeetbhum:\*  
7: em\_eeetbhum:\*  
8: em\_eeetbhum:\*  
9: gb\_eeet1:\*  
10: gb\_eeet2:\*  
11: gb\_eeet3:\*  
12: gb\_eeet4:\*  
13: gb\_eeet5:\*  
14: gb\_eeet6:\*  
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25: em\_ges\_hum:\*  
26: em\_ges\_hum:\*  
27: em\_ges\_hum:\*  
28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107.8	48.3	4614	29	AY404475 Homo sapi
2	99.8	44.8	496	28	AY404475 Homo sapi
3	83.6	37.5	4556	29	AY404477 Mus muscu
4	59.8	26.8	800	29	EX238165 Danio rer

5	59.6	26.7	616	28	AZ623890	AZ623890 IM0462J06
6	53.6	24.0	407	29	FR0002725	286508 F. rubripes
7	53.6	24.0	472	29	AI016157	AI016157 oc3j607.8
8	52.6	23.6	619	29	FR0002754	286537 F. rubripes
9	52.4	23.5	763	14	CA383436	CA383436.663616 NC
10	52.4	23.5	763	14	CA358980	CA358980.631834 NC
11	52.3	23.3	864	29	CNS05DWR	ALJ32964 Tetradon
12	50.6	22.7	751	13	BU226444	BU226444.60396353
13	50.6	22.5	574	14	CB608527	CB608527 AMGNUNC.N
14	48.2	21.6	519	14	CB534807	CB534807.768167 MA
15	48.2	21.6	833	13	BU116614	BU116614.603139753
16	48.2	21.5	717	29	CE190928	CE190928 tigr-g88-
17	47.6	21.3	5943	29	AY416499	AY416499 Homo sapi
18	47.2	21.2	576	12	BG548184	BG548184.602575340
19	46.6	20.9	746	13	CD348085	CD348085 UI-M-FY0-
20	46.6	20.9	746	13	BU117962	BU117962.603143496
21	46.4	20.8	633	14	CB457889	CB457889.716006 MA
22	45.4	20.4	969	29	CNS03TDH	AL259694 Tetradon
23	44.8	20.1	437	29	FR0002733	286516 F. rubripes
24	43.6	19.6	349	29	CE172038	CE172038 tigr-g88-
25	43.6	19.6	526	29	CE574768	CE574768 tigr-g88-
26	43.4	19.5	689	10	BF347024	BF347024.602021819
27	43.3	19.3	641	13	BX481709	BX481709 DFX2686F
28	42.6	19.1	4675	11	AK083220	AK083220 Mus muscu
29	42.6	18.8	532	9	AI137939	AI137939 UI-R-A1-d
30	41.6	18.7	470	10	BB855798	BB855798 BB855798
31	41.4	18.6	518	10	BB856854	BB856854 BB856854
32	41.4	18.6	717	29	CNS01812	AL108785 Drosophila
33	41.2	18.5	5666	29	AY416501	AY416501 Mus muscu
34	41.1	18.4	593	13	BW228855	BW228855 BW228855
35	40.8	18.3	318	10	BB592602	BB592602 BB592602
36	40.8	18.3	586	29	CE185451	CE185451 tigr-g88-
37	40.6	18.2	503	29	CE235101	CE235101 tigr-g88-
38	40.4	18.1	494	29	CE798323	CE798323 tigr-g88-
39	40.2	18.0	804	29	CNS0085D	AL051748 Drosophila
40	40.0	17.9	463	29	CE117510	CE117510 tigr-g88-
41	39.8	17.8	1004	14	CD386828	CD386828 AGNCOURT
42	39.4	17.7	692	12	BI759571	BI759571.603046989
43	39.2	17.6	224	13	BU927029	BU927029.86894909
44	39.2	17.6	380	13	BQ337986	BQ337986 QV3-NN102
45	39.2	17.6	496	29	CE392736	CE392736 tigr-g88-

#### ALIGNMENTS

RESULT 1	AY404475	4614 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY404475				
DEFINITION	Homo sapiens SCN11A gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY404475				
VERSION	AY404475.1	GI:39760452			
KEYWORDS	GSS				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., 1 (bases 1 to 4614)				
AUTHORS	Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)				
TITLE	JOURNAL				
REFERENCE	PUBMED				
AUTHORS	2 (bases 1 to 4614) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission				
TITLE					



Db	Query Match	Best Local Similarity	Score	Length	800;
Db	3194 CTGCCTCATTTTTCGTGCTCATATTTTGTATCTCTGGAGTAATATT--TTTTCCTGGAG	26.8%;	69.1%;	Pred. No. 0.0011;	DB 29; Length 800;
Qy	172 TTGGGAAATGCATTCAATGGAACAGACTTTTAGAATTT	96; Conservative	0; Mismatches	42; Indels	1; Gaps
Db	3252 TTTGGAAATGCATT--AATGGAACAGACATATAATAT				3250
RESULT 4					
LOCUS	BX338165			800 bp	DNA linear GSS 29-JAN-2003
DEFINITION	Danio rerio genomic clone DKEX-286P24, genomic survey sequence.				
ACCESSION	BX338165				
VERSION	BX338165.1			GI:28160499	
KEYWORDS	GSS.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Actinopterygii; Neopterygii; Teleostei; Osteariophysi;				
TITLE	Cypriniformes; Cyprinidae; Danio.				
JOURNAL	1 (bases 1 to 800)				
COMMENT	Humphray,S.J., Huckle,E. and Durham,J.L.				
FEATURES	Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome				
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	/db_xref="taxon:7955"				
	/clone="DKEX-286P24"				
	/tissue_type="Testis"				
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ORIGIN					
Query Match					
Best Local Similarity	26.8%;				
Score	69.1%;				
Length	800;				
Matches	96; Conservative				
	0; Mismatches				
	42; Indels				
	1; Gaps				
Qy	35 TTGCTTTTGTTCATTAAGTGTGTGTCATAGCTCTGATAGTGCCATCTCCATTC				94
Db	174 TTGGCTTCTGTGTTTGTATGAGGTAGTGAAGCGCTCTTCTTGAGCCATCTTCA				232
Qy	95 CTGAATGTTTGTCTGTCTGCTCAATTTTCGGCTCGATTTTGTATTCGGAGTAAAC				154
Db	233 ATGAATGTGTTGCTGTGTGCTGTATCTTGGCTGATCTTCAGCATCATGGGGTGAAC				292
Qy	155 TTGCTTTTCCCTGGAATTT				173
Db	293 CTCCTTCCCGGAAATATT				311
RESULT 5					
LOCUS	AZ623890			616 bp	DNA linear GSS 13-DEC-2000
DEFINITION	IM0462J06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic				
ACCESSION	clone UUGC1M0462J06 F, genomic survey sequence.				
VERSION	AZ623890				
KEYWORDS	AZ623890.1			GI:11746080	
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Mus musculus				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 616)				
	Dunn,D., Aoyagi,A., Barber,M., Bascorn,T., Duval,B., Hamil,C.,				
	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,				
	Reilly,W., Rose,M., Rose,R., Stokes,R., Tingey,A., von				
	Niederhausern,A. and Wright,D., Weiss,R.				

JOURNAL	COMMENT	FEATURES	source
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0462 row: j column: 06 Seq primer: CGTTGTAAACGACGGCCACT Class: plasmid ends High quality sequence stop: 616.		
LOCATION/Qualifiers			
1. 616			
/organism="Mus musculus"			
/mol_type="genomic DNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="MUGC1M0462J06"			
/sex="Male"			
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"			
/clone_lib="Mouse 10kb plasmid UUGC1M library"			
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
ORIGIN			
Query Match	26.7%; Score 59.6; DB 28; Length 616;		
Best Local Similarity	63.9%; Pred. No. 0.0012;		
Matches 106; Conservative	0; Mismatches 59; Indels 1; Gaps 1;		
34	TTTGCTTTGTTTCCATTAAGTGGTGCATGCTCTCATTAGTGCATACCTCCATT 93		
Db	F. rubripes F. rubripes GSS sequence, clone 010M03ab3, genomic survey sequence.		
59	TCTTCTTCTGTTTCCACACAGTAGTGATGATCCTTGATGGCGCATTCCTCCA-T 117		
94	CCTGAATGTTTGGCTTGCTGCTCCTCATTTTGGCTCGTATTTGATTTCTGGAGTATA 153		
Db	CATGAAGCTCCTCCTCGTGGCTCATCTTCTGCTCATCTTCAGATCATAGGTGAA 177		
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154	CTTCTCTTTCTGGAATAATTGGGAATGCATTCATGGAACAGAC 199		
178	CCTCTTGGCCGGGAATTTTCGAGATGTGCGACACCAAGCAAC 223		
RESULT 6			
FR0002725/c			
LOCUS	FR0002725 407 bp DNA linear GSS 27-FEB-1997		
DEFINITION	F. rubripes GSS sequence, clone 010M03ab3, genomic survey sequence.		
ACCESSION	Z86508		
VERSION	Z86508.1 GI:1883420		
KEYWORDS	GSS: genome survey sequence.		
SOURCE	Takifugu rubripes (Fugu rubripes)		
ORGANISM	Takifugu rubripes		





QY 173 TTGGGAATGATTCATGGA 193  
 Db 365 TTGGCCCTGGCTCAACCGA 385

RESULT 9  
 CA383436  
 LOCUS 672 bp mRNA linear EST 06-NOV-2002  
 DEFINITION 663616 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT29H17\_B\_D09 5', mRNA sequence.  
 ACCESSION CA383436  
 VERSION CA383436.1 GI:24707883  
 KEYWORDS EST.  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM Oncorhynchus mykiss (rainbow trout)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 672)  
 Rexroad, C.E. and Keeler, J.W.  
 Sequence analysis of a rainbow trout normalized cDNA library  
 Unpublished (2002)  
 Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccgwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alc option. Vector identified by cross\_match v0.990329.  
 Seq primer: AGCGATACAAATTTTCACACAGA.  
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ORIGIN  
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 Best Local Similarity 69.7%; Pred. No. 0.052; Indels 1; Gaps 1;  
 Matches 85; Conservative 0; Mismatches 36;

QY 39 TTTGTTTTCATAGAGTGATGCTCATAGTGCATATCCCATTCCTGA 98  
 Db 552 TTTTGAAGGATGAGGCTGTAGTCAAGCCCTGTGGAGCACTCCCTCATTT-ATGA 610

QY 99 ATGTTTGCTTGTCTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGATATCTCC 158  
 Db 611 ATGTTTGCTGTTGCTCATCTTTTGGCTGATTTTCAATATGAGATCAACTGT 670

QY 159 TT 160  
 Db 671 TT 672

RESULT 10  
 CA358980 763 bp mRNA linear EST 05-NOV-2002  
 LOCUS 631834 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT5D21\_B\_B11 5', mRNA sequence.  
 ACCESSION CA358980  
 VERSION CA358980.1 GI:24604167  
 KEYWORDS EST.  
 SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 763)  
 Rexroad, C.E. and Keeler, J.W.  
 Sequence analysis of a rainbow trout normalized cDNA library  
 Unpublished (2002)  
 Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccgwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alc option. Vector identified by cross\_match v0.990329.  
 Seq primer: AGCGATACAAATTTTCACACAGA.  
 Location/Qualifiers  
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ORIGIN  
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 Best Local Similarity 69.7%; Pred. No. 0.051; Indels 1;  
 Matches 85; Conservative 0; Mismatches 36;

QY 39 TTTGTTTTCATAGAGTGATGCTCATAGTGCATATCCCATTCCTGA 98  
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QY 99 ATGTTTGCTTGTCTGCTCATTTTCTGCTCGATTTTGTATTTCTGGAGATATCTCC 158  
 Db 158 ATGTTTGCTGTTGCTCATCTTTTGGCTGATTTTCAATATGAGATCAACTGT 217

QY 159 TT 160  
 Db 218 TT 219

RESULT 11  
 CA358980 864 bp DNA linear GSS 01-SEP-2000  
 LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone 030G19 of library B from Tetradon nigroviridis, genomic survey sequence.  
 ACCESSION AL332964  
 VERSION AL332964.1 GI:8226722  
 KEYWORDS GSS: genome survey sequence.  
 SOURCE Tetradon nigroviridis  
 ORGANISM Tetradon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodonidae; Tetraodon.  
 1  
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizaes, C., Wincker, P., Broctier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)  
 JOURNAL 20296633  
 MEDLINE 10833645  
 PUBMED

REFERENCE  
AUTHORS 2  
Roest Crolius, H., Jallion, O., Dastiva, C., Ozouf-Costaz, C.,  
Pirames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
Saurin, W., Bernot, A. and Weissenbach, J.  
TITLE  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish *Tetraodon nigroviridis*  
JOURNAL  
Genome Res. 10 (7), 939-949 (2000)  
MEDLINE  
20359837  
PUBMED  
10899143  
REFERENCE  
3 (bases 1 to 864)  
Genoscope.  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the *Tetraodon nigroviridis*  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.  
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Best Local Similarity 64.6%; Pred. No. 0.062;  
Matches 93; Conservative 0; Mismatches 50; Indels 1; Gaps 1;  
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DB 441 TCCGTTCTTTCGTCATATTCAGGTGTGTGACGCCCTGAGGTCATACCCCTC 500  
QY 90 CATTCCTGAATGTTTGTCTGTCTGCTCATTTTTCGTCGATTTGTATTCGGAG 149  
DB 501 CATATGAACGTGCTACTGTGTGTCTCATCTTCGCTCATCTTCACATCATGCGG 559  
QY 150 TATACCTCTTTCCTCGAAATTT 173  
DB 560 TCAACCTGTTTGTGCGAAGTATT 583  
RESULT 12  
BU226444 751 bp mRNA linear EST 26-NOV-2002  
LOCUS BU226444  
DEFINITION 603946353P1 CSEQCHN23 Gallus gallus cDNA clone CHEST899j14 5', mRNA  
sequence.  
ACCESSION BU226444 GI:25463376  
VERSION BU226444  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 751)  
Boardman, P.E., Sanz-Bzquez, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
JOURNAL  
MEDLINE  
12445392  
PUBMED  
12445392  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409

FEATURES  
source  
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/organism="Gallus gallus"  
/mol\_type="mRNA"  
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/dev\_stage="22"  
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/clone\_1lb="CSEQCHN23"  
/note="Organ: heads; Vector: Bluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was bluntended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996) : 791, except that a significantly longer  
reannealing hybridization was used."  
ORIGIN  
Query Match 22.7%; Score 50.6; DB 13; Length 751;  
Best Local Similarity 72.5%; Pred. No. 0.13;  
Matches 79; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
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DB 296 AGGGTGTGTAATGCTCTTGTAGAGCAATTCATCTA-TCATGATGATATTCGTGT 354  
QY 112 CTGCCTCATTTTCTGAGCTGTATTTTGTATTCGGAGTATATCTTCTT 160  
DB 355 TTGCTTATTTCTGAGCTCATCTTCAGCATCATGAGATATATCTCTT 403  
RESULT 13  
CB608527 574 bp mRNA linear EST 16-MAY-2003  
LOCUS CB608527  
DEFINITION AMGNNUC:NRDGL-00143-D3-A nrdgl (10855) Rattus norvegicus cDNA clone  
nrdgl-00143-d3 5', mRNA sequence.  
ACCESSION CB608527 GI:29548140  
VERSION CB608527  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 574)  
Amgen EST Program.  
Amgen Rat EST Program  
Unpublished (2003)  
COMMENT  
Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00143 row: d column: 3.  
location/Qualifiers  
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dorsal root ganglia"  
ORIGIN

Email: Simon.Hubbard@umist.ac.uk.

QY 160 T 160

Db 525 T 525

Wed Mar 24 11:10:38 2004

us-09-646-224a-13.rst

Page 8

Search completed: March 22, 2004, 23:12:48  
Job time : 1321.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 1297.82 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-14

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_hlg: \*  
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8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
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32: em\_hlg\_other: \*  
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41: em\_hgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	244	100.0	244	6 BD138452	BD138452 Mammalian
3	226.4	92.8	167476	9 AC116038	AC116038 Homo sapi
4	76.8	31.5	210800	2 AC127824	AC127824 Rattus no
5	76.8	31.5	243048	2 AC127215	AC127215 Rattus no
6	65.4	26.8	241289	2 AC124662	AC124662 Mus muscu
7	53.2	21.8	146144	2 AC138446	AC138446 Felis cat
8	51.8	21.2	139245	2 AC137540	AC137540 Felis cat
9	51.8	21.2	142025	2 AC137541	AC137541 Felis cat
10	50.4	20.7	144218	2 AC144468	AC144468 Canis fam
11	50.4	20.7	223041	2 AC144469	AC144469 Canis fam
12	50.2	20.6	156655	2 AC144605	AC144605 Canis fam
13	50.2	20.6	208456	2 AC144470	AC144470 Canis fam
14	49.2	20.2	203255	2 AC117294	AC117294 Rattus no
15	49.2	20.2	232282	2 AC094738	AC094738 Rattus no
16	49.2	20.2	236613	2 AC135877	AC135877 Rattus no
17	49.2	20.1	103065	9 AC137625	AC137625 Homo sapi
18	48.8	20.0	156678	2 AC145026	AC145026 Sus scrofa
19	48.8	20.0	204398	10 AL844526	AL844526 Mouse DNA
20	48.6	19.9	128632	10 BX284648	BX284648 Mouse DNA
21	48.6	19.9	128632	10 AC110223	AC110223 Mus muscu
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23	48.4	19.8	204990	2 AC138163	AC138163 Bos tauru
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25	48	19.7	1312	6 AX164264	AX164264 Sequence
26	48	19.7	168493	9 AC013463	AC013463 Homo sapi
27	48	19.7	168493	9 AC013463	AC013463 Homo sapi
28	47.8	19.6	124919	2 AC139738	AC139738 Felis cat
29	47.4	19.4	480	6 AX164230	AX164230 Sequence
30	47.4	19.4	701	6 F327224S20	F327224S20 Sequence
31	47.4	19.4	188616	9 AC011303	AC011303 Homo sapi
32	47.2	19.3	385	9 HUMSCN4A17	LO4233 Homo sapien
33	47.2	19.3	37115	2 AC139098	AC139098 Homo sapi
34	47.2	19.3	44566	2 AC139088	AC139088 Homo sapi
35	47.2	19.3	101990	9 AC127029	AC127029 Homo sapi
36	47.2	19.3	162473	9 AC005803	AC005803 Homo sapi
37	47	19.3	856	6 E36123	E36123 Nucleic aci
38	47	19.3	3701	6 AR340648	AR340648 Sequence
39	47	19.3	3701	6 BD217793	BD217793 Regulatio
40	47	19.3	5419	9 HSA417790	AJ417790 Homo sapi
41	47	19.3	5728	6 BD012083	BD012083 Human bod
42	47	19.3	5728	6 BD082952	BD082952 Human bod
43	47	19.3	5728	6 AF150882	AF150882 Homo sapi
44	47	19.3	5860	6 AR340678	AR340678 Sequence
45	47	19.3	6237	9 AF188679	AF188679 Homo sapi

ALIGNMENTS

RESULT 1  
LOCUS AX017230  
DEFINITION Sequence 14 from Patent WO947670.  
ACCESSION AX017230  
VERSION AX017230.1 GI:10042150  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Tate, S.N., Grose, D.T. and Hick, C.A.  
Mammalian sodium channel proteins  
Patent: WO 9947670-A 14 23-SEP-1999;  
JOURNAL

TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS (GB); HICK CAROLINE ANNE (GB)

## FEATURES

source

1.244  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 244; DB 6; Length 244;  
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Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAGATATTCATGTTTCTGCTTTTGGACGACATTTAAGGCTGATGAT 60  
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QY 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
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QY 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
DB 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
QY 241 CCTA 244  
DB 241 CCTA 244

RESULT 2  
LOCUS BD138452 244 bp DNA linear PAT 18-SEP-2002  
DEFINITION Mammalian sodium channel protein.  
ACCESSION BD138452  
VERSION BD138452.1 GI:23233397  
KEYWORDS JP 2002508941-A/13.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1 (bases 1 to 244)  
AUTHORS Grose,D.T., Hick,C.A. and Tate,S.N.  
TITLE Mammalian sodium channel protein  
JOURNAL Patent: JP 2002508941-A 13 26-MAR-2002;  
GLAXO GROUP LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2002508941-A/13  
PD 26-MAR-2002  
PR 18-MAR-1999 JP 2000536653  
PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N1/09,A61K45/00,A61P17/04,A61P25/02,C07K14/705,C07K16/28, PC  
C12N1/15,  
PC C12N1/19,C12N1/21,C12N5/10,C12Q1/02,G01N33/15,G01N33/50,G01N33/ PC  
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CC Mammalian sodium channel protein  
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## FEATURES

source

## ORIGIN

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Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
DB 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
QY 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
DB 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
QY 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
DB 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
QY 241 CCTA 244  
DB 241 CCTA 244

RESULT 3  
LOCUS AC116038/c 167476 bp DNA linear PRI 07-OCT-2003  
DEFINITION Homo sapiens chromosome 3 clone RP11-134J21, complete sequence.  
ACCESSION AC116038  
VERSION AC116038.3 GI:37537604  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Unpublished  
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
REFERENCE 3 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
COMMENT On Oct 7, 2003 this sequence version replaced gi:21622736.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgchgs@u.washington.edu  
----- Project Information  
Center project name: chr-3  
Center clone name: RP11-134J21 (bc0780)  
----- Summary Statistics  
Sequencing vector: plasmid; 100% of reads  
Chemistry: Dye-terminator ET; 45% of reads

QY 1 ATCAGATATTCATGTTTCTGCTTTTGGACGACATTTAAGGCTGATGAT 60  
DB 1 ATCAGATATTCATGTTTCTGCTTTTGGACGACATTTAAGGCTGATGAT 60  
QY 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
DB 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
QY 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
DB 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
QY 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
DB 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
QY 241 CCTA 244  
DB 241 CCTA 244

QY 1 ATCAGATATTCATGTTTCTGCTTTTGGACGACATTTAAGGCTGATGAT 60  
DB 1 ATCAGATATTCATGTTTCTGCTTTTGGACGACATTTAAGGCTGATGAT 60  
QY 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
DB 61 ATCGTTTATGACGCTGTTGATTCACAGAGTGAGTCAAGTCTTACATGTTGGCAGT 120  
QY 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
DB 121 GTTATGTCAGTCAAGATATCATGATGATGATGATGATGATGATGATGAT 180  
QY 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
DB 181 CCAGAGCTGGGGTCTCTGCTTTGCTTTGGAACAAACATATGATGATGATGAT 240  
QY 241 CCTA 244  
DB 241 CCTA 244

Chemistry: Dye-terminator Big Dye; 55% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 167467 bases at least Q40  
 Consensus quality: 167476 bases at least Q30  
 Consensus quality: 167476 bases at least Q20  
 Insert size: 167476; sum-of-contigs  
 Quality coverage: 18.9x in Q20 bases; sum-of-contigs

## Overlapping Sequences:

5' : Rp11-1114A3 AC137625, 2001-bp overlap  
 3' : Rp11-182A24 (UMGC:bc0782) AC123903, 41341-bp overlap

## Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
 all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglIII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8629	2732	2741	2234	2259
6	<800	6382	6514	2067	2008
2248	2299	512	<800	5097	5007
9345	9792	449	<800	2317	2259
2016	2003	2707	2741	2813	2744
4889	4771	4809	4878	2537	2550
3455	3447	184	<800	1923	2008
245	<800	5818	5899	2486	2550
72	<800	1364	1346	4036	3992
4175	4167	999	990	2583	2550
72	<800	3014	3028	8136	8039
6640	6560	4721	4667	2738	2744
4710	4771	727	745	4704	4629
3468	3447	179	<800	2649	2744

687	<800	7123	7158	2550	2550
3049	3091	2078	2040	5020	4862
762	<800	1891	1888	6949	6960
553	<800	8072	8171	4636	4629
5080	5088	92	<800	3588	3544
6613	6560	3674	3639	604	<800
8963	9211	5478	5397	5748	6106
331	<800	240	<800	953	943
2328	2299	5050	4878	4728	4629
2038	2003	1053	1068	178	<800
712	<800	3231	3264	1222	1220
1368	1370	86	<800	694	<800
182	<800	5444	5397	3022	3007
1620	1560	1265	1228	4079	3992
775	<800	438	<800	1294	1220
2583	2686	1436	1408	2044	2008
2709	2686	5528	5397	3725	3544
19834	19753	475	<800	790	<800
8729	8629	2310	2371	4232	4223
2264	2299	5177	5089	396	<800
651	<800	391	<800	4714	4629
7181	7213	166	<800	2486	2550
6166	6159	3594	3639	14	<800
500	<800	1172	1188	4240	4223
8764	8629	316	<800	879	917
57	<800	4023	4039	317	<800
3737	3718	1975	2040	161	<800
3711	3718	324	<800	1198	1220
9961	9792	1341	1346	1967	2008
560	<800	4463	4430	344	<800
8662	8629	3569	3639	6314	6531
1565	1560	1229	1188	2731	2744
309	<800	7414	7557	3335	3339
835	822	511	<800	253	<800
1568	1560	602	<800	1242	1220
731	766	1501	1555	4557	4629
		6843	6824	3630	3727







Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 Project Information  
 Center project name: GDUK  
 Center clone name: CH230-10N16  
 Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 229285 bases at least Q40  
 Consensus quality: 231657 bases at least Q30  
 Consensus quality: 233138 bases at least Q20  
 Estimated insert size: 236807; sum-of-coverage estimation  
 Quality coverage: 7x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 2 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 241919: contig of 241919 bp in length  
 \* 241920 242019: gap of unknown length  
 \* 242020 243048: contig of 1029 bp in length.

FEATURES  
 source  
 1..243048  
 location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clone="CH230-10N16"  
 1..1569  
 misc\_feature  
 /note="wgs\_contig"  
 240939..241455  
 /note="clone boundary  
 clone\_end:Sp6  
 site:  
 end\_sequence:BH308290"

ORIGIN  
 Query Match 31.5%; Score 76.8; DB 2; Length 243048;  
 Best Local Similarity 70.8%; Pred. No. 9.2e-14;  
 Matches 102; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

19 TTTTCGCTTTTTCGAGCAAAATTAAAGGCTGATGATGCTTTATGCACTGTT 78  
 |||||  
 29578 TTTTCACTCTGTTTCAGGCAACCTATTAAGGCTGCTGGAATCATGATGATCTGCTGTC 29519  
 |||||  
 79 GATTCACAGAGAGTGTAGTCTTACCATGTTCCGAGTGTATGTCATGCAAGTCAGAG 138  
 |||||  
 29518 GATTCACAGAGAGTGTAGTCTTACCATGTTCCGAGTGTATGTCATGTCATGCAAGTCAGAG 29459  
 |||||  
 139 ATATCATGACTACATGACAGCTCC 162  
 |||||  
 29458 GTGCTATGATGTGTGACGCGCC 29435  
 |||||

RESULT 6  
 AC124662 241289 bp DNA linear HTG 22-NOV-2003  
 LOCUS AC124662 Mus musculus chromosome 9 clone RP24-409K22 map 9, \*\*\* SEQUENCING  
 DEFINITION IN PROGRESS \*\*\*; 11 unordered pieces.  
 AC124662  
 AC124662.5 GI:38490569  
 HTG; HTGS PHASE1; HTGS FULLTOP; HTGS ACTIVEFIN.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 241289)  
 Birten,B., Nusbaum,C. and Lander,E.  
 TITLE Mus musculus chromosome 9, clone RP24-409K22

JOURNAL  
 2 (bases 1 to 241289)  
 Birten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,  
 Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
 Chazaro,B., Choepel,Y., Collange,M., Collins,S., Collymore,A.,  
 Cook,A., Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., Fitzgerald,M., Fitzhugh,M., Gage,D.,  
 Galagan,J., Gardina,S., Gande,S., Gord,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,  
 Johnson,R., Jones,C., Kamet,A., Karatas,A., Kells,C., Larocque,K.,  
 Lamasares,R., Landers,T., Lenoczky,J., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,J., Margolis,N.,  
 Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,  
 Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
 Pollara,V., Raymond,C., Rella,R., Riebeck,M., Riley,R., Rite,C.,  
 Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,  
 Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,  
 Stojanovic,N., Strauss,N., Subramanian,A., Talamas,U., Testfaye,S.,  
 Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,  
 Vasilev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,U., Zembek,L., Zimmer,A. and Zody,M.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 3 (bases 1 to 241289)  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 Direct Submission

1 241289  
 Birten,B., Nusbaum,C., Lander,E., Abouelell,A., Allen,N.,  
 Anderson,S., Atschili,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., Deatellano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardina,S.,  
 Graham,L., Grand-Pierre,N., Haler,N., Hagos,B.,  
 Hall,D., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamet,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrim,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
 Rachupka,A., Ramasamy,U., Raymond,C., Rella,R., Rite,C., Rogov,P.,  
 Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talamas,U., Testfaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vasilev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,U., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission  
 Submitted (22-NOV-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 22, 2003 this sequence version replaced gi:38153914.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIDR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: L26677  
 Center clone name: 409\_K\_22

NOTE: This is a 'working draft' sequence. It currently  
 consists of 11 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 56842: contig of 56842 bp in length

56843 56942: gap of 100 bp  
56943 95966: contig of 39024 bp in length  
56967 96066: gap of 100 bp  
95967 133016: contig of 36950 bp in length  
133017 133116: gap of 100 bp  
133117 138788: contig of 5672 bp in length  
138789 138889: gap of 100 bp  
138889 157002: contig of 18114 bp in length  
157003 157102: gap of 100 bp  
157103 162695: contig of 5593 bp in length  
162696 162796: gap of 100 bp  
162796 165266: contig of 2471 bp in length  
165267 187706: gap of 100 bp  
187707 187806: gap of 100 bp  
187807 210027: contig of 22221 bp in length  
210028 210127: gap of 100 bp  
210128 224271: contig of 14144 bp in length  
224272 224372: gap of 100 bp  
224372 241289: contig of 16918 bp in length.

Location/Qualifiers  
1. 241289  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="9"  
/map="9"  
/clone="RP24-409K22"  
/clone\_11b="RPC1-24 Male Mouse BAC"

ORIGIN  
Query Match 26.8%; Score 65.4; DB 2; Length 241289;  
Best Local Similarity 66.6%; Pred. No. 5.2e-10;  
Matches 105; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 18 TTTTCGTTTTCGAGGACCAATTAAAGGCTGATGATATCGTTTATGAGCGCT 77  
Db 217443 TTTTCGTTTTCGAGGACCAATTAAAGGCTGATGATATGAGGCTGCT 217502

QY 78 TGATTCACAGAGGTGAGT--CAGTGTCTACATGTTCCGACAGTGTATGTCAGTCA 135  
Db 217503 TGATTCACAGAGGTGAGTAAAGTCTCAGTGTCTAGAGTGTATGTCAGTCA 217562

QY 136 GAGATATCATGACTACATGACAGTCCAGAACT 168  
Db 217563 GCGGTACTATGAGTTCGACAGCGCCCTACT 217595

RESULT 7  
AC138446 146144 bp DNA linear HTG 05-FEB-2003  
LOCUS Felis catus clone RP86-556K17, WORKING DRAFT SEQUENCE, 5 ordered  
DEFINITION pieces.  
AC138446  
AC138446.2 GI:28209439  
VERSION HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
KEYWORDS Felis catus (cat)  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
1 (bases 1 to 146144)  
Ahter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
Carliaga,K., Coleman,B., Engle,J., Grantle,S., Guan,X., Gupta,J.,  
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,  
Laric,P., Lee-Ilan,S.-O., Legaspi,R., Maduro,Q.L., Maduro,V.B.,  
Masiello,C., Maskeri,B., McDowell,J.,  
Paguigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,  
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,  
Stentrop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,  
Wehrby,K.D., Wiggins,L., Young,A. and Green,E.D.  
NISC Comparative Sequencing Initiative

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

2 (bases 1 to 146144)  
Green,E.D.  
Direct Submission  
Submitted (03-JAN-2003) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Galtersburg, MD 20877, USA  
3 (bases 1 to 146144)  
Green,E.D.  
Direct Submission  
Submitted (05-FEB-2003) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Galtersburg, MD 20877, USA  
On Feb 5, 2003 this sequence version replaced gi:27476134.  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: nisc\_zoo@nih.gov  
----- Project Information  
Center project name: dzm  
Center clone name: 556K17

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 145261 bases at least Q40  
Consensus quality: 145617 bases at least Q40  
Consensus quality: 145697 bases at least Q20  
Insert size: 142000; agarose-fp  
Insert size: 145744; sum-of-contigs  
Quality coverage: 9.18x in Q20 bases; agarose-fp  
Quality coverage: 8.95x in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 11576: contig of 11576 bp in length  
1 11577 11676: gap of unknown length  
1 11677 74352: contig of 62676 bp in length  
1 74353 74452: gap of unknown length  
1 74453 78922: contig of 4470 bp in length  
1 78923 79022: gap of unknown length  
1 79023 142614: contig of 63592 bp in length  
1 142615 142715: gap of unknown length  
1 142715 146144: contig of 3430 bp in length.

Location/Qualifiers  
1. 146144  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9685"  
/clone="RP86-556K17"  
/clone\_11b="RP86"  
1. 11576  
/note="assembly fragment  
missing 77 clone end on 5' end of insert"  
11677. 74352

misc\_feature  
misc\_feature  
misc\_feature

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7453..78922  
/note="assembly_fragment"  
misc_feature         /note="assembly_fragment"  
79023..142614  
/note="assembly_fragment"  
misc_feature         /note="assembly_fragment"  
142715..146144  
/note="assembly_fragment"  
clone_end:SP6  
vector_side:right"  
  
ORIGIN  
Query Match      21.8%; Score 53.2; DB 2; Length 146144;  
Best Local Similarity 78.0%; Pred. No. 5.3e-06;  
Matches 64; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 21 TCTGCTTTTTCAGGCACAAATTAAAGGCTTGATGATATCGTTTATGACACTGTGA 80  
|||||  
Db 112354 TCTGACTTTTTTACAGGCCACCACTTTAAGGATGATGATCATGTATGACACTGTGA 1124133  
|||||  
QY 81 TTCCACAGAGGTGACTCAGT 102  
|||||  
Db 112414 TTCAGAAAACGTAAAGCTATT 112435  
|||||  
  
RESULT 8  
AC137540/c 139245 bp DNA linear HTG 18-DEC-2002  
LOCUS Fells catus clone RP86-386P20, WORKING DRAFT SEQUENCE, 9 ordered  
DEFINITION Pieces.  
AC137540  
VERSION AC137540.2 GI:27228821  
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.  
SOURCE Fells catus (cat)  
ORGANISM Fells catus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
REFERENCE  
AUTHORS 1 (bases 1 to 139245)  
Akhter,N., Antomellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
Carriaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,  
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,B.,  
Latric,P., Lee-Lin,S.-O., Legaspi,R., Maduro,Q.L., Maduro,V.B.,  
Marquis,E.H., Maselli,C., Maskeri,B., McDowell,J.,  
Paguirigan,C., Pearson,R., Porhoy,M.E., Prasad,A.,  
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,  
Stattrop,S., Thomas,J.W., Thomas,P.J., Touchman,D.W., Vogt,J.L.,  
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 139245)  
Green,E.D.  
DIRECT SUBMISSION  
Submitted (22-NOV-2002) NIH Intramural Sequencing Center, 8717  
Grovermont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 139245)  
Green,E.D.  
DIRECT SUBMISSION  
Submitted (18-DEC-2002) NIH Intramural Sequencing Center, 8717  
Grovermont Circle, Gaithersburg, MD 20877, USA  
On Dec 18, 2002 this sequence version replaced gi:25167123.  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc_zoo@hgri.nih.gov  
----- Project Information  
Center project name: dzt  
Center clone name: 386P20
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```

data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 137738 bases at least Q40
Consensus quality: 138102 bases at least Q30
Consensus quality: 138333 bases at least Q20
Insert size: 125000; agarose-fp
Insert size: 138445; sum-of-contigs
Quality coverage: 9.74x in Q20 bases; agarose-fp
Quality coverage: 8.80x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1
* 7979 8078: gap of unknown length
* 8079 10289: contig of 2211 bp in length
* 10290 10389: gap of unknown length
* 10390 41759: contig of 31370 bp in length
* 41760 41859: gap of unknown length
* 41860 66912: contig of 25053 bp in length
* 66913 67013 67012: gap of unknown length
* 67013 68082: contig of 1070 bp in length
* 68083 68182: gap of unknown length
* 68183 69342: contig of 1160 bp in length
* 69343 69442: gap of unknown length
* 69443 86961: contig of 17519 bp in length
* 86962 87061: gap of unknown length
* 87062 96862: contig of 9801 bp in length
* 96863 96962: gap of unknown length
* 96963 139245: contig of 42283 bp in length.
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* Location/Qualifiers
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* 1. 139245
* /organism="Pala catus"
* /mol_type="genomic DNA"
* /db_xref="taxon:9685"
* /clone="RP86-386P20"
* /clone_1lb="RP86"
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* 1. 45684
* /note="clone overlaps with GenBank Accession Number
* AC137541 clone RP86-558L14 (center project name d2s)"
*
* 1. 7978
* /note="assembly_fragment
* clone_end:SP6
* vector_side:left"
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* 8079..10289
* /note="assembly_fragment"
* 10390..41759
* /note="assembly_fragment"
* 41860..66912
* /note="assembly_fragment"
* 67013..68082
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* 68183..69342
* /note="assembly_fragment"
* 69443..86961
* /note="assembly_fragment"
* 87062..96862

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clone\_end:17  
vector\_side:right"

ORIGIN

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Best Local Similarity 74.7%; Pred. No. 1.5e-05;  
Matches 65; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 10 ATTGATGTTTTCGCTTTTTCAGGACAAATTTAAGGCGGATGATATGCTTAT 69  
DB 18980 ATTGATGTTTATGTTATTTATTAAGGCAACATTTAAGGATGATGATATATGAT 18921

QY 70 GCAGCTGTTGATTCACAGAGTGAGT 96  
DB 18920 GCAGCTGTTGATTCGTTAATGTAAGT 18894

RESULT 9 AC137541 142025 bp DNA linear HTG 18-DEC-2002  
AC137541/c Felis catus clone RP86-558L14, WORKING DRAFT SEQUENCE, 3 ordered  
LOCUS pieces.

ACCESSION AC137541.2 GI:27228822  
VERSION HTG; HTGS PHASE2; HTGS\_DRAFT.  
KEYWORDS Felis catus (cat)  
SOURCE Felis catus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE 1 (bases 1 to 142025)  
AUTHORS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,  
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
Carlaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,  
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,  
Margulies, E.H., Masello, C., Maskeri, B., McDowell, J.,  
Margulies, C., Pearson, R., Portnoy, M.E., Prasad, A.,  
Pugitigan, N., Schandler, K., Schueler, M.G., Simon, C.,  
Stratford, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
Wehrby, K.D., Wiggins, L., Young, A. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 142025)  
Green, E.D.  
Direct Submission  
Submitted (22-NOV-2002) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 142025)  
Green, E.D.  
Direct Submission  
Submitted (18-DEC-2002) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gaithersburg, MD 20877, USA  
On Dec 18, 2002 this sequence version replaced gi:25167124.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
COMMENT

Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc\_zoo@nigrl.nih.gov  
Project Information  
Center project name: dzt  
Center clone name: 558L14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average

coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 141628 bases at least Q40  
Consensus quality: 141751 bases at least Q30  
Consensus quality: 141818 bases at least Q20  
Insert size: 130000; agarose-1p  
Insert coverage: 141825; sum-of-contigs  
Quality coverage: 12.59x in Q20 bases; agarose-1p  
Quality coverage: 11.54x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 7831: contig of 7831 bp in length  
\* 7832 7931: gap of unknown length  
\* 7932 71572: contig of 63641 bp in length  
\* 71573 71672: gap of unknown length  
\* 71673 142025: contig of 70353 bp in length.  
Location/Qualifiers  
1. 142025  
/organism="Felis catus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9685"  
/clone="RP86-558L14"  
/clone\_1b="RP86"  
1. 7831  
/note="assembly\_fragment  
clone\_end:17  
vector\_side:left"  
7932. 71572  
/note="assembly\_fragment"  
71673. 142025  
/note="assembly\_fragment  
clone\_end:SP6  
vector\_side:right"  
95993. 142025  
/note="clone overlaps with GenBank Accession Number  
AC137540 clone RP86-386P20 (center project name dzt)"

ORIGIN

Query Match 21.2%; Score 51.8; DB 2; Length 142025;  
Best Local Similarity 74.7%; Pred. No. 1.5e-05;  
Matches 65; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 10 ATTGATGTTTTCGCTTTTTCAGGACAAATTTAAGGCGGATGATATGCTTAT 69  
DB 115420 ATTGATGTTTATGTTATTTATTAAGGCAACATTTAAGGATGATGATATATGAT 115361

QY 70 GCAGCTGTTGATTCACAGAGTGAGT 96  
DB 115360 GCAGCTGTTGATTCGTTAATGTAAGT 115334

RESULT 10 AC144468 144218 bp DNA linear HTG 24-MAY-2003  
AC144468/c Canis familiaris clone RP81-263K15, WORKING DRAFT SEQUENCE, 5  
LOCUS ordered pieces.  
ACCESSION AC144468 AC144468.2 GI:31072038  
VERSION HTG; HTGS PHASE2; HTGS\_DRAFT.  
KEYWORDS











Quality coverage: 12.09x in Q20 bases; agarose-fp  
Quality coverage: 9.61x in Q20 bases; sum-of-coverage

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 36929: contig of 36929 bp in length  
\* 36930 37029: gap of unknown length  
\* 37030 85159: contig of 48130 bp in length  
\* 85160 85259: gap of unknown length  
\* 85260 139957: contig of 54698 bp in length  
\* 139958 140057: gap of unknown length  
\* 140058 143501: contig of 3444 bp in length  
\* 143502 143601: gap of unknown length  
\* 143602 160252: contig of 16651 bp in length  
\* 160253 160353: gap of unknown length  
\* 160353 164593: contig of 4241 bp in length  
\* 164594 164694: gap of unknown length  
\* 164694 178529: contig of 13836 bp in length  
\* 178530 178629: gap of unknown length  
\* 178630 203001: contig of 24372 bp in length  
\* 203002 203101: gap of unknown length  
\* 203102 208456: contig of 5355 bp in length.

## FEATURES

## SOURCE

1. 208456  
/organism="Canis familiaris"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:9615"  
/clone="RP81-35514"  
/clone\_id="RP81"  
1. 36929  
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37030..85159  
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/note="assembly\_fragment"  
130279..208456  
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AC144605 clone RP81-249M20 (center project name eab)"  
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140058..143501  
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vector\_side:right"

## ORIGIN

Query Match 20.6%; Score 50.2; DB 2; Length 208456;  
Best Local Similarity 73.6%; Pred. No. 5.3e-05;  
Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

25 CTTTTCGACGCGCATTTAAGGCGCGATGATATCGCTTTGATTC 84  
DB CTTTTCGACGCGCATTTAAGGCGCGATGATATCGCTTTGATTC 71007  
85 ACAGAGTGAAGTCAAGTGTCTTACCATG 111  
DB AGAAATGTAAGTATTTCTTGATCTG 70980

## RESULT 14

## AC117294

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

AC117294 203255 bp DNA linear HTG 11-OCT-2002  
Rattus norvegicus clone CH230-251M17, WORKING DRAFT SEQUENCE, 2  
unordered pieces.

AC117294.5 GI:23681496  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTUP.  
Rattus norvegicus (Norway rat)

Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Eucleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1 (bases 1 to 203255)

Muzny,D.,Marle,M.,Mezzer,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,  
Allen,C.,Allen,H.,Albrooke,S.,Amin,A.,Anguiano,D.,  
Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,  
Baldwin,D.,Bandaraike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,  
Biswal,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,  
Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderson,E.,  
Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,  
Chacko,J.,Chavez,D.,Chen,G.,Chen,Y.,Chen,Y.,Chen,Z.,Chu,J.,  
Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,  
Davila,M.,L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,  
Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Divya,K.,  
Diaper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Dvali,B.,Eaves,K.,  
Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Faller,T.,Fan,G.,  
Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,  
Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Guvarata,W.,  
Gebregeorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,M.,Guevara,W.,  
Gunnarsson,P.,Haaland,W.,Hamil,C.,Hamilton,C.,Hamilton,K.,  
Harvey,Y.,Havlik,P.,Hawes,A.,Henderson,N.,Hernandez,J.,  
Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgson,A.,Hogues,M.,  
Hollins,B.,Howells,S.,Huliyil,S.,Hume,J.,Idlebird,D.,Jackson,A.,  
Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jollivet,A.,  
Karpachy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovar,C.,  
Kowis,C.,Kraft,C.U.,Lebow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,  
Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,  
Lorenshuwa,L.,Loulesged,H.,Lozano,R.J.,Lu,X.,Ma,J.,  
Mabeshwari,M.,Mahindartine,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,  
Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,  
Mawhney,S.,McLeod,M.P.,McNeill,T.Z.,Meenen,E.,  
Moloshayevic,A.,Miner,G.,Mingja,E.,Montemayor,J.,Moore,S.,  
Morgan,M.,Morris,K.,Morris,S.,Mundasa,M.,Murphy,M.,Nair,L.,  
Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,  
Nwokwelenh,O.,Okunolu,G.,Olarunsooan,A.,Pal,S.,Parks,K.,  
Paeternak,S.,Paul,H.,Perez,A.,Perez,L.,Pfennoch,C.,  
Plopper,F.,Polidexter,A.,Popovic,D.,Primus,E.,Pu,L.,L.,  
Piazo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,  
Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,  
Rivers,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Ruiz,S.J.,  
Sanders,W.,Savery,G.,Scherer,S.,Scott,G.,Shatman,S.,Shen,H.,  
Shetty,J.,Shvartsbeyn,A.,Sison,I.,Sitter,C.D.,Snajb,D.,  
Sneed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,R.,Sosa,J.,  
Steimle,M.,Strong,R.,Sutton,A.,Svatek,A.,Tabor,P.,Taylor,C.,  
Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Trejos,Z.,Umanli,K.,  
Valas,R.,Vera,V.,Villaana,D.,Waldron,L.,Walker,B.,Wang,J.,  
Wang,O.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,  
Williams,G.,Willson,R.,Wleczky,R.,Wooden,H.,Worley,K.,  
Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,  
Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhao,S.,Dunn,D.,von  
Niederhausern,A.,Welles,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,  
Weinstock,G. and Gibbs,R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 203255)  
Worley,K.C.  
Direct Submission  
Submitted (10-APR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA





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QY 1 ATCAGATTATTCATGTTTTCGCTTTTTCGAGGACCAATTTAAGGCTGATGAT 60  
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 DB 1 ATCAGATTATTCATGTTTTCGCTTTTTCGAGGACCAATTTAAGGCTGATGAT 60  
 |||||  
 QY 61 ATCGTTTATGACGCTGTTGATTCCACAGAGTGAGTCACTGTTTCAATGTTTCGACAT 120  
 |||||  
 DB 61 ATCGTTTATGACGCTGTTGATTCCACAGAGTGAGTCACTGTTTCAATGTTTCGACAT 120  
 |||||  
 QY 121 GTTATGTCAGTCAAGTCAAGATATCATGACATGACAGTCCAGAACTGGCGTCATAGTT 180  
 |||||  
 DB 121 GTTATGTCAGTCAAGTCAAGATATCATGACATGACAGTCCAGAACTGGCGTCATAGTT 180  
 |||||  
 QY 181 CCAGACAGCTGGGGTCTCTGCTTGTTCCTTTGGACAAAACACTATGAGATACCACTG 240  
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 DB 181 CCAGACAGCTGGGGTCTCTGCTTGTTCCTTTGGACAAAACACTATGAGATACCACTG 240  
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 QY 241 CCTA 244  
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 DB 241 CCTA 244

## RESULT 2

AAH55850  
 ID AAH55850 standard; DNA; 438 BP.

AAH55850;

04-SEP-2001 (first entry)

Human SCN3A genomic DNA fragment SEQ ID NO:94.

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;  
 diagnosis; mutation; chromosome 2q23-q31; neurological disorder;  
 anticonvulsant; neuroprotective; ds.

Homo sapiens.

MO200138564-A2.

31-MAY-2001.

24-NOV-2000; 2000WO-CA001404.

26-NOV-1999; 99US-0167623P.

(UWMC-) UNIV MCGILL.

Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;

WPI; 2001-355945/37.

Determining a predisposition to epilepsy and/or development of epilepsy  
 comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA  
 variant, equivalent, or mutation which shows a linkage disequilibrium.

Disclosure; Page 183; 268bp; English.

The present invention describes a method (M1) of determining an  
 individual's predisposition to epilepsy and/or development of epilepsy,  
 as well as predicting the individual's response to medication. The method  
 comprises determining the genotype of at least one gene selected from  
 SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which  
 shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium  
 channel genes located on chromosome 2. The idiopathic generalised  
 epilepsy (IGE) gene is more specifically localised on chromosome 2q23-  
 q31. Compounds identified as modulators of the biological activity of  
 SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy  
 or other neurological disorders. They have anticonvulsant and  
 neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679  
 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,  
 oligonucleotides and proteins given in the exemplification of the present  
 invention

SEQ Sequence 438 BP; 155 A; 52 C; 65 G; 166 T; 0 U; 0 Other;  
 Query Match 19.7%; Score 48; DB 5; Length 438;  
 Best Local Similarity 68.8%; Pred. No. 3.4e-05;  
 Matches 66; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 ATCAGATTATTCATGTTTTCGCTTTTTCGAGGACCAATTTAAGGCTGATGAT 60  
 |||||  
 DB 153 ATTTTATGACCAATTTAATAATATATGTTATTACAGGCCACATTTAAGGCTGATGAT 212  
 |||||  
 QY 61 ATCGTTTATGACGCTGTTGATTCCACAGAGTGAGT 96  
 |||||  
 DB 213 ATTATGATATGACGCTGTTGATTCAAGAGTGTAACT 248  
 |||||

## RESULT 3

AAH55818  
 ID AAH55818 standard; DNA; 480 BP.

AAH55818;

04-SEP-2001 (first entry)

Human SCN2A genomic DNA fragment SEQ ID NO:60.

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;  
 diagnosis; mutation; chromosome 2q23-q31; neurological disorder;  
 anticonvulsant; neuroprotective; ds.

Homo sapiens.

MO200138564-A2.

31-MAY-2001.

24-NOV-2000; 2000WO-CA001404.

26-NOV-1999; 99US-0167623P.

(UWMC-) UNIV MCGILL.

Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;

WPI; 2001-355945/37.

Determining a predisposition to epilepsy and/or development of epilepsy  
 comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA  
 variant, equivalent, or mutation which shows a linkage disequilibrium.

Disclosure; Page 148; 268bp; English.

The present invention describes a method (M1) of determining an  
 individual's predisposition to epilepsy and/or development of epilepsy,  
 as well as predicting the individual's response to medication. The method  
 comprises determining the genotype of at least one gene selected from  
 SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which  
 shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium  
 channel genes located on chromosome 2. The idiopathic generalised  
 epilepsy (IGE) gene is more specifically localised on chromosome 2q23-  
 q31. Compounds identified as modulators of the biological activity of  
 SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy  
 or other neurological disorders. They have anticonvulsant and  
 neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679  
 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,  
 oligonucleotides and proteins given in the exemplification of the present  
 invention

Sequence 480 BP; 172 A; 59 C; 64 G; 185 T; 0 U; 0 Other;

Query Match 19.4%; Score 47.4; DB 5; Length 480;  
 Best Local Similarity 78.1%; Pred. No. 5.5e-05;  
 Matches 57; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACATTTAAGGCTGATGATATCGTTATGACGCTGTGATCC 84  
 DB 166 CTTTTCGACGACGCTTTAAGGATGATGATATGATGACGCTGTGATCA 225  
 QY 85 ACAGAGGTGAGTC 97  
 DB 226 CGAAATGTAGTC 238  
 RESULT 4  
 ID AAX60242 standard; cDNA; 856 BP.  
 AC AAX60242;  
 XX 11-AUG-1999 (first entry)  
 DE cDNA encoding type 5 sodium channel protein designated PMS.  
 XX  
 KM Type 5 sodium channel; PMS; nervous system; plexiform;  
 KM dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
 KM diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
 KM neuropathic pain; migraine; headache; ss.  
 XX  
 OS Homo sapiens.  
 PS FR2771103-A1.  
 XX  
 PD 21-MAY-1999.  
 PF 19-NOV-1998; 98FR-00014551.  
 XX  
 PR 20-NOV-1997; 97US-0066225P.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;  
 DR WPI; 1999-315739/27.  
 DR P-PSDB; AAY16577.  
 XX  
 PT Isolated DNA encoding sodium channel of the nervous system.  
 XX  
 PS Claim 1; Fig 3A; 90pp; French.  
 CC The present sequence encodes a type 5 sodium channel protein designated  
 CC PMS. The protein is a sodium ion channel of the nervous system, and is  
 CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
 CC used to identify inhibitors of sodium channel proteins that are resistant  
 CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
 CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
 CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
 XX  
 SQ Sequence 856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;  
 Query Match 19.3%; Score 47; DB 2; Length 856;  
 Best Local Similarity 90.9%; Pred. No. 9.2e-05;  
 Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 36 GGCACATTTAAGGCTGATGATATCGTTATGACGCTGTGATCCACAGAG 90  
 DB 559 GGCACATTTAAGGCTGATGATATGATATGACGCTGTGATCCACAGAG 613  
 RESULT 5  
 ID AAX87602 standard; cDNA; 3638 BP.  
 AC AAX87602;  
 XX 26-OCT-1999 (first entry)  
 DE Human sodium channel Nan partial cDNA.

XX  
 KM Nan; sodium channel; ion transport; human; dorsal root ganglia; pain;  
 KM paraesthesia; hyperexcitability; therapy; SCN1A gene; ss.  
 XX  
 OS Homo sapiens.  
 PS W09938889-A2.  
 XX  
 PD 05-AUG-1999.  
 PF 29-JAN-1999; 99MO-US002008.  
 XX  
 PR 29-JAN-1998; 98US-0072990P.  
 PR 20-NOV-1998; 98US-0109402P.  
 XX  
 PA (UYVA) UNIV YALE.  
 XX  
 PI Dib-Hajj S, Waxman S;  
 DR WPI; 1999-479168/40.  
 DR P-PSDB; AAY06598.  
 XX  
 PT New isolated nucleic acids encoding sodium channels, used to develop  
 PT products for treating acute or chronic pain or hyperexcitability  
 PT phenomena.  
 XX  
 PS Claim 1; Fig 8A1-2; 91pp; English.  
 XX  
 CC This is the nucleotide sequence of a partial cDNA clone which codes for a  
 CC portion (see AAY06598) of human Nan, a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The Nan channel cDNA was obtained from human DRG tissue  
 CC cDNA by PCR amplification (see also AAX87620-22). Rat, mouse and human  
 CC Na nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98)  
 CC are provided. The invention also includes expression vectors and  
 CC transformed host cells, methods for identifying tissues and cells that  
 CC express Nan, methods for identifying agents that modulate Nan channel  
 CC activity or Nan channel mRNA transcription or translation, and a method  
 CC for using such agents to treat acute or chronic pain, paraesthesia and  
 CC hyperexcitability phenomena. The preferential expression of Nan in  
 CC sensory DRG and trigeminal neurons provides a target for selectively  
 CC modifying the behaviour of these nerve cells while not affecting other  
 CC nerve cells in the brain and spinal cord. The gene is named SCN1A  
 XX  
 SQ Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;  
 Query Match 19.3%; Score 47; DB 2; Length 3638;  
 Best Local Similarity 90.9%; Pred. No. 0.00016;  
 Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 36 GGCACATTTAAGGCTGATGATATCGTTATGACGCTGTGATCCACAGAG 90  
 DB 3099 GGCACATTTAAGGCTGATGATATGATATGACGCTGTGATCCACAGAG 3153  
 RESULT 6  
 ID AAF30104 standard; cDNA; 3701 BP.  
 AC AAF30104;  
 XX  
 DT 30-APR-2001 (first entry)  
 DE Human sodium channel Nan partial cDNA.  
 XX  
 KM Sodium channel; Nan; human; tetrodotoxin resistant; pain; paraesthesia;  
 KM hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 PS  
 FH Key Location/Qualifiers  
 FT CDS 1..3699

/\*tag= a  
/partial

WO200105831-A1.

25-JAN-2001.

14-JUL-2000; 2000WO-US019342.

16-JUL-1999; 99US-00354147.

(UYVA ) UNIV YALE.

Dib-Hajj S, Waxman SG;  
WPI; 2001-103147/11.  
P-PSDB; AAB20125.

Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paresthesia and/or hyperexcitability phenomena.

Example 4; Fig 8A; 162bp; English.

The present sequence is that of a partial cDNA for a novel human tetrodotoxin resistant sodium channel, termed NaN (see AAB20125). The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). A full-length sequence is given in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paresthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN polypeptides

Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;

Query Match 19.3%; Score 47; DB 4; Length 3701;  
Best Local Similarity 90.9%; Pred. No. 0.00016;  
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 36 GGCAACATTTAAGGCTGGATGATATCGTTATGACAGCTGTGATTCACACAGAG 90  
|||||  
DB 3162 GGCAACATTTAAGGCTGGATGATATATATATGACAGCTGTGATTCACACAGAG 3216

RESULT 7  
AAL42750  
ID AAL42750 standard; cDNA; 5728 BP.

AC AAL42750;

DT 19-JUL-2002 (first entry)

DE Human sodium channel subunit SCN12A-s coding sequence.

KW Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
KW human nervous system; chromosome 3p23-21.3; excitatory cell;  
KW drug development; familial hyperglycaemia; QT extending syndrome type 3;  
KW motor endplate disease.

OS Homo sapiens.

XX

Key Location/Qualifiers  
FT CDS 200..4534  
/\*tag= a  
/product= "Human sodium channel subunit SCN12A-s"

WO200190355-A1.

29-NOV-2001.

11-JUL-2000; 2000WO-JP004629.

23-MAY-2000; 2000JP-00152085.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Kanazawa I, Goto J, Jeong S;  
WPI; 2002-393394/42.  
P-PSDB; AAO14926.

Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.

Claim 7; Page 55-70; 118pp; Japanese.

The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A-s sodium channel subunit

Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;

Query Match 19.3%; Score 47; DB 6; Length 5728;  
Best Local Similarity 90.9%; Pred. No. 0.00019;  
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 36 GGCAACATTTAAGGCTGGATGATATCGTTATGACAGCTGTGATTCACACAGAG 90  
|||||  
DB 3958 GGCAACATTTAAGGCTGGATGATATATATATGACAGCTGTGATTCACACAGAG 4012

RESULT 8  
AAF30101  
ID AAF30101 standard; cDNA; 5860 BP.

AC AAF30101;

DT 30-APR-2001 (first entry)

DE Human sodium channel NaN cDNA.

KW Sodium channel; NaN; human; tetrodotoxin resistant; pain; paresthesia;  
KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 31..5402

PN WO200105831-A1.

PD 25-JAN-2001.

PF 14-JUL-2000; 2000WO-US019342.

XX



PR 16-JUL-1999; 99US-00354147.  
XX (UTYA ) UNIV YALE.  
PA  
PI Dib-Hajj S, Waxman SG;  
XX  
XX WPI: 2001-103147/11.  
DR P-PSDB; AAB20121.  
XX  
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
PT channels, useful for preventing, diagnosing and treating pain,  
PT paraesthesia and/or hyperexcitability phenomena.  
XX  
PS Claim 1, Fig 11A, 162pp; English.  
XX  
XX The present sequence is that of cDNA encoding a novel human tetrodotoxin  
CC resistant sodium channel, termed Nan (see AAB20121). The cDNA was  
CC isolated from a human dorsal root ganglia tissue cDNA library by PCR  
CC amplification (see also AAB30122-23). Nan belongs to the a-subunit  
CC voltage-gated sodium channel protein family and produces a TTX-R sodium  
CC current. Such channels underlie the generation and propagation of  
CC impulses in excitable cells such as neurons and muscle fibres.  
CC Preferential expression of Nan on sensory neurons innervating the body  
CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
CC neurons, makes it a very useful target for diagnostic and/or therapeutic  
CC uses in relation to acute and/or chronic pain pathologies. A claimed  
CC method of treating pain, paraesthesia and/or hyperexcitability phenomena  
CC in a human or animal subject involves administering an agent that alters  
CC sodium current flow through Nan channels, or which modulates  
CC transcription or translation of Nan mRNA, in dorsal root ganglia or  
CC trigeminal neurons. Nan nucleic acids are used in gene therapy to correct  
CC disorders associated with decreased sodium channel expression or  
CC (antibense) to down-regulate Nan expression, in the diagnosis of disease,  
CC and in the recombinant production of Nan polypeptides  
XX  
SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
XX  
Query Match 19.3%; Score 47; DB 4; Length 5860;  
Best Local Similarity 90.9%; Pred. No. 0.00019;  
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 36 GGCAATTAAAGGCTGGATGATTCGTTATGACAGCTGTGATCCACAGAG 90  
DB 3789 GGCAATTAAAGGCTGGATGATTCGTTATGACAGCTGTGATCCACAGAG 3843  
XX  
RESULT 9  
ADD32193  
ID ADD32193 standard; cDNA; 5860 BP.  
XX  
AC ADD32193;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
XX  
XX expression vector; Na v 1.9 sodium channel protein;  
KM sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 31..5406  
FT /\*tag= a  
FT CDS /product= "Na v 1.9 sodium channel protein"  
XX  
XX MO2003080570-A2.  
XX  
XX 02-OCT-2003.  
XX  
XX 20-MAR-2003; 2003WO-US008611.  
XX  
XX 20-MAR-2002; 2002US-0365550P.  
XX  
XX

XX  
PA (TRAN-) TRANSMOLECULAR INC.  
XX  
XX Gonda MA, Greenwood JD;  
XX  
XX WPI: 2003-876895/81.  
DR P-PSDB; ADD32194.  
XX  
XX Expression vector useful for stable cloning and expression of Nav1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
PT fragment.  
XX  
PS Disclosure; SEQ ID NO 3; 125pp; English.  
XX  
XX The present invention describes an expression vector comprising a nucleic  
CC acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
CC its fragment, and producing a sodium current when transfected in a cell.  
CC Also described: (1) a recombinant cell comprising the plasmid selected  
CC from pRAN, pCMV-rhan-GFP, pLG338M-rhan and the plasmid described above;  
CC (2) a method of making a cell or cell line that produces a Na v 1.9  
CC sodium channel-dependent sodium current by: (a) providing a cell that has  
CC been transfected with the expression vector; and (b) culturing the cell  
CC under conditions that allow expression of Na v 1.9 sodium channel protein  
CC to produce a sodium current into the transfected cell; (3) a method of  
CC screening for an agent that modulates sodium current in a cell by: (a)  
CC exposing the cell or cell line produced by the method to the agent; and  
CC (b) measuring sodium current following exposure to the agent, where an  
CC alteration in the level of sodium current is indicative of an agent  
CC capable of modulating sodium current in a cell; and (4) a recombinant  
CC cell comprising the expression vector. The expression vectors are useful  
CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a human Na v 1.9 sodium channel protein, which  
XX is used in the exemplification of the present invention.  
XX  
SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
XX  
Query Match 19.3%; Score 47; DB 9; Length 5860;  
Best Local Similarity 90.9%; Pred. No. 0.00019;  
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 36 GGCAATTAAAGGCTGGATGATTCGTTATGACAGCTGTGATCCACAGAG 90  
DB 3789 GGCAATTAAAGGCTGGATGATTCGTTATGACAGCTGTGATCCACAGAG 3843  
XX  
RESULT 10  
AAL42749  
ID AAL42749 standard; cDNA; 6528 BP.  
XX  
AC AAL42749;  
XX  
DT 19-JUL-2002 (first entry)  
XX  
DE Human sodium channel subunit SCN12A coding sequence.  
XX  
XX Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
KM human nervous system; chromosome 3p23-21.3; excitatory cell;  
KM drug development; familial hyperglycaemia; QT extending syndrome type 3;  
XX motor encephle disease.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 200..5575  
FT /\*tag= a  
FT CDS /product= "Human sodium channel subunit SCN12A"  
XX  
XX MO200190355-A1.  
XX  
XX 29-NOV-2001.  
XX  
XX



PS Disclosure; Page 59-63; 64pp; English.

XX  
CC The invention provides an altered ion channel protein having acquired  
CC sensitivity to a gating agent. The altered ion channel protein can be  
CC expressed by standard recombinant methodology. The altered ion channel  
CC protein can be derived from a rat, mouse or human unaltered, gating agent  
CC insensitive ion channel proteins. The altered protein is useful in  
CC screening assays for the identification of modulators capable of  
CC modulating an unaltered gating agent insensitive ion channel protein. The  
CC modulator identified by the assay is preferably an antagonist of the  
CC altered protein, which is useful in the manufacture of a medicament for  
CC the treatment of pain, inflammation or hypersensitivity, and for treating  
CC a mammalian patient, particularly human. The present sequence represents  
CC a DNA encoding a human sensory neurone specific (SNS) 1, a sodium ion  
CC channel protein

XX  
SQ Sequence 5874 BP; 1434 A; 1552 C; 1428 G; 1460 T; 0 U; 0 Other;

XX  
Query Match 17.0%; Score 41.4; DB 4; Length 5874;  
Best Local Similarity 72.0%; Pred. No. 0.012;  
Matches 54; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 20 TTCTGCTTTTTCGACGACCAATTAAAGGCTGATGATATCGTTTATGACGCTGTG 79  
DB 4073 TTGCACTTCTGACAGTGCGCAACCTTAAAGGCTGATGACATTAATGATGACGCTGTG 4132  
QY 80 ATTCCACAGAGGTGA 94  
DB 4133 ATTCGCGGAGGTCA 4147

RESULT 13  
AAF57016  
ID AAF57016 standard; cDNA; 5874 BP.  
XX  
AC AAF57016;  
DT 14-MAY-2001 (first entry)  
XX  
DE Human hPN3 cDNA sequence.  
XX  
KW Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;  
KW tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; human;  
KW sodium channel protein; peripheral nervous system; allodynia; neuropathy;  
KW hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerability;  
KW analgesic; anti-HIV; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..5871  
FT /\*tag= a  
FT /\*product= "hPN3"  
XX  
PN US6184349-B1.  
XX  
PD 06-FEB-2001.  
XX  
PF 15-APR-1997; 97US-00843417.  
XX  
PR 11-OCT-1995; 95US-00511828.  
XX  
PA (SYNT ) SYNTX USA INC.  
XX  
PI Herman R, Delgado SG, Fish LM, Sangameswaran L, Rabert DK;  
XX  
DR WPI: 2001-202004/20.  
XX  
DR P-PSDB; AAB61956.  
XX  
PT New rat and human tetrodotoxin-resistant, voltage-gated sodium channel  
PT proteins, present in peripheral nerve tissue, useful as a therapeutic  
PT target for compounds treating peripheral nervous system disorders.  
XX

PS Disclosure; Fig 5A-K; 86pp; English.

XX  
CC The invention provides purified and isolated rat and human peripheral  
CC nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins.  
CC The rat peripheral nerve sodium channel type 3 (PN3) protein or its human  
CC homolog are useful for the development of antibodies against PN3 which  
CC are useful in affinity chromatography to purify recombinant sodium  
CC channel proteins or polypeptides, or as a research tool. The PN3 proteins  
CC are useful as therapeutic targets for compounds to treat disorders of the  
CC peripheral nervous system such as allodynia, hyperalgesia, diabetic  
CC neuropathy, traumatic injury and acquired immunodeficiency syndrome  
CC (AIDS)-associated neuropathy. The present sequence represents the cDNA  
CC encoding the human hPN3 protein

XX  
SQ Sequence 5874 BP; 1434 A; 1553 C; 1428 G; 1459 T; 0 U; 0 Other;

XX  
Query Match 17.0%; Score 41.4; DB 4; Length 5874;  
Best Local Similarity 72.0%; Pred. No. 0.012;  
Matches 54; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 20 TTCTGCTTTTTCGACGACCAATTAAAGGCTGATGATATCGTTTATGACGCTGTG 79  
DB 4073 TTGCACTTCTGACAGTGCGCAACCTTAAAGGCTGATGACATTAATGATGACGCTGTG 4132  
QY 80 ATTCCACAGAGGTGA 94  
DB 4133 ATTCGCGGAGGTCA 4147

RESULT 14  
ABX13103  
ID ABX13103 standard; cDNA; 5874 BP.  
XX  
AC ABX13103;  
DT 10-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding voltage-gated sodium channel Nav1.8.  
XX  
KW Human; ss; gene; voltage gated sodium channel; VGSC; Nav1.8; p11;  
KW small calcium binding protein; analgesia; chronic pain; osteoarthritis;  
KW rheumatoid arthritis; neuropathic pain; cancer pain;  
KW tri geminal neuralgia; hyperalgesia; inflammatory pain; nociceptive pain;  
KW tabes dorsalis; phantom limb pain; spinal cord injury pain; central pain;  
KW post-herpetic pain; HIV pain; non-cardiac chest pain;  
KW irritable bowel syndrome; bowel disorder.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 2041..5871  
FT /\*tag= a  
FT /\*product= "Nav1.8"  
XX  
PN WO2003016917-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 20-AUG-2002; 2002WO-GB003852.  
XX  
PR 20-AUG-2001; 2001GB-00020238.  
XX  
PA (UNLO ) UNIV COLLEGE LONDON.  
XX  
PI Okuse K, Baker M, Poon L, Wood JN, Malik-Hall M;  
XX  
DR WPI: 2003-278589/27.  
XX  
DR P-PSDB; ABG76193.  
XX  
PT Identifying a voltage gated sodium channel (VGSC) modulator for producing  
PT analgesia and for relieving chronic pain, e.g. osteoarthritis or HIV  
PT pain, comprises bringing into contact a VGSC, a p11 peptide and a test  
PT compound.  
XX





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Db 605 TTGTTGACGGCAACATTTAAGGCTGATGATATATATATGACAGCTGTTGATTCACA 546
Qy 88 GAGGTGAGTCACTGTTCTTACCATGTTCCGACAGTGTATAGTCAAGATATATACGA 147
Db 545 GAGGTGAGTCACTGTTCTTACCATGTTCCGACAGTGTATAGTCAAGATATATACGA 486
Qy 148 CTACATGACAGTCCAGAACTGGCGTCAATAGTTCAGACAGCTGGGGTCTGCTGTTGT 207
Db 485 CTACATGACAGTCCAGAACTGGCGTCAATAGTTCAGACAGCTGGGGTCTGCTGTTGT 426
Qy 208 TCCTTTGGAAACAAACACTATGATGATACCACTGCCCTA 244
Db 425 TTCTTTGGAAACAAACACTATGATGATACCACTGCCCTA 389

RESULT 2
US-10-388-470-6
; Sequence 6, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3699)
; OTHER INFORMATION: partial human Nan cDNA sequence
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (922)
; OTHER INFORMATION: Y = c or t. Xaa at amino acid position 308 is
; OTHER INFORMATION: Leu.
US-10-388-470-6

Query Match 19.3%; Score 47; DB 15; Length 3701;
Best Local Similarity 90.9%; Pred. No. 4,1e-05;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 36 GGCAACATTTAAGGCTGATGATATCGTTATGACAGCTGTTGATTCACAGAG 90
Db 3162 GGCAACATTTAAGGCTGATGATATATATATATGACAGCTGTTGATTCACAGAG 3216

RESULT 3
US-10-388-470-41
; Sequence 41, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
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; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human Nan
US-10-388-470-41

Query Match 19.3%; Score 47; DB 15; Length 5860;
Best Local Similarity 90.9%; Pred. No. 5,1e-05;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 36 GGCAACATTTAAGGCTGATGATATCGTTATGACAGCTGTTGATTCACAGAG 90
Db 3789 GGCAACATTTAAGGCTGATGATATATATATGACAGCTGTTGATTCACAGAG 3843

RESULT 4
US-10-220-120-104
; Sequence 104, Application US/10220120
; Publication No. US20040048253A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purni
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHLEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENMALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Antissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKREHER, Theresa K.
; APPLICANT: DAFRO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YAP, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: JACKSON, Stuart
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1113 PCT
; CURRENT APPLICATION NUMBER: US/10/220,120
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,698; 60/184,770; 60/184,774;
```

60/184,693; 60/184,771; 60/184,813; 60/184,773; 60/184,776;  
60/184,769; 60/184,768; 60/184,837; 60/184,697; 60/184,841;  
60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/205,221;  
60/204,815; 60/203,785; 60/204,821; 60/204,908; 60/204,226;  
60/204,525; 60/205,285; 60/205,232; 60/205,323; 60/205,287;  
60/205,324; 60/205,286  
PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;  
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;  
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;  
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;  
2000-05-17; 2000-05-12; 2000-05-16; 2000-05-15;  
2000-05-16; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;  
2000-05-17; 2000-05-17  
NUMBER OF SEQ. ID NOS: 422  
SOFTWARE: PERL Program  
SEQ ID NO 104  
LENGTH: 8530  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: incyle ID No. US20040048253A1 LI:410188.1:2000MAY01  
FEATURE:  
NAME/KEY: unseq  
LOCATION: 6797, 7046, 7252, 7311, 7325-7326, 7502-7503, 7563  
OTHER INFORMATION: a, t, c, g, or other  
US-10-220-120-104  
Query Match 17.0%; Score 41.4; DB 12; Length 8530;  
Best Local Similarity 72.0%; Pred. No. 0.0051;  
Matches 54; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 20 TTTCTCTTTTTCGACGACCAATTAAAGGCTGATGATATCGTTATGACGCTGTG 79  
DB 4391 TTGACCTTTCGACGCTGCAACCTTTAAAGCTGATGACATATATGACGCTGTG 4450  
QY 80 ATTCCACAGAGCTA 94  
DB 4451 ATTCCGCGAGGTCA 4465  
RESULT 5  
US-10-209-776-1  
Sequence 1, Application US/10209776  
Publication No. US20030096360A1  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
Delgado, Stephen G  
Fish, Linda M  
Sangameswaran, Lakshmi  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Syntex Corporation, Patent Department A2-200  
STREET: 3401 Hillview Avenue P.O. Box 10850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/209,776  
FILING DATE: 01-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,828  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Perles, Rohan  
REGISTRATION NUMBER: 35,752  
REFERENCE/DOCKET NUMBER: 28340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-852-1698  
TELEFAX: (415)-496-3529  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6344 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: Dorsal root ganglia  
CELL TYPE: Peripheral nerve  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-209-776-1  
Query Match 16.3%; Score 41.2; DB 14; Length 6344;  
Best Local Similarity 74.3%; Pred. No. 0.0051;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 25 CTTTTCGACGACCAATTAAAGGCTGATGATATCGTTATGACGCTGTGATTC 84  
DB 4103 CTCTTCAGCTGCGCACTTCAAGGCTGATGACATATATGATGACGCTGTGATTC 4162  
QY 85 ACAGAGTGA 94  
DB 4163 GGAGAGTCA 4172  
RESULT 6  
US-10-202-824-1  
Sequence 1, Application US/10202824  
Publication No. US20030176648A1  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschultz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: EHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6524 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-202-824-1

Query Match 16.9%; Score 41.2; DB 14; length 6527;  
Best Local Similarity 74.3%; Pred. No. 0.0052;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 25 CTTTTCAGGAGGCAATTAAAGGCTGATGATATCGTTTATGACAGCTGTGATTC 84  
DB 4287 CTTCTTCAGGTGGCACTTCAAGGCTGATGACATATGATGACGCTGTGATTC 4346

OY 85 ACAGAGGTGA 94  
DB 4347 GGAGAGATCA 4356

RESULT 7  
US-10-202-824-7  
; Sequence 7, Application US/10202824  
; Publication No. US20030176648A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, John N.  
; Akopian, Armen N.  
; TITLE OF INVENTION: Ion Channel  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Pharmaceuticals  
; STREET: 1800 Concord Pike, P.O. Box 15437  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/202,824  
; FILING DATE: 26-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,656  
; FILING DATE: 24-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hohenschultz, Liza D.  
; REGISTRATION NUMBER: 33,712  
; REFERENCE/DOCKET NUMBER: PHM.70086  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (302) 886-7466  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6527 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 204..6077  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-202-824-7

Query Match 16.9%; Score 41.2; DB 14; length 6527;  
Best Local Similarity 74.3%; Pred. No. 0.0052;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 25 CTTTTCAGGAGGCAATTAAAGGCTGATGATATCGTTTATGACAGCTGTGATTC 84  
DB 4287 CTTCTTCAGGTGGCACTTCAAGGCTGATGACATATGATGACGCTGTGATTC 4346

OY 85 ACAGAGGTGA 94  
DB 4347 GGAGAGATCA 4356

RESULT 8  
US-10-202-824-5  
; Sequence 5, Application US/10202824  
; Publication No. US20030176648A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, John N.  
; Akopian, Armen N.  
; TITLE OF INVENTION: Ion Channel  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Pharmaceuticals  
; STREET: 1800 Concord Pike, P.O. Box 15437  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/202,824  
; FILING DATE: 26-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,656  
; FILING DATE: 24-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hohenschultz, Liza D.  
; REGISTRATION NUMBER: 33,712  
; REFERENCE/DOCKET NUMBER: PHM.70086  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (302) 886-7466  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7052 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 204..6602  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-202-824-5

Query Match 16.9%; Score 41.2; DB 14; length 7052;  
Best Local Similarity 74.3%; Pred. No. 0.0054;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 25 CTTTTCAGGAGGCAATTAAAGGCTGATGATATCGTTTATGACAGCTGTGATTC 84  
DB 4812 CTTCTTCAGGTGGCACTTCAAGGCTGATGACATATGATGACGCTGTGATTC 4871

OY 85 ACAGAGGTGA 94  
DB 4872 GGAGAGATCA 4881

RESULT 9  
US-09-840-125-3  
; Sequence 3, Application US/09840125  
; Patent No. US2002061524A1



GENERAL INFORMATION:  
APPLICANT: Splawski, Igor  
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND  
FILE REFERENCE: 2323-155  
CURRENT APPLICATION NUMBER: US/09/840,125  
PRIORITY FILING DATE: 2001-04-24  
PRIORITY APPLICATION NUMBER: 09/634,920  
PRIORITY FILING DATE: 2000-08-09  
PRIORITY APPLICATION NUMBER: 60/147,488  
PRIORITY FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 6048  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(6048)  
US-09-840-125-3

Query Match 15.2%; Score 37.2; DB 9; Length 6048;  
Best Local Similarity 72.7%; Pred. No. 0.12; Mismatches 18; Indels 0; Gaps 0;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTGTTCAGGACGACATTTAAGGCTGATGATATCGTTATGACGCTGTGATTC 84  
DB 4234 CTTCTGACGAGTGCGACATTTAAAGGCTGATGACATTTATGATGACGCTGTGACTCC 4293  
QY 85 ACAGAG 90  
DB 4294 AGGGGG 4299

RESULT 10  
US-09-896-994-1  
Sequence 1, Application US/09896994  
Publication No. US20030074024A1  
GENERAL INFORMATION:  
APPLICANT: Ken Stokes  
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1 is  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/896,994  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/514,907  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legarda  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: MEET-0029/P-3586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6048 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-896-994-1

Query Match 15.2%; Score 37.2; DB 10; Length 6048;  
Best Local Similarity 72.7%; Pred. No. 0.12; Mismatches 18; Indels 0; Gaps 0;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTGTTCAGGACGACATTTAAGGCTGATGATATCGTTATGACGCTGTGATTC 84  
DB 4234 CTTCTGACGAGTGCGACATTTAAAGGCTGATGACATTTATGATGACGCTGTGACTCC 4293  
QY 85 ACAGAG 90  
DB 4294 AGGGGG 4299

RESULT 11  
US-10-077-054-1  
Sequence 1, Application US/10077054  
Publication No. US20030157600A1  
GENERAL INFORMATION:  
APPLICANT: Makielaki, Jonathan C  
TITLE OF INVENTION: Sodium Channel Alpha Subunits  
FILE REFERENCE: 960296,98032  
CURRENT APPLICATION NUMBER: US/10/077,054  
PRIORITY FILING DATE: 2002-02-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 6091  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (10)..(6054)  
US-10-077-054-1

Query Match 15.2%; Score 37.2; DB 14; Length 6091;  
Best Local Similarity 72.7%; Pred. No. 0.12; Mismatches 18; Indels 0; Gaps 0;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTGTTCAGGACGACATTTAAGGCTGATGATATCGTTATGACGCTGTGATTC 84  
DB 4240 CTTCTGACGAGTGCGACATTTAAAGGCTGATGACATTTATGATGACGCTGTGACTCC 4299  
QY 85 ACAGAG 90  
DB 4300 AGGGGG 4305

RESULT 12  
US-10-101-510-617  
Sequence 617, Application US/10101510  
Publication No. US20030148295A1  
GENERAL INFORMATION:  
APPLICANT: WAN, JACKSON  
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
FILE REFERENCE: 15117,0012  
CURRENT APPLICATION NUMBER: US/10/101,510  
PRIORITY FILING DATE: 2002-03-20  
PRIORITY APPLICATION NUMBER: 60/276,947  
PRIORITY FILING DATE: 2001-03-20  
NUMBER OF SEQ ID NOS: 805  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 617  
LENGTH: 8490

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (6774)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7021)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7227)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7286)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7300)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7477)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7538)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8167)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-101-510-617

Query Match 15.2%; Score 37.2; DB 14; Length 8490;  
Best Local Similarity 72.7%; Pred. No. 0.14;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACCAATTAAAGGCTGATGATATCGTTTATGCACTGTTGATTC 84  
DB 4384 CTTCTGACGGTGCGCAACATTTAAAGGCTGATGACATTAATGATGACGCTGTGACTCC 4443  
QY 85 ACAGAG 90  
DB 4444 AGGGGG 4449

RESULT 13  
US-10-333-191-1  
Sequence 1, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
FILE REFERENCE: 2323-154-11  
CURRENT APPLICATION NUMBER: US/10/333,191  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 8491  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 15.2%; Score 37.2; DB 15; Length 8491;  
Best Local Similarity 72.7%; Pred. No. 0.14;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACCAATTAAAGGCTGATGATATCGTTTATGCACTGTTGATTC 84  
DB 4384 CTTCTGACGGTGCGCAACATTTAAAGGCTGATGACATTAATGATGACGCTGTGACTCC 4443  
QY 85 ACAGAG 90  
DB 4444 AGGGGG 4449

RESULT 14  
US-10-333-191-3  
Sequence 3, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
FILE REFERENCE: 2323-154-11  
CURRENT APPLICATION NUMBER: US/10/333,191  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 8491

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-3

Query Match 15.2%; Score 37.2; DB 15; Length 8491;  
Best Local Similarity 72.7%; Pred. No. 0.14;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACCAATTAAAGGCTGATGATATCGTTTATGCACTGTTGATTC 84  
DB 4384 CTTCTGACGGTGCGCAACATTTAAAGGCTGATGACATTAATGATGACGCTGTGACTCC 4443  
QY 85 ACAGAG 90  
DB 4444 AGGGGG 4449

RESULT 15  
US-09-917-800A-1604  
Sequence 1604, Application US/09917800A  
Patent No. US20020119462A1  
GENERAL INFORMATION:  
APPLICANT: Mendick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Castle, Arthur

US-09-917-800A-1604  
Sequence 1604, Application US/09917800A  
Patent No. US20020119462A1  
GENERAL INFORMATION:  
APPLICANT: Mendick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Castle, Arthur

```

; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1604
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013119
; US-09-917-800A-1604

Query Match      15.1%; Score 36.8; DB 9; Length 6822;
Best Local Similarity 73.4%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 17;

QY      36 GGCACATTTAAGGCTGATGATATCGTTTATGACAGCTGTGATTCACAGAGTGAG 95
DB      4505 GGCACATTTCAAGGCTGATGATGACATCATGTATGACAGCTGTGATTCGCGGACGTCAA 4564
QY      96 TCAG 99
DB      4565 ACTG 4568

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Search completed: March 23, 2004, 05:14:28  
 Job time : 189.443 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:45:54 ; Search time 1838.64 Seconds  
(without alignments)  
4669.435 Million cell updates/sec

Title: US-09-646-224A-14

Perfect score: 244  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	244	100.0	244	27	US-09-666-224A-14	Sequence 14, Appl
2	226.4	92.8	576	75	US-60-186-189-98	Sequence 98, Appl
3	226.4	92.8	6925	73	US-60-207-214-72	Sequence 72, Appl
4	226.4	92.8	115159	106	US-60-466-412-84151	Sequence 84151, A
5	202.6	83.0	605	26	US-09-634-306B-185132	Sequence 185132, A
6	202.6	83.0	605	43	US-10-027-632-185132	Sequence 185132, A
7	123.4	50.2	278	72	US-60-160-190-43	Sequence 43, Appl
8	122.4	50.2	278	72	US-60-160-190-415	Sequence 65, Appl
9	50.2	20.6	460	72	US-60-160-190-415	Sequence 415, Appl
10	49	20.1	4740	76	US-60-207-214-137	Sequence 137, Appl
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16	49	20.1	107943	103	US-60-466-412-84152	Sequence 84152, A
17	48	19.7	438	53	US-09-718-355D-94	Sequence 94, Appl
18	48	19.7	438	53	US-10-664-422-94	Sequence 94, Appl
19	48	19.7	438	53	US-10-664-423-94	Sequence 94, Appl
20	48	19.7	438	53	US-10-664-423-94	Sequence 94, Appl
21	48	19.7	21347	79	US-60-230-445-603-94	Sequence 440, Appl
22	47.4	19.4	480	30	US-09-718-355D-60	Sequence 60, Appl
23	47.4	19.4	480	53	US-10-664-422-60	Sequence 60, Appl
24	47.4	19.4	480	53	US-10-664-423-60	Sequence 60, Appl
25	47.4	19.4	480	53	US-10-664-423-60	Sequence 60, Appl
26	47.4	19.4	548	72	US-60-160-190-533	Sequence 533, Appl
27	47.4	19.4	601	39	US-09-949-016-178472	Sequence 178472, A
28	47.4	19.4	20696	79	US-60-210-445-53	Sequence 178473, A
29	47.4	19.4	33768	77	US-60-213-177-320	Sequence 33, Appl
30	47.4	19.4	33768	77	US-60-213-177-321	Sequence 330, Appl
31	47.4	19.4	32768	79	US-60-230-445-34	Sequence 321, Appl
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35	47.4	19.4	33768	79	US-60-233-937-2	Sequence 2, Appl
36	47.4	19.4	33768	79	US-60-233-937-3	Sequence 3, Appl
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38	47.4	19.4	99830	39	US-09-949-016-16859	Sequence 16859, A
39	47.2	19.3	567	73	US-60-173-463-161	Sequence 161, Appl
40	47.2	19.3	662	73	US-60-173-463-166	Sequence 166, Appl
41	47.2	19.3	662	74	US-60-173-463-256	Sequence 256, Appl
42	47.2	19.3	662	74	US-60-181-426-274	Sequence 274, Appl
43	47.2	19.3	662	77	US-60-198-554-259	Sequence 259, Appl
44	47.2	19.3	788	77	US-60-213-177-25	Sequence 25, Appl
45	47.2	19.3	788	79	US-60-230-445-136	Sequence 126, Appl

## ALIGNMENTS

RESULT 1  
 US-09-646-224A-14  
 : Sequence 14, Application US/09646224A  
 : GENERAL INFORMATION:  
 : APPLICANT: Glaxo Wellcome PLC  
 : APPLICANT: Tate, Simon N  
 : APPLICANT: Grose, David T  
 : APPLICANT: Hicks, Carolin A  
 : TITLE OF INVENTION: Ion Channels  
 : FILE REFERENCE: PG3432  
 : CURRENT APPLICATION NUMBER: US/09/646,224A  
 : CURRENT FILING DATE: 2000-09-14  
 : PRIOR APPLICATION NUMBER: GB 9805793.8  
 : PRIOR FILING DATE: 1998-03-18  
 : NUMBER OF SEQ ID NOS: 35  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 14  
 :  
 : LENGTH: 244  
 : TYPE: DNA  
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? ORGANISM: Homo sapiens
US-09-646-224A-14

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Best Local Similarity 100.0%; Pred. No. 2,2e-63;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 ATCGTTTATGACGCTGTGATTCACACAGAGGTAGTCAAGTGTTCACATGTTGGCAGT 120
Db 61 ATCGTTTATGACGCTGTGATTCACACAGAGGTAGTCAAGTGTTCACATGTTGGCAGT 120

OY 121 GTTATGGTCAAGTCACAGATATCATCATACATGACACAGTCCACAGACTGGCGTCATAGTT 180
Db 121 GTTATGGTCAAGTCACAGATATCATCATACATGACACAGTCCACAGACTGGCGTCATAGTT 180

OY 181 CCAGCAGCTGGGGTCTCTGCTTGTTCCTTTGGAAACAAACATATGAGATACCACCTG 240
Db 181 CCAGCAGCTGGGGTCTCTGCTTGTTCCTTTGGAAACAAACATATGAGATACCACCTG 240

OY 241 CCTA 244
Db 241 CCTA 244

RESULT 2
US-60-196-189-98
? Sequence 98, Application US/60196189
? GENERAL INFORMATION:
? APPLICANT: Bonazzi, Vivien
? TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
? TITLE OF INVENTION: AND USES THEREOF
? FILE REFERENCE: CL000441
? CURRENT APPLICATION NUMBER: US/60/196,189
? CURRENT FILING DATE: 2000-04-11
? NUMBER OF SEQ ID NOS: 442
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 98
? LENGTH: 576
? TYPE: DNA
? ORGANISM: HUMAN
US-60-196-189-98

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Best Local Similarity 95.5%; Pred. No. 6,9e-58;
Matches 233; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Query Match	92.8%;	Score 226.4;	DB 75;	Length 576;
Best Local Similarity	95.5%;	Pred. No. 6.9e-58;		
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QY	1	ATCAGTATTATTCATGTTTTCGCTTTTTCGACAGGCACAAATTAAAGGCTGGATGAT	60	
Db	170	ATTGTGATTATTCATGTTTTCGCTTTTTCGACAGGCACAAATTAAAGGCTGGATGAT	229	
QY	61	ATCGTTATCAGCTGTGTAATCCACAGAGGTAGTCAAGTCTCAACATGTTGGCAGT	120	
Db	230	ATTATATATCAGCTGTGTAATCCACAGAGGTAGTCAAGTCTCAACATGTTGGAGT	289	
QY	121	GTTATGCTCAAGTCAGAGATATCATGACATGACAGTCAGAACTGGCGTCATAGTT	180	
Db	290	GTTATGCTCAAGTCAGAGATATCATGACATGACATGACAGTCAGAACTGGCGTCATAGTT	349	
QY	181	CCAGCAGCTGGGGTCTCTGCGCTGTGTTCTCTTGGAAACAAACACTATAGAGATACACAGT	240	
Db	350	CCAGCAGCTGGGGTCTCTGCGCTGTGTTCTCTTGGAAACAAACACTATAGAGATACCACTG	409	
QY	241	CCTA 244		
Db	410	CCTA 413		
RESULT 3				

US-60-207-214-72

Sequence 72, Application US/60207214  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: AND USUS THEREOF  
FILE REFERENCE: CL000581  
CURRENT APPLICATION NUMBER: US/60/207,214  
CURRENT FILING DATE: 2000-05-26  
NUMBER OF SEQ ID NOS: 622  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 72  
LENGTH: 6925  
TYPE: DNA  
ORGANISM: HUMAN  
US-60-207-214-72

Query Match 92.8%; Score 226.4; DB 76; Length 6925;  
Best Local Similarity 95.5%; Pred. No. 1.7e-57;  
Matches 233; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATCAGTATTATTCAGTGTTCCTTTTTCGAGGACAAATTTAAGGCTGGATGAT 60  
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Db 3705 ATTGTATTATTCATGTTTCTCTGCTTTTGTGAGGCAACATTTAAGGCTGGATGAT 3764  
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QY 61 ATCGTTTATGACGCTGTTGATTCACAGAGGTGAGTGTGTTACCATGTTGGCAGT 120  
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Db 3765 ATTATATATGACGCTGTTGATTCACAGAGGTGAGTGTGTTACCATGTTGGCAGT 3824  
|||  
QY 121 GTTATGTCAGTACAGATATCATGACTACATGACAGTCACAACTGGGCTCATAGTT 180  
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Db 3825 GTTATGTCAGTACAGATATCATGACTACATGACAGTCACAACTGGGCTCATAGTT 3884  
|||  
QY 181 CCACAGCTGGGGTCTCTGCTGCTTCTCTTCTTGGAAACAAACCTATGAGATACCACTG 240  
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Db 3885 CCACAGCTGGGGTCTCTGCTGCTTCTCTTCTTGGAAACAAACCTATGAGATACCACTG 3944  
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QY 241 CCTA 244  
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Db 3945 CCTA 3948  
|||

RESULT 4

US-60-466-412-84151  
Sequence 84151, Application US/60466412  
GENERAL INFORMATION:  
APPLICANT: CARBIL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: C1001466  
CURRENT APPLICATION NUMBER: US/60/466,412  
CURRENT FILING DATE: 2003-04-30  
NUMBER OF SEQ ID NOS: 429241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84151  
LENGTH: 115159  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1) (115159)  
OTHER INFORMATION: n = A,T,C or G  
US-60-466-412-84151

Query Match 92.8%; Score 226.4; DB 103; Length 115159;  
Best Local Similarity 95.5%; Pred. No. 4.4e-57;  
Matches 233; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATCAGTATTATTCAGTGTTCCTTTTTCGAGGACAAATTTAAGGCTGGATGAT 60  
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QY 61 ATCGTTTATGACGCTGTTGATTCACAGAGGTGAGTGTGTTACCATGTTGGCAGT 120

Db 85377 ATTATATATGACGCTGTTGATTCACAGAGGTGAGTGTGTTACCATGTTGGAGT 85436

QY 121 GTTATGTCAGTACAGATATCATGACTACATGACAGTCACAACTGGGCTCATAGTT 180

Db 85437 GTTATGTCAGTACAGATATCATGACTACATGACAGTCACAACTGGGCTCATAGTT 85496

QY 181 CCACAGCTGGGGTCTCTGCTGCTTCTCTTCTTGGAAACAAACCTATGAGATACCACTG 240

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QY 241 CCTA 244

Db 85557 CCTA 85560

RESULT 5

US-09-634-306B-185132/C  
Sequence 185132, Application US/09634306B  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/09/634,306B  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 185132  
LENGTH: 605  
TYPE: DNA  
ORGANISM: Human  
US-09-634-306B-185132

Query Match 83.0%; Score 202.6; DB 26; Length 605;  
Best Local Similarity 95.9%; Pred. No. 1.3e-50;  
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 28 TTTTTCGAGGACAAATTTAAGGCTGATGATATCGTTATGACGCTGTTGATTCACA 87

Db 605 TTGTTGACGACCAATTTAAGGCTGATGATATTTATATGACGCTGTTGATTCACA 546

QY 88 GAGGTGATGATGTTTACCATGTTGCGGAGTTATGATGATGATGATGATGATGATGATGAT 147

Db 545 GAGGTGATGATGTTTACCATGTTTCTGAGTGTATGATGATGATGATGATGATGATGATGAT 486

QY 148 CTACATGACAGTCACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207

Db 485 CTACATGACAGTCACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426

QY 208 TCCCTTGGAAACAAACCTATGAGATACCACTGCTTA 244

Db 425 TCCCTTGGAAACAAACCTATGAGATACCACTGCTTA 389

RESULT 6

US-10-027-632-185132/C

Sequence 185132, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185132  
; LENGTH: 605  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-185132

Query Match 83.0%; Score 202.6; DB 43; Length 605;  
Best Local Similarity 95.9%; Pred. No. 1.3e-50;  
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY	28	TTTTTGACGACAAATTTAAGGCTGATGATATGTTATGACGCTGTTGATTCACA	87
DB	605	TTGTTGACGACAACTTTAAGGCTGATGATATTAATATAGCAGCTGTTGATTCACA	546
QY	88	GAGGTGATCAGTGTTCACCATGTTGGCAGTGTTCATGTCATCAGATATCAGA	147
DB	545	GAGGTGATCAGTGTTCACCATGTTGGCAGTGTTCATGTCATCAGATATCAGA	486
QY	148	CTACATGACAGTCCAGACTGGCTCATATGTTCCAGCAGCTGGGCTTCTGCTTGT	207
DB	485	CTACATGACAGTCCAGACTGGCTCATATGTTCCAGCAGCTGGGCTTCTGCTTGT	426
QY	208	TCCTTTGACAAAACACTATGATGATACCACTGCTTA	244
DB	425	TTCTTTGACAAAACACTATGATGATACCACTGCTTA	389

RESULT 7  
US-60-160-190-43/c  
; Sequence 43, Application US/60160190  
; GENERAL INFORMATION:  
; APPLICANT: BONAZZI, VIVIEN  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
; FILE REFERENCE: CLO000115  
; CURRENT APPLICATION NUMBER: US/60/160,190  
; CURRENT FILING DATE: 1998-10-19  
; NUMBER OF SEQ ID NOS: 2384  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-160-190-43

Query Match 50.2%; Score 122.4; DB 72; Length 278;  
Best Local Similarity 92.1%; Pred. No. 2.6e-26;  
Matches 129; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY	1	ATCAGTATATTCATGTTTCTGCTTTTTCGAGGACACATTTAAGGCTGATGAT	60
DB	140	ATTGTATATTCATGTTTCTGCTTTTTCGAGGACACATTTAAGGATGATGAT	81
QY	61	ATCGTTATGACGCTGTTGATTCACAGAGGTGAGTCAGTGTTCATCAGTTCGACGT	120
DB	80	ATTATATATGACGCTGTTGATTCACAGAGGTGAGTCAGTGTTCATCAGTTCGACGT	21
QY	121	GTTATGTCACAGTCAGAT	140
DB	20	GTTATGTCACAGTCAGAT	1

RESULT 8  
US-60-169-841-65/c  
; Sequence 65, Application US/60169841  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
; FILE REFERENCE: CLO00163  
; CURRENT APPLICATION NUMBER: US/60/169,841  
; CURRENT FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 2910  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: Human  
US-60-169-841-65

Query Match 50.2%; Score 122.4; DB 72; Length 278;  
Best Local Similarity 92.1%; Pred. No. 2.6e-26;  
Matches 129; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY	1	ATCAGTATATTCATGTTTCTGCTTTTTCGAGGACACATTTAAGGCTGATGAT	60
DB	140	ATTGTATATTCATGTTTCTGCTTTTTCGAGGACACATTTAAGGATGATGAT	81
QY	61	ATCGTTATGACGCTGTTGATTCACAGAGGTGAGTCAGTGTTCATCAGTTCGACGT	120
DB	80	ATTATATATGACGCTGTTGATTCACAGAGGTGAGTCAGTGTTCATCAGTTCGACGT	21
QY	121	GTTATGTCACAGTCAGAT	140
DB	20	GTTATGTCACAGTCAGAT	1

RESULT 9  
US-60-160-190-415/c  
; Sequence 415, Application US/60160190  
; GENERAL INFORMATION:  
; APPLICANT: BONAZZI, VIVIEN  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
; FILE REFERENCE: CLO000115  
; CURRENT APPLICATION NUMBER: US/60/160,190  
; CURRENT FILING DATE: 1998-10-19  
; NUMBER OF SEQ ID NOS: 2384  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 415  
; LENGTH: 460  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-160-190-415

Query Match 20.6%; Score 50.2; DB 72; Length 460;  
Best Local Similarity 77.2%; Pred. No. 0.0003;  
Matches 61; Conservative 0; Mismatches 18; Indels 0; Gaps 0;





; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-2171

Query Match 20.1%; Score 49; DB 103; Length 5080;  
Best Local Similarity 69.1%; Pred. No. 0.0016;  
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 36 GGCAATTTAAGGCTGATGATATCGTTATGACAGTGTGATTCACAGAGTGAG 95  
Db 3913 GGCAATTTAAGGCTGATGATATCGTTATGACAGTGTGATTCACAGAGTGAG 3972

OY 96 TCAGTGTCTACATGTTCCGAGTGTATGCTCAAG 132  
Db 3973 ATGTCAAGTCTCGTTCGACATAGTCACAGCCAG 4009

## RESULT 15

US-60-466-412-2171  
; Sequence 2171, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-466-412-2171

Query Match 20.1%; Score 49; DB 103; Length 5080;  
Best Local Similarity 69.1%; Pred. No. 0.0016;  
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 36 GGCAATTTAAGGCTGATGATATCGTTATGACAGTGTGATTCACAGAGTGAG 95  
Db 3913 GGCAATTTAAGGCTGATGATATCGTTATGACAGTGTGATTCACAGAGTGAG 3972

OY 96 TCAGTGTCTACATGTTCCGAGTGTATGCTCAAG 132  
Db 3973 ATGTCAAGTCTCGTTCGACATAGTCACAGCCAG 4009

Search completed: March 23, 2004, 04:00:29  
Job time : 1849.78 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 16:13:34 ; Search time 309.212 Seconds  
(without alignments)  
414.412 Million cell updates/sec

Title: US-09-646-224A-14

Perfect score: 1 atcagatatttcacgtttt.....ctatgagatcacctgcctta 244

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapex 1.0

Searched: 1155024 seqs, 262583689 residues

Total number of hits satisfying chosen parameters: 2310048

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents NA New:\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	45	18.4	201	US-60-548-091-19213
2	45	18.4	100374	US-60-548-091-5675
3	41.4	17.0	5874	US-10-487-337-5
4	41.2	16.9	6524	US-10-487-337-1
5	37.2	15.2	4852	US-60-548-091-267
6	37.2	15.2	4855	US-60-548-091-266
7	36.2	14.8	600	US-60-545-213-3899
8	36.2	14.8	600	US-60-545-213-8171
9	35.8	14.7	201	US-60-548-091-5535
10	35.6	14.6	201	US-60-548-091-5580
11	35.6	14.6	4855	US-60-548-091-268
12	35	14.3	201	US-60-548-091-5511
13	34.8	14.3	156796	US-10-796-280-12574
14	31.8	13.0	339880	PCT-US03-32805-1
15	31.4	12.9	634888	PCT-US03-34801-1
16	30.4	12.5	1338	US-09-830-230A-96
17	30.4	12.5	1410	US-09-830-230A-95
18	30.2	12.4	454	US-10-767-701-21297
19	30	12.3	15857	US-10-100-683-12496
20	30	12.3	287340	US-10-767-471-10885
21	29.8	12.2	541	US-10-779-543-19243
22	29.6	12.1	2133	US-10-417-884A-1413
23	29.6	12.1	12917	US-10-796-280-12530
24	29.6	12.1	23939	US-10-796-280-12212
25	29.6	12.1	28786	US-60-548-091-5615
26	29.2	12.0	1173	PCT-US04-03545-39

C	27	29	11.9	444922	7	US-60-550-051-3005	Sequence 3005, Ap
C	28	28.8	11.8	4403	5	US-09-796-692B-4717	Sequence 4717, Ap
C	29	28.6	11.7	327636	7	US-60-550-051-2994	Sequence 2994, Ap
C	30	28.4	11.6	28786	6	US-10-767-471-10789	Sequence 10789, A
C	31	28.4	11.6	39320	6	US-10-767-471-10789	Sequence 10789, A
C	32	28.4	11.6	41973	6	US-10-767-471-10733	Sequence 10733, A
C	33	28.4	11.6	41973	6	US-10-767-471-10733	Sequence 10733, A
C	34	28.4	11.6	44848	6	US-10-781-758-42	Sequence 12385, A
C	35	28.4	11.6	44848	6	US-10-785-116-42	Sequence 42, Appl
C	36	28.4	11.6	154875	6	US-10-765-790-107	Sequence 107, Appl
C	37	28.4	11.6	230097	6	US-10-796-280-12390	Sequence 12390, A
C	38	28.4	11.6	1184710	6	US-10-796-280-12394	Sequence 12394, A
C	39	28.2	11.6	5091	6	US-10-100-683-12022	Sequence 12022, A
C	40	28.2	11.6	46917	6	US-10-100-683-12022	Sequence 10663, A
C	41	28.2	11.6	123504	6	US-10-767-471-10685	Sequence 10914, A
C	42	28	11.5	40000	6	US-10-767-471-10914	Sequence 12198, A
C	43	28	11.5	172943	6	US-10-796-280-12198	Sequence 44126, A
C	44	27.8	11.4	201	6	US-10-796-280-44126	Sequence 13164, A
C	45	27.8	11.4	15205	6	US-10-100-683-13164	Sequence 13164, A

ALIGNMENTS

RESULT 1  
US-60-548-091-19213  
; Sequence 19213, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CI001506  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19213  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-19213  
Query Match 18.4% Score 45; DB 7; Length 201;  
Best Local Similarity 66.3%; Pred. No. 1.6e-05;  
Matches 63; Conservative 31; Indels 0; Gaps 0;  
Db 2 TCAGTATTATTCAGTGTTCGCTTTTTCGAGCAGCATTTAAGGCTGATGATA 61  
18 TAAATGATTGTCTTAATCTTCTTTCCCGACACATTAAAGCTGATGACA 77  
Qy 62 TCGTTATGACGCTGTGATTCACAGAGGTGAGT 96  
Db 78 TTATGATGACGCTGTGATTCACAGAGGTGAGT 112  
RESULT 2  
US-60-548-091-5675  
; Sequence 5675, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CI001506  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5675  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION: (1)...(100374)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-60-548-091-5675

Query Match 18.4%; Score 45; DB 7; Length 100374;  
Best Local Similarity 66.3%; Pred. No. 0.0018;  
Matches 63; Conservative 1; Mismatches 31; Indels 0; Gaps 0;

QY 2 TCAGATATTCAGCTTTTTCGCTTTTTCGAGGACAACTTAAGGCTGATGATA 61

DB 85173 TAAATGATGCTTATATCTGCTTTTCTCCAGGCAACTTAAGGCTGATGACA 85232

QY 62 TCGTTATGACGCTGTGATCCAGAGTGAGT 96

DB 85233 TTATGTATGCACTGTGACTCCGGGGGTAAGT 85267

RESULT 3  
US-10-487-337-5

Sequence 5, Application US/10487337

GENERAL INFORMATION:

APPLICANT: Kenji OKUSE

APPLICANT: Mark BAKER

APPLICANT: Louis POON

APPLICANT: John Nicholas WOOD

APPLICANT: Misha Malik-HALL

TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS

FILE REFERENCE: 117-492 / N.86242A GCW

CURRENT APPLICATION NUMBER: US/10/487,337

CURRENT FILING DATE: 2004-02-20

PRIOR APPLICATION NUMBER: PCT/GB02/03852

PRIOR FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: GB 0120238.1

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 5874

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(5874)

OTHER INFORMATION:

US-10-487-337-5

Query Match 17.0%; Score 41.4; DB 6; Length 5874;  
Best Local Similarity 72.0%; Pred. No. 0.00093;  
Matches 54; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 20 TTCGCTTTTTCGAGGACAACTTAAGGCTGATGATTCGTTATGACGCTGTTG 79

DB 4073 TTGCACTTCTGACAGTGCAACTTTAAAGCTGATGACATTTATGATGACGCTGTTG 4132

QY 80 ATTCACAGAGGTGA 94

DB 4133 ATTCGCGAGGTCA 4147

RESULT 4  
US-10-487-337-1

Sequence 1, Application US/10487337

GENERAL INFORMATION:

APPLICANT: Kenji OKUSE

APPLICANT: Mark BAKER

APPLICANT: Louis POON

APPLICANT: John Nicholas WOOD

APPLICANT: Misha Malik-HALL

TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS

FILE REFERENCE: 117-492 / N.86242A GCW

CURRENT APPLICATION NUMBER: US/10/487,337

CURRENT FILING DATE: 2004-02-20

PRIOR APPLICATION NUMBER: PCT/GB02/03852

PRIOR FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: GB 0120238.1

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 6524

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (204)..(6074)

OTHER INFORMATION:

US-10-487-337-1

Query Match 16.9%; Score 41.2; DB 6; Length 6524;  
Best Local Similarity 74.3%; Pred. No. 0.0011;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTTTCGAGGACAACTTAAGGCTGATGATATCGTTATGACGCTGTTGATTC 84

DB 4287 CTCTTCAGGTGGACACTTAAAGCTGATGACATATGATGACGCTGTTGATTC 4346

QY 85 ACAGAGGTGA 94

DB 4347 GGAGGATCA 4356

RESULT 5  
US-60-548-091-267

Sequence 267, Application US/60548091

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CLO01506

CURRENT APPLICATION NUMBER: US/60/548,091

CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 267

LENGTH: 4852

TYPE: DNA

ORGANISM: Homo sapiens

US-60-548-091-267

Query Match 15.2%; Score 37.2; DB 7; Length 4852;  
Best Local Similarity 72.7%; Pred. No. 0.022;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTTTCGAGGACAACTTAAGGCTGATGATATCGTTATGACGCTGTTGATTC 84

DB 3126 CTTCGAGGTGGCAACTTTAAAGCTGATGACATTTATGATGACGCTGATTC 3185

QY 85 ACAGAG 90

DB 3186 AGGGGG 3191

RESULT 6  
US-60-548-091-266

Sequence 266, Application US/60548091

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CLO01506

CURRENT APPLICATION NUMBER: US/60/548,091

CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 266

LENGTH: 4855

TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-266

Query Match 15.2%; Score 37.2; DB 7; Length 4855;  
Best Local Similarity 72.7%; Pred. No. 0.022;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTC 84  
DB 3129 CTTCTGACGAGTGGCAACATTTAAAGCTGATGACATTTATGACAGCTGTGACTCC 3188  
QY 85 ACAGAG 90  
DB 3189 AGGGGG 3194

## RESULT 7

US-60-545-213-3899  
Sequence 3899, Application US/60545213  
GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mount, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042099)  
CURRENT APPLICATION NUMBER: US/60/545,213  
CURRENT FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3899  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-545-213-3899

Query Match 14.8%; Score 36.2; DB 7; Length 600;  
Best Local Similarity 77.2%; Pred. No. 0.02;  
Matches 44; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 37 GCACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTCACAGAGTG 93  
DB 304 GCCACATTTCAAGATGATGATATATGATCGACAGATTGATCCAGAAATGTG 360

## RESULT 8

US-60-545-213-8171  
Sequence 8171, Application US/60545213  
GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mount, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042099)  
CURRENT APPLICATION NUMBER: US/60/545,213  
CURRENT FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8171  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-545-213-8171

Query Match 14.8%; Score 36.2; DB 7; Length 600;  
Best Local Similarity 77.2%; Pred. No. 0.02;  
Matches 44; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 37 GCACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTCACAGAGTG 93  
DB 304 GCCACATTTCAAGATGATGATATATGATCGACAGATTGATCCAGAAATGTG 360

## RESULT 9

US-60-548-091-5535  
Sequence 5535, Application US/60548091  
GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5535  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-5535

Query Match 14.7%; Score 35.8; DB 7; Length 201;  
Best Local Similarity 78.2%; Pred. No. 0.018;  
Matches 43; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 36 GCACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTCACAGAG 90  
DB 5 GCACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTCACAGAGGGG 59

## RESULT 10

US-60-548-091-5580  
Sequence 5580, Application US/60548091  
GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5580  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-5580

Query Match 14.6%; Score 35.6; DB 7; Length 201;  
Best Local Similarity 71.2%; Pred. No. 0.021;  
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 25 CTTTTCGACGACATTTAAGGCTGATGATCGTTATGACAGCTGTGATTC 84  
DB 51 CTTCTGACGAGTGGCAACATTTAAAGCTGATGACATTTATGATGACAGRTGACTCC 110

QY 85 ACAGAG 90  
DB 111 AGGGGG 116

## RESULT 11

US-60-548-091-268  
Sequence 268, Application US/60548091  
GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 268  
LENGTH: 4855  
TYPE: DNA

ORGANISM: Homo sapiens  
US-60-548-091-268

Query Match 14.6%; Score 35.6; DB 7; Length 4855;  
Best Local Similarity 71.2%; Pred. No. 0.073;  
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

25 CTTTTCGAGGCGCATTTAAGGCTGAGTATGCTTTATGACGCTGTGATCC 84  
Db 3129 CTTTCGAGGCTGAGTATTTAAGGCTGAGTATGCTTTATGACGCTGTGATCC 3188

QY 85 ACAGAG 90  
Db 3189 AGGGGG 3194

RESULT 12  
US-60-548-091-5511  
Sequence 5511, Application US/60548091  
GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: STROKE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001506  
CURRENT APPLICATION NUMBER: US/60/548,091  
CURRENT FILING DATE: 2004-02-27  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5511  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-5511

Query Match 14.3%; Score 35; DB 7; Length 201;  
Best Local Similarity 74.6%; Pred. No. 0.033;  
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

25 CTTTTCGAGGCGCATTTAAGGCTGAGTATGCTTTATGACGCTGTGATCC 83  
Db 143 CTTTCGAGGCTGAGTATTTAAGGCTGAGTATGCTTTATGACGCTGTGATCC 201

RESULT 13

US-10-796-280-12574  
Sequence 12574, Application US/10796280  
GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001510  
CURRENT APPLICATION NUMBER: US/10/796,280  
CURRENT FILING DATE: 2004-03-10  
NUMBER OF SEQ ID NOS: 68533  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12574  
LENGTH: 156796  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-796-280-12574

Query Match 14.3%; Score 34.8; DB 6; Length 156796;  
Best Local Similarity 57.3%; Pred. No. 0.53;  
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

19 TTTTCGCTTTTTCGAGGCGCATTTAAGGCTGAGTATGCTTTATGACGCTGT 78  
Db 97839 TATGTAATATTATTTTCAGGCTCAACATACACAGAAGTCTGTAATGCTATG 97838

QY 79 GATTCACAGAGGTGAGTCTTACCATGTTCCGAGCTTATGCT 128  
Db 97839 GATTCAGAGTCTGAGTCTTACCATGTTCCGAGCTTATGCT 97838

RESULT 14  
PCT-US03-32805-1/C

Sequence 1, Application PC/TUS0332805  
GENERAL INFORMATION:  
APPLICANT: decode genetics ehf.  
APPLICANT: Heigadottir, Anna  
APPLICANT: Guicher, Jeffrey R.  
APPLICANT: Manolescu, Andrei  
TITLE OF INVENTION: Susceptibility Gene for Myocardial  
FILE REFERENCE: 2345, 2048002  
CURRENT APPLICATION NUMBER: PCT/US03/32805  
CURRENT FILING DATE: 2003-10-16  
PRIOR APPLICATION NUMBER: 60/419,432  
PRIOR FILING DATE: 2002-10-17  
NUMBER OF SEQ ID NOS: 535  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1

LENGTH: 398800  
TYPE: DNA  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (70677)...(70776)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (154988)...(155087)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 248521  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (272544)...(272643)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (279545)...(279644)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (300892)...(300991)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (327555)...(327654)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (332849)...(332948)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (341698)...(341698)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (345190)...(345289)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (350504)...(350603)  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (391524)...(391623)

OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (396625)... (396724)  
OTHER INFORMATION: n = A,T, C or G  
PCT-US03-32805-1

Query Match 13.0%; Score 31.8; DB 1; Length 398800;  
Best Local Similarity 53.7%; Pred. No. 7.7;  
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 1 ATCAGTATTTATTCAGTCTTTCTGCTTTTTCAGGACATTTAAGGCTGATGGAT 60  
DB 259702 ATCAGTATTTATTCAGTCTTTCTGCTTTTTCAGGACATTTAAGGCTGATGGAT 259643  
OY 61 ATCGTTATGCAAGCTGTGATTCACAGAGGTGAGTGTTCATGCTTCCAGT 120  
DB 259642 TTCATTGTTGGACATGGGTCCAGTATGGGTGGAATGTTTCCATGTTGGAATG 259583  
OY 121 GTT 123  
DB 259582 GGT 259580

RESULT 15  
PCT-US03-34801-1  
Sequence 1, Application PC/TUS0334801  
GENERAL INFORMATION:  
APPLICANT: decode genetics ehf.  
APPLICANT: Reyniadorffir, Inga  
APPLICANT: Gulcher, Jeffrey R.  
APPLICANT: Grant, Struan F.  
APPLICANT: Thorleifsson, Gudmar  
TITLE OF INVENTION: Human Type II Diabetes Gene - S11c-3  
FILE REFERENCE: 2345, 2046002  
CURRENT APPLICATION NUMBER: PCT/US03/34801  
CURRENT FILING DATE: 2003-10-31  
PRIOR APPLICATION NUMBER: 60/423,541  
PRIOR FILING DATE: 2002-11-01  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 634888  
TYPE: DNA  
ORGANISM: homo sapiens  
PCT-US03-34801-1

Query Match 12.9%; Score 31.4; DB 1; Length 634888;  
Best Local Similarity 49.7%; Pred. No. 12;  
Matches 80; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OY 48 GGGCTGATGATATCGTTTATGACGCTGTGATTCACAGAGGTGAGTGTTCATC 107  
DB 78193 GGGCTGAGGAAATTCACCAAGGCTCTGCTGCTCTCTCTGAGCAATGGCTGAGT 78252  
OY 108 CATGTTCCGAGTGTATGATGATCAAGTCAAGATATCATGATGACAGTCCAGAC 167  
DB 78253 GCTAACCTGCAATGATGATGAGCTCTGATATACCAACATGATGAAGGACTGATC 78312  
OY 168 TGGCTCATAGTTCAGACAGCTGGGCTTCTGCTTGT 208  
DB 78313 TGGAGACATCTCTCTTAAGCAAAATTCGATATATGTT 78353

Search completed: March 23, 2004, 04:50:26  
Job time : 328.212 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 1431.61 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-14

Perfect score: 244  
Sequence: 1 atcagttatcatcatgtttc.....ctatgagataaccactgccta 244

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

BST:  
1: em\_eebha:\*  
2: em\_eechum:\*  
3: em\_eeclin:\*  
4: em\_eeclmu:\*  
5: em\_eeclrov:\*  
6: em\_eeclp1:\*  
7: em\_eecltro:\*  
8: em\_hnc:\*  
9: gb\_eecl1:\*  
10: gb\_eecl2:\*  
11: gb\_hnc:\*  
12: gb\_eecl3:\*  
13: gb\_eecl4:\*  
14: gb\_eecl5:\*  
15: em\_eeclum:\*  
16: em\_eeclom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.2	20.6	709	29	CE215453 tigr-gss-
2	49	20.1	4614	29	AY404475 Homo sapi
3	48.4	19.8	800	29	BX238165 Danio rer
4	48	19.7	3772	29	AY404476 Pan trogl

5	45.4	18.6	256	28	AZ861116
6	41.2	16.9 <td>574</td> <td>14 <td>CB608527</td> </td>	574	14 <td>CB608527</td>	CB608527
7	40.6	16.6 <td>1084</td> <td>28 <td>CC295710</td> </td>	1084	28 <td>CC295710</td>	CC295710
8	40.2	16.5 <td>519</td> <td>14 <td>CB534807</td> </td>	519	14 <td>CB534807</td>	CB534807
9	40.2	16.5 <td>689</td> <td>10 <td>BF347024</td> </td>	689	10 <td>BF347024</td>	BF347024
10	40	16.4 <td>430</td> <td>14 <td>CB761310</td> </td>	430	14 <td>CB761310</td>	CB761310
11	38.2	15.7 <td>521</td> <td>14 <td>CB720975</td> </td>	521	14 <td>CB720975</td>	CB720975
12	38	15.6 <td>833</td> <td>13 <td>BU116614</td> </td>	833	13 <td>BU116614</td>	BU116614
13	37.8	15.5 <td>480</td> <td>12 <td>BM494034</td> </td>	480	12 <td>BM494034</td>	BM494034
14	37.2	15.2 <td>908</td> <td>13 <td>BQ946179</td> </td>	908	13 <td>BQ946179</td>	BQ946179
15	37.2	15.2 <td>4675</td> <td>11 <td>AK083220</td> </td>	4675	11 <td>AK083220</td>	AK083220
16	37.2	15.2 <td>5666</td> <td>29 <td>AY416501</td> </td>	5666	29 <td>AY416501</td>	AY416501
17	36.6	15.0 <td>442</td> <td>14 <td>CB789718</td> </td>	442	14 <td>CB789718</td>	CB789718
18	36.6	15.0 <td>633</td> <td>14 <td>CB457889</td> </td>	633	14 <td>CB457889</td>	CB457889
19	36.2	14.8 <td>283</td> <td>14 <td>BB874422</td> </td>	283	14 <td>BB874422</td>	BB874422
20	35.8	14.7 <td>876</td> <td>29 <td>CNS04PFU</td> </td>	876	29 <td>CNS04PFU</td>	CNS04PFU
21	35.6	14.6 <td>624</td> <td>9 <td>AV838090</td> </td>	624	9 <td>AV838090</td>	AV838090
22	35.6	14.6 <td>690</td> <td>13 <td>BM000524</td> </td>	690	13 <td>BM000524</td>	BM000524
23	35.6	14.6 <td>725</td> <td>13 <td>BM134994</td> </td>	725	13 <td>BM134994</td>	BM134994
24	35.6	14.6 <td>751</td> <td>13 <td>BU226444</td> </td>	751	13 <td>BU226444</td>	BU226444
25	35.6	14.6 <td>767</td> <td>13 <td>BM128695</td> </td>	767	13 <td>BM128695</td>	BM128695
26	35.6	14.6 <td>768</td> <td>13 <td>BM015229</td> </td>	768	13 <td>BM015229</td>	BM015229
27	35.4	14.5 <td>657</td> <td>28 <td>AQ597108</td> </td>	657	28 <td>AQ597108</td>	AQ597108
28	35	14.3 <td>313</td> <td>10 <td>BA462246</td> </td>	313	10 <td>BA462246</td>	BA462246
29	34.8	14.3 <td>985</td> <td>10 <td>BF314635</td> </td>	985	10 <td>BF314635</td>	BF314635
30	34.8	14.3 <td>989</td> <td>10 <td>BF794594</td> </td>	989	10 <td>BF794594</td>	BF794594
31	34.6	14.2 <td>379</td> <td>10 <td>AW552297</td> </td>	379	10 <td>AW552297</td>	AW552297
32	34.4	14.1 <td>979</td> <td>12 <td>BG341991</td> </td>	979	12 <td>BG341991</td>	BG341991
33	34.4	14.1 <td>5943</td> <td>29 <td>AY416499</td> </td>	5943	29 <td>AY416499</td>	AY416499
34	34.2	14.0 <td>594</td> <td>14 <td>CB824846</td> </td>	594	14 <td>CB824846</td>	CB824846
35	34.2	14.0 <td>595</td> <td>14 <td>CB357217</td> </td>	595	14 <td>CB357217</td>	CB357217
36	34.2	14.0 <td>619</td> <td>13 <td>BQ784002</td> </td>	619	13 <td>BQ784002</td>	BQ784002
37	34.2	14.0 <td>676</td> <td>12 <td>BM102967</td> </td>	676	12 <td>BM102967</td>	BM102967
38	34.2	14.0 <td>677</td> <td>13 <td>BU973179</td> </td>	677	13 <td>BU973179</td>	BU973179
39	34.2	14.0 <td>817</td> <td>12 <td>BI890389</td> </td>	817	12 <td>BI890389</td>	BI890389
40	34.2	14.0 <td>913</td> <td>14 <td>CA471335</td> </td>	913	14 <td>CA471335</td>	CA471335
41	34.2	14.0 <td>4556</td> <td>29 <td>AY404477</td> </td>	4556	29 <td>AY404477</td>	AY404477
42	34	13.9 <td>401</td> <td>9 <td>AL723537</td> </td>	401	9 <td>AL723537</td>	AL723537
43	34	13.9 <td>584</td> <td>29 <td>TA162H09P</td> </td>	584	29 <td>TA162H09P</td>	TA162H09P
44	34	13.9 <td>600</td> <td>14 <td>CB379189</td> </td>	600	14 <td>CB379189</td>	CB379189
45	34	13.9 <td>611</td> <td>14 <td>CB238724</td> </td>	611	14 <td>CB238724</td>	CB238724

#### ALIGNMENTS

RESULT 1  
LOCUS CE215453 709 bp DNA linear GSS 25-SEP-2003  
DEFINITION tigr-gss-dog-17000372977459 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE215453  
VERSION CE215453.1 GI:35371122  
KEYWORDS GSS  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 709)  
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.N. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research, TIGR, 9712 Medical Center Drive,  
Department of Eukaryotic Genomics, Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org

[illegible]

QY	DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
96	TCAGTGTTCACATGTTGGCAGTGTATGATGCA	132												
3507	ATGTCAAGGTCCTCGTGTTCACATGTCACACCCAG	3543												
RESULT 3														
LOCUS	BX238165	800 bp	DNA	linear	GSS 29-JAN-2003									
DEFINITION	Danio rerio genomic clone DKEX-286P24, genomic survey sequence.													
ACCESSION	BX238165													
VERSION	BX238165.1	GI:28160499												
KEYWORDS	GSS.													
SOURCE	Danio rerio (zebrafish)													
ORGANISM	Danio rerio													
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.													
AUTHORS	1 (bases 1 to 800)													
TITLE	Humphray, S.J., Huckle, E. and Durham, J.L.													
JOURNAL	Submitted (27-JUN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphrays@sanger.ac.uk Unpublished													
COMMENT	This sequence was generated from the SP6 end of BAC 286P24. 286P24 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/projects/D_rerio/.													
FEATURES	Location/Qualifiers													
source	1..800													
	/organism="Danio rerio"													
	/mol_type="genomic DNA"													
	/db_xref="taxon:7955"													
	/clone="DKEX-286P24"													
	/rissue_type="Testis"													
	/note="vector pindigobAC-536"													
Query Match	19.8%; Score 48.4; DB 29; Length 800;													
Best Local Similarity	68.4%; Pred. No. 0.054; Mismatches 31; Indels 0; Gaps 0;													
Matches	67; Conservative 0; Mismatches 31; Indels 0; Gaps 0;													
QY	6 TATTATTCATGTTTCTGCTTTTTCAGGACCAATTAAAGGCTGGATGATATCGT	65												
DB	524 TTTTATTCATCTATCTATCTTACTTTTCCCAAGGCCACATTTAAAGATGATGACATCAT	583												
QY	66 TTATGCAGCTGTGATTCACACAGGCGGATGACATGTT	103												
DB	584 GTACGCAGCTGTAGATTCCTCGTAGTGAAGTGTGTTT	621												
RESULT 4														
LOCUS	AY404476	3772 bp	DNA	linear	GSS 16-DEC-2003									
DEFINITION	Pan troglodytes SCN1LA gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.													
ACCESSION	AY404476													
VERSION	AY404476.1	GI:39760453												
KEYWORDS	GSS.													
SOURCE	Pan troglodytes (chimpanzee)													
ORGANISM	Pan troglodytes													
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.													
AUTHORS	1 (bases 1 to 3772)													
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tenebaum, D.M., Cavello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Carey, J.M.													
JOURNAL	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios													
PUBMED	Science 302 (5652), 1960-1963 (2003)													
REFERENCE	14671302													
REFERENCE	2 (bases 1 to 3772)	</												

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriter, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.C., Adams, M.D., and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source Location/Qualifiers  
1..3772  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..3772  
/gene="SCN11A"  
/locus\_tag="HCM1903"

ORIGIN

Query Match 19.7%; Score 48; DB 29; Length 3772;  
Best Local Similarity 30.7%; Pred. No. 0.06;  
Matches 51; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 37 GCACAAATTAGAGCTGGATGATATCGTTATGACAGCTGTTGATTCACAGAGTGTAGT 96  
Db 3448 GCACAAATTAGAGCTGGATGATATCGTTATGATGACAGCTGTTGATTCACAGAGNNNNN 3507

QY 97 CAGTGTCTACATGTTCCGACAGTGTATGCTCAAGTCAGATATCATGACTACATGAGA 156  
Db 3508 NNN 3567

QY 157 CAGTCCAGAACTGGCGTCATAGTTCCAGACAGCTGGGTTCTCTGCC 202  
Db 3568 NNN 3613

RESULT 5 256 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0167K19F Mouse 10kb plasmid UGCM1 library Mus musculus genomic  
DEFINITION clone UUGC2M0167K19 F, genomic survey sequence.  
ACCESSION A2861116  
VERSION A2861116  
KEYWORDS A2861116.1 GI:13057114  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 256)  
Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamil, C., Iejam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0167 row: K column: 19  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 256.  
Location/Qualifiers  
1..256  
/organism="Mus musculus"  
/mol\_type="genomic DNA"

FEATURES  
source

/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0167K19"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCM1 library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|bp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 18.6%; Score 45.4; DB 28; Length 256;  
Best Local Similarity 77.5%; Pred. No. 0.34;  
Matches 55; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 27 TTTTTCAGACCAATTAAAGCTGGATGATATCGTTATGACAGCTGTTGATTCAC 86  
Db 112 TTTTTCAGACCACTTAAAGCTGGATGATATGATGACAGCTGTCATCTCG 171

QY 87 AGAGTGAGTC 97  
Db 172 AGATGTAGTC 182

RESULT 6 574 bp mRNA linear EST 16-MAY-2003  
LOCUS CB608527  
DEFINITION AMGNNUC:NRDGL-00143-D3-A nrdgl (10855) Rattus norvegicus cDNA clone  
ACCESSION CB608527  
VERSION CB608527  
KEYWORDS CB608527.1 GI:29548140  
SOURCE EST.  
ORGANISM Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 574)  
Angen EST Program.  
Angen Rat EST Program  
Unpublished (2003)  
Contact: Dan Fitzpatrick  
Angen, Inc  
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00143 row: d column: 3.  
Location/Qualifiers  
1..574  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrdgl-00143-d3"  
/issue\_type="Dorsal Root Ganglia"  
/clone\_1lb="nrdgl (10855)"  
/note="Vector: DSPORT1; Site\_1: SalI; Site\_2: NotI; rat dorsal root ganglia"

FEATURES  
source

ORIGIN

Query Match 16.9%; Score 41.2; DB 14; Length 574;  
Best Local Similarity 74.3%; Pred. No. 3.7;  
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 CTTTTCGAGGCAACATTTAAGGCTGATGATATCGTTTATGACGCTGTTGATCC 84  
DB 336 CTTTTCGAGGCTGACACCTTCAAGGCTGATGACATATATGACGCTGTTGATCC 395

QY 85 ACAGAGGTGA 94  
DB 396 GGAGAGATCA 405

RESULT 7  
CC295710 1084 bp DNA linear GSS 13-MAY-2003  
LOCUS CH261-146M14, RM1.1 CH261 Gallus gallus genomic clone CH261-146M14,  
DEFINITION genomic survey sequence.  
ACCESSION CC295710  
VERSION CC295710.1 GI:30667151  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 1084)  
AUTHORS Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)  
JOURNAL Contact: Richard K. Wilson  
COMMENT Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert length: 182000 Std Error: 0.00  
Seq primer: RM1 TAGGACTCATATAGGAGAGA  
Class: BAC ends  
High quality sequence start: 20  
High quality sequence stop: 745.  
Location/Qualifiers  
1. 1084  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/strain="Red Jungle Fowl"  
/db\_xref="taxon:9031"  
/clone="CH261-146M14"  
/sex="female"  
/cell\_line="UCD001, inbred 256"  
/clone\_11b="CH261"  
/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CH261 Female Chicken library - for library and clone  
ordering information: <http://www.chori.org/bacpac>"

ORIGIN

Query Match 16.6%; Score 40.6; DB 28; Length 1084;  
Best Local Similarity 73.2%; Pred. No. 4.9;  
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 26 TTTTTCGAGGCAACATTTAAGGCTGATGATATCGTTTATGACGCTGTTGATCCA 85  
DB 605 TCTTTCATAGGCTACATTAAAGATGATGATATCATGATGACGCTGATTTCTC 664

QY 86 CAGAGGTGAGT 96  
DB 665 GCAATGTAGT 675

RESULT 8  
CBS34807 519 bp mRNA linear EST 16-MAY-2003  
LOCUS CBS34807/c  
DEFINITION 768167 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.

ACCESSION CBS34807  
VERSION CBS34807.1 GI:29400892  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 519)  
AUTHORS Smith, T.P.L., Roberts, A.J., Echeerikamp, S.E., Chitko-McKown, C.G.,  
Wray, J.E. and Keele, J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
Unpublished (2003)  
JOURNAL Contact: Smith TPL  
COMMENT USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alc option. Vector identified with  
cross\_match v0.990329.  
Plate: LAM8018 row: M column: 21  
Seq primer: TAGAAGCAGCAGTCAGG.  
Location/Qualifiers  
1. 519  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_11b="MARC 6BOV"  
/note="Vector: pCDNA3.1; Site\_1: EcoRI; Site\_2: NotI;  
library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

ORIGIN

Query Match 16.5%; Score 40.2; DB 14; Length 519;  
Best Local Similarity 70.1%; Pred. No. 6.6;  
Matches 54; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 18 TTTTTCGCTTTTTCGAGGCAACATTTAAGGCTGATGATATCGTTTATGACGCTGT 77  
DB 207 TCTTCGATGCTGCTCAAGTGCAACATTTAAGGCTGATGACATTTATGTCAGCTGT 148

QY 78 TGATTTCAAGAGGTGA 94  
DB 147 TGATTCACGAGATGTTA 131

RESULT 9  
BF347024 689 bp mRNA linear EST 22-NOV-2000  
LOCUS BF347024  
DEFINITION 602021819P1 NCI CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4157189  
5', mRNA sequence.  
ACCESSION BF347024  
VERSION BF347024.1 GI:11294619  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 689)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL Contact: Robert Strusberg, Ph.D.  
Email: cga@db-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.



Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology

(UMIST) PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..833

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Compton Line 151"

/db\_xref="taxon:9031"

/clone="CHSST129j14"

/sex="Female"

/tissue\_type="cerebrum"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSECH15"

/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) (Stratagene) vector to accommodate cDNA produced with the I-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BglI and BamHI sites [5'gagcggtcgagccgcgagtcgagaaagaaag] (5'aattcttttctcgatccggtcgagtcgagcgc]"

## ORIGIN

Query Match 15.6%; Score 38; DB 13; Length 833;  
Best Local Similarity 81.5%; Pred. No. 23;  
Matches 44; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

37 GCACATTTAAGGCTGATGATATCGTTTTCGAGCTGTTGATTCACAGAGT 90  
|||||  
694 GCAACATTCACAGCGCTGATGATGATCATCATGTGACGAGCTGATTCACAGAGT 747

RESULT 13  
BM494034 480 bp mRNA linear EST 11-FEB-2002  
LOCUS IpcGBrl\_10\_C01\_21 Ictalurus punctatus Brain primary library  
DEFINITION Ictalurus punctatus cDNA clone IpcGBrl\_10\_C01\_21\_06Mar00\_006 5',  
mRNA sequence.  
BM494034  
BM494034.1 GI:18645215

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Ictalurus punctatus (channel catfish)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
Ictaluridae; Ictalurus.  
1 (bases 1 to 480)  
Nonnenmann, D.J. and Waldbieser, G.C.  
Characterization of a brain cDNA library from adult channel catfish  
(Ictalurus punctatus)  
Unpublished (2002)  
Contact: Waldbieser GC  
Catfish Genetics Research Unit  
USDA-Agricultural Research Service  
141 Experiment Station Road, Stoneville, MS 38776, USA  
Tel: 662 686 3593  
Fax: 662 686 3567  
Email: gwaldbieser@ars.usda.gov

Single pass sequencing. Bases called with Phred v0.000925.c. Low  
quality bases and vector trimmed with Lucy v1.16.  
Plate: Brl\_10 row: C column: 1  
Seq primer: M3 Reverse.  
Location/Qualifiers

FEATURES

1..480  
/organism="Ictalurus punctatus"

## ORIGIN

Query Match 15.5%; Score 37.8; DB 12; Length 480;  
Best Local Similarity 78.9%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

36 GCACATTTAAGGCTGATGATATCGTTTTCGAGCTGTTGATTCACAGAGT 92  
|||||  
154 GGCACCGTTTAAAGTTGATGATCATGTATGACGCGGTGATTCACAGAGT 210

RESULT 14  
BQ946179 908 bp mRNA linear EST 21-AUG-2002  
LOCUS AGENCOURT\_8926526 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6469275  
DEFINITION 5', mRNA sequence.  
BQ946179  
BQ946179.1 GI:22361657

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 908)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: gsgabbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMU at:  
http://image.llnl.gov  
Plate: LHM13998 row: C column: 04  
High quality sequence stop: 596.  
Location/Qualifiers

## FEATURES

source

1..908  
/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:6469275"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 15.2%; Score 37.2; DB 13; Length 908;  
Best Local Similarity 72.7%; Pred. No. 36;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

25 CTTTTCGAGCGCAATTTAAGGCTGATGATATCGTTTTCGAGCTGTTGATTC 84  
|||||  
102 CTTTCAGTGGCAACCTTAAAGCTGATGATCATGTATGACGCTGTAGATTCC 161

DB 85 ACAGAG 90

Db 162 CGAAG 167

RESULT 15  
AK083220  
LOCUS  
DEFINITION  
AK083220 4675 bp mRNA linear HTC 20-SEP-2003  
Mus musculus adult male hippocampus cDNA, RIKEN full-length  
enriched library, clone: C630029C19 product: sodium channel,  
voltage-gated, type VIII, alpha polypeptide, full insert sequence.  
AK083220  
VERSION  
KEYWORDS  
AK083220.1 GI:26101130  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, Y., Nishi, K., Kitagawa, T., Tashiro, H., Itoh, A.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 4675)  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,

## COMMENT

Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp).  
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>.  
URL: <http://fantom.gsc.riken.go.jp/>.

## FEATURES

## SOURCE

1..4675

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="PANTOM:DB:C630029C19"

/db\_xref="MGJ:2417601"

/db\_xref="taxon:10090"

/clone="C630029C19"

/sex="male"

/tissue\_type="hippocampus"

/clone\_id="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

&lt;1..3589

/note="putative

sodium channel, voltage-gated, type VIII, alpha

polypeptide (MGJ|MGJ:103169, GB|NM\_011323, evidence:

BLASTN, 99%, match=3589)"

## ORIGIN

## misc\_feature

Query Match 15.2%; Score 37.2; DB 11; Length 4675;  
Best Local Similarity 72.7%; Pred. No. 32;  
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY

25 CTTTTCGACGACATTTAAGGCGTGATGATTCGTTATGAGCGTGTGATTC 84

DB

1861 CTTTTCGACGACGACCTTCAAGGCTGATGACATCATGTATGACGCTGTGATTC 1920

QY

85 ACAGAG 90

DB

1921 CGAAG 1926

Search completed: March 22, 2004, 23:13:02  
Job time : 1445.61 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 2175.44 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-15

Perfect score: 409  
1 attcaccaccagcccgccca.....gtccccaagaagaatcc 409

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_hcg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_atg:\*

12: gb\_ay:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_atg:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rnd:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

38: em\_by:\*

39: em\_hugo\_hum:\*

40: em\_hugo\_mus:\*

41: em\_hugo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	409	100.0	409	6	AX017231	AX017231 Sequence
2	409	100.0	409	6	BD138453	BD138453 Mammalian
3	364.8	89.2	167476	9	AC116038	AC116038 Homo sapi
4	143.4	35.1	241289	2	AC124662	AC124662 Mus muscu
5	134.4	32.9	856	6	E36123	E36123 Nucleic aci
6	134.4	32.9	3701	6	AR340648	AR340648 Sequence
7	134.4	32.9	3701	6	BD217793	BD217793 Regulatio
8	134.4	32.9	5419	9	HSAA17790	AJ417790 Homo sapi
9	134.4	32.9	5728	6	BD012083	BD012083 Human sod
10	134.4	32.9	5728	6	BD082952	BD082952 Human sod
11	134.4	32.9	5728	6	AF150882	AF150882 Homo sapi
12	134.4	32.9	5860	6	AR340678	AR340678 Sequence
13	134.4	32.9	6237	9	AF188679	AF188679 Homo sapi
14	134.4	32.9	6528	6	BD012082	BD012082 Human sod
15	134.4	32.9	6528	6	BD082951	BD082951 Human sod
16	134.4	32.9	6528	9	AF109737	AF109737 Homo sapi
17	124.8	30.5	243048	2	AC127215	AC127215 Rattus no
18	124	30.3	210800	2	AC127824	AC127824 Rattus no
19	94.8	23.2	221399	10	AL604045	AL604045 Mouse DNA
20	88	21.5	5822	6	AR340647	AR340647 Sequence
21	88	21.5	5822	6	BD217792	BD217792 Regulatio
22	88	21.5	5858	10	AF118044	AF118044 Mus muscu
23	88	21.5	5921	10	AB031389	AB031389 Mus muscu
24	85.2	20.8	637	6	AX164265	AX164265 Sequence
25	85.2	20.8	2156	9	F30116519	AF330134 Homo sapi
26	85.2	20.8	168493	9	AC013463	AC013463 Homo sapi
27	84.2	20.6	238	9	HUMSCNA19	LO1980 Human type
28	84.2	20.6	297	2	HUMSCNA418	LO4233 Homo sapien
29	84.2	20.6	37115	2	AC139098	AC139098 Homo sapi
30	84.2	20.6	44566	2	AC123682	AC123682 Homo sapi
31	84.2	20.6	87944	2	AC023662	AC023662 Homo sapi
32	84.2	20.6	101990	9	AC127029	AC127029 Homo sapi
33	84.2	20.6	162473	9	AC005803	AC005803 Homo sapi
34	83.8	20.5	5887	10	MM0278787	AJ278787 Mus muscu
35	83.8	20.5	208074	2	AC104290	AC104290 Rattus no
36	83.8	20.5	225821	2	AC122968	AC122968 Rattus no
37	83.8	20.5	227323	2	AC117350	AC117350 Rattus no
38	83.6	20.4	236549	2	AC111914	AC111914 Rattus no
39	83.6	20.4	252804	2	AC133055	AC133055 Rattus no
40	83.2	20.3	5334	6	E36125	E36125 Nucleic aci
41	83.2	20.3	178483	2	AC147399	AC147399 Canis fam
42	82.8	20.2	162474	5	AL929294	AL929294 Zebrafish
43	81.8	20.0	18757	2	AC142568	AC142568 Felis cat
44	81.6	20.0	5849	10	RNO237852	AJ237852 Rattus no
45	81.6	20.0	5875	6	AR340646	AR340646 Sequence

# ALIGNMENTS

RESULT 1

AX017231 409 bp DNA linear PAT 07-SEP-2000

LOCUS AX017231

DEFINITION Sequence 15 from Patent WO947670.

ACCESSION AX017231

VERSION AX017231.1 GI:10042151

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Tate, S.N., Grose, D.T. and Hick, C.A.

TITLE Mammalian sodium channel proteins

JOURNAL Patent: WO 9947670-A 15 23-SEP-1999;

Pred. No. is the number of results predicted by chance to have a

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS (GB) ; HICK CAROLINE ANNE (GB)

## FEATURES

Location/Qualifiers  
1. .409  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 409; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1,9e-83;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCACCCAGGCGCCGACATGCATCTCCAGAGCTGCGAAAAGTGAAGAC 60  
DB 1 ATCCACCCAGGCGCCGACATGCATCTCCAGAGCTGCGAAAAGTGAAGAC 60  
QY 61 AGGCTCCCAACAGGGGCTATGGCTGTAGGAAGAGCTATGATCAATGTTGCTCTAA 120  
DB 61 AGGCTCCCAACAGGGGCTATGGCTGTAGGAAGAGCTATGATCAATGTTGCTCTAA 120  
QY 121 GAAACACCTTGCTCTTCTAGATGAAGTGAATGCTTATATTTTCTCCAGTAATTG 180  
DB 121 GAAACACCTTGCTCTTCTAGATGAAGTGAATGCTTATATTTTCTCCAGTAATTG 180  
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QY 361 GGTGTCCTGATTTGGTAAATGTAATCTCTGCTCTCCAAAGAGGATCC 409  
DB 361 GGTGTCCTGATTTGGTAAATGTAATCTCTGCTCTCCAAAGAGGATCC 409

RESULT 2  
BD138453 409 bp DNA linear PAT 18-SRP-2002  
LOCUS Mammalian sodium channel protein.  
DEFINITION BD138453  
ACCESSION BD138453.1 GI:23233398  
VERSION JP 2002508941-A/14.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 409)  
AUTHORS Grose,D.T., Hick,C.A. and Tate,S.N.  
TITLE Mammalian sodium channel protein  
JOURNAL Patent: JP 2002508941-A 14 26-MAR-2002;  
GLAXO GROUP LTD

COMMENT  
OS Homo sapiens (human)  
PN JP 2002508941-A/14  
PD 26-MAR-2002  
PF 18-MAR-1998 JP 2000536653  
PR 18-MAR-1998 GB 9805793.8  
PT DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
C12N1/15,  
PC  
C12N1/19, C12N1/21, C12N5/10, C12Q1/02, G01N33/15, G01N33/50, G01N33/ PC  
68, C12N15/00, C12N5/00  
CC Mammalian sodium channel protein  
FH Key Location/Qualifiers  
FT source 1. .409

FT /organism="Homo sapiens (human)".  
Location/Qualifiers  
1. .409  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 409; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1,9e-83;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCACCCAGGCGCCGACATGCATCTCCAGAGCTGCGAAAAGTGAAGAC 60  
DB 1 ATCCACCCAGGCGCCGACATGCATCTCCAGAGCTGCGAAAAGTGAAGAC 60  
QY 61 AGGCTCCCAACAGGGGCTATGGCTGTAGGAAGAGCTATGATCAATGTTGCTCTAA 120  
DB 61 AGGCTCCCAACAGGGGCTATGGCTGTAGGAAGAGCTATGATCAATGTTGCTCTAA 120  
QY 121 GAAACACCTTGCTCTTCTAGATGAAGTGAATGCTTATATTTTCTCCAGTAATTG 180  
DB 121 GAAACACCTTGCTCTTCTAGATGAAGTGAATGCTTATATTTTCTCCAGTAATTG 180  
QY 181 TTTTCTCTTATTAATAAAATTTCTAACAGAAAGAACAGCAGAGTTGAGAGCA 240  
DB 181 TTTTCTCTTATTAATAAAATTTCTAACAGAAAGAACAGCAGAGTTGAGAGCA 240  
QY 241 ATTCACCTGGTTACATTTCTGTAAGTCTTATCAATCTTGGCTCATCTCTGAA 300  
DB 241 ATTCACCTGGTTACATTTCTGTAAGTCTTATCAATCTTGGCTCATCTCTGAA 300  
QY 301 TCTCTTCATTTGGCGTTATATGACAACTTCAACAGCAGAAAAGATAGTATCTG 360  
DB 301 TCTCTTCATTTGGCGTTATATGACAACTTCAACAGCAGAAAAGATAGTATCTG 360  
QY 361 GGTGTCCTGATTTGGTAAATGTAATCTCTGCTCTCCAAAGAGGATCC 409  
DB 361 GGTGTCCTGATTTGGTAAATGTAATCTCTGCTCTCCAAAGAGGATCC 409

RESULT 3  
AC116038 167476 bp DNA linear PRI 07-OCT-2003  
LOCUS Homo sapiens chromosome 3 clone RP11-13J21, complete sequence.  
DEFINITION AC116038  
ACCESSION AC116038.3 GI:37537604  
VERSION HTG.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Unpublished  
2 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 167476)  
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
4 (bases 1 to 167476)  
REFERENCE Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and

TITLE  
JOURNAL

## COMMENT

Haugen, E. D.  
 Direct Submission  
 Submitted (07-Oct-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 On Oct 7, 2003 this sequence version replaced gi:21622736.

## Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu

Project Information

Center project name: chr-3

Center clone name: RP11-134J21 (bc0780)

## Summary Statistics

Sequencing vector: plasmid; 100% of reads  
 Chemistry: Dye-terminator ET; 45% of reads  
 Chemistry: Dye-terminator Big Dye; 55% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 167467 bases at least Q40  
 Consensus quality: 167476 bases at least Q30  
 Consensus quality: 167476 bases at least Q20  
 Insert size: 167476; sum-of-contigs  
 Quality coverage: 18.9x in Q20 bases; sum-of-contigs

## Overlapping Sequences:

5: RP11-114A3 AC137625, 2001-bp overlap  
 3: RP11-182A24 (UWGC:bc0782) AC123903, 41341-bp overlap

## Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
 all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.  
 The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI

HindIII

BglIII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8629	2732	2741	2234	2259
6	<800	6382	6514	2067	2008
2248	2299	512	<800	5097	5007
9345	9792	449	<800	2317	2259
2016	2003	2707	2741	2813	2744
4889	4771	4809	4878	2537	2550

3455	3447	184	<800	1923	2008
245	<800	5818	5899	2486	2550
72	<800	1364	1346	4036	3992
4175	4167	999	990	2583	2550
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3468	3447	179	<800	2649	2744
687	<800	7123	7158	2550	2550
3049	3091	2078	2040	5020	4862
762	<800	1891	1888	6949	6960
553	<800	8072	8171	4636	4629
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8963	9211	5478	5397	5748	6106
331	<800	240	<800	953	943
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1368	1370	86	<800	694	<800
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775	<800	438	<800	1294	1220
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2709	2686	5528	5397	3725	3544
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7181	7213	166	<800	2486	2550
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500	<800	1172	1188	4240	4223
8764	8629	316	<800	879	917
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Query Match	89.2%; Best Local Similarity	Score 364.8; 97.8%;	DB 9; Pred. No. 1.5e-73;	Length 167476; Matches 391; Conservative	DB 9; Mis-matches 7;	Indels 2;	Gaps 2;
QY 1	ATCCACCCCAAGGCCCCGACATGCACTCCCAAGCTGAGCTGCGAATACTGAAAGAC	60					
Db 101567	ATTCACCCCAAGGCCCCGACATGCACTCCCAAGCTGAGCTGCGAATACTGAAAGAC	101509					
QY 61	AGGCTCCCAACAGGGCTATGAGTGTGAAAGAGCTATGATGCAATGTTGCTGCTAA	120					
Db 101508	AGGCTCCCAACAGGGCTATGAGTGTGAAAGAGCTATGATGCAATGTTGCTGCTAA	101449					
QY 121	GAACACCTTGCTCTTCTAGAAAGAGTGAATGCTTATATTTTCTCCAGTATTTG	180					
Db 101448	GAACACCTTGCTCTTCTAGAAAGAGTGAATGCTTATATTTTCTCCAGTATTTG	101389					
QY 181	TTTTTTCTCTTATTTAAAAAATTTCTAACAGAAAGAACCAAGCCAGAGTTGAGAGCA	240					
Db 101388	TTTTTTCTCTTATTTAAAAAATTTCTAACAGAAAGAACCAAGCCAGAGTTGAGAGCA	101329					
QY 241	ATTCACTCGGTTACATTT-CTTGTGATGCTTTATATCTTTGGCTCATTTCTTCACTTGA	239					
Db 101328	ATTCACTCGGTTACATTTCTTGTGATGCTTTATATCTTTGGCTCATTTCTTCACTTGA	101268					
QY 300	ATCTCTTCATTTGGCGTTATCATTTGACCAATTCACCAACAGAGAAAAAGATAGTATCT	359					
Db 101268	ATCTCTTCATTTGGCGTTATCATTTGACCAATTCACCAACAGAGAAAAAGATAGTATCT	101208					
QY 360	GAGGTGCTTGATTTGGTATATTTGATCTCTGCTCCCAA 399						
Db 101208	GAGGTGCTTGATTTGGTATATTTGATCTCTGCTCCCAA 101169						
RESULT 4							
AC124662	241289 bp	DNA	linear	HTG 22-NOV-2003			
LOCUS	Mus musculus chromosome 9 clone RP24-409K22 map 9, *** SEQUENCING						
DEFINITION	IN PROGRESS ***, 11 unordered pieces.						
ACCESSION	AC124662						
VERSION	AC124662.5	GI:38490569					
KEYWORDS	HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
AUTHORS	1 (bases 1 to 241289)						
TITLE	Birken, B., Nusbaum, C. and Landry, E.						
	Mus musculus chromosome 9, clone RP24-409K22						

**JOURNAL**  
**REFERENCE**  
**AUTHORS**  
 2 (bases 1 to 241289)  
 Birtzen,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,  
 Bouhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
 Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,  
 Cook,A., Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., Fitzgerald,M., Fitzhugh,W., Gage,D.,  
 Galegan,J., Gargyua,S., Ginde,S., Gird,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,  
 Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,  
 Lamaras,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,J., Margulis,N.,  
 Matthews,C., McCarthy,M., McSwan,P., McKernan,K., Meldrum,J.,  
 Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Nicou,R., Norby,C., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Plunkhang,P., Pierre,N.,  
 Pollara,V., Raymond,C., Retta,R., Riaback,M., Riley,R., Rise,C.,  
 Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,  
 Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,  
 Stojanovic,N., Strauss,N., Sudirmanian,A., Talama,J., Testaye,S.,  
 Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,D.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.,J.,  
 Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 241289)  
 Birtzen,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
 Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boguslavsky,L., Bouhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Cornut,B., Deatellano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galegan,J., Gargyua,S.,  
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karatas,A., Kells,C., Lander,E., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrum,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norby,C., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Plunkhang,P., Pierre,N.,  
 Ruchpaka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talama,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (22-NOV-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 22, 2003 this sequence version replaced gi:38153914.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/JM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L26677  
 Center clone name: 409\_K\_22  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 1 56842: contig of 56842 bp in length

56843 56942: gap of 100 bp  
56943 56966: contig of 39024 bp in length  
56967 56967: gap of 100 bp  
56967 133016: contig of 36950 bp in length  
56967 133017: gap of 100 bp  
56967 133116: contig of 5672 bp in length  
56967 138789: gap of 100 bp  
56967 138888: gap of 100 bp  
56967 157002: contig of 18114 bp in length  
56967 157003: gap of 100 bp  
56967 157103: contig of 5593 bp in length  
56967 162695: gap of 100 bp  
56967 162696: contig of 2471 bp in length  
56967 165366: gap of 100 bp  
56967 165367: gap of 100 bp  
56967 187706: contig of 22340 bp in length  
56967 187707: gap of 100 bp  
56967 187807: contig of 22221 bp in length  
56967 210027: contig of 100 bp  
56967 210127: gap of 100 bp  
56967 210128: contig of 14144 bp in length  
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/clone\_11b="RPC1-24 Male Mouse BAC"

Query Match 35.1%; Score 143.4; DB 2; Length 241289;  
Best Local Similarity 70.2%; Pred. No. 8.6e-23;  
Matches 221; Conservative 0; Mismatches 91; Indels 3; Gaps 2;

89 GGAAGAGGCTTNGTAGTCAATGCTGCTAAGAAACCTTGGCTCTGATAGTA 148  
220169 GCAGATCTATGCTTAACTCTGCGGAAATCCACTGCTGCTTGAATGAGCA 220228  
149 GTTAGAATGCTTAAATTTTCTCCAGTAATGTT--TTTCTCTTATTAATAAATTC 206  
220229 GCTAGGGAGCTTATCTTTTCCCTTCAGTAATGTTTCTCTCATTAATAACATCC 220288  
207 TAAACAGAAAGCAACAGCAGAGTTTGAAGCAATTCACCTCGTTACATTT-CTTGT 265  
220289 CAACAGAAAGATGAGCAGCCGCTTGAAGCAATTCATACCTTACTTCTGTG 220348  
266 GTCTTATCATCTTGGCTCATCTTCTCACTGAAATCTCTTATTTGGGTTATCATTTGAC 325  
220349 GTTTTATCATCTTGGCTCATCTTCTCACTGAAATCTTATTCGATTAATTTGAC 220408  
326 AACTTCAACCAACAGCAAGAAAGTAAGTATCTGGTGTCTTGAATTTGGTAATTGAT 385  
220409 AACTTCAATCAGCAGCAAGAAAGTAAGTATGCACTGGCTGCTGCTGCTCTCAC 220468  
386 CTCTGTCTCTCAAG 400  
220469 CGGGGTGAGCAATG 220483

RESULT 5  
E36123 856 bp DNA linear PAT 18-JUN-2001  
LOCUS Nucleic acid encoding sodium channel of nerve tissue.  
DEFINITION E36123  
ACCESSION E36123  
VERSION E36123.1 GI:13022506  
KEYWORDS JP 199235186-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 856)  
Paul,S.D., Linda,M.P., Rina,K., Douglas,K.R. and Lakemi,S.

32.9%; Score 134.4; DB 6; Length 856;  
Best Local Similarity 90.1%; Pred. No. 1.6e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

202 ATTCTTCAAGAAAGCAACAGCAGAGTTTGAAGCAATTCACCTGGTTACATTT-CT 260  
603 ATTCCACAGAAAGCAACAGCAGAGTTTGAAGCAATTCACCTGGTTACATTTACT 662  
261 TCGTAGCTTATCATCTTTGGCTCATCTTCACTGAAATCTTCAATTTGGCGTTATCA 320  
663 TCGTAGCTTATCATCTTTGGCTCATCTTCACTGAAATCTTCAATTTGGCGTTATCA 722  
321 TTGACAATTCACCAACAGCAAGAAAGTAAGTATCTGGTGTCTTGT 372  
723 TTGACAATTCACCAACAGCAAGAAAGTAAGTATCTGGTGTCTTGT 774

RESULT 6  
AR340648 3701 bp DNA linear PAT 17-AUG-2003  
LOCUS Sequence 6 from patent US 6573067.  
DEFINITION AR340648  
ACCESSION AR340648  
VERSION AR340648.1 GI:33732380  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3701)  
AUTHORS Dib-Hajj,S. and Waxman,S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 6 03-JUN-2003;  
FEATURES  
1. 3701  
Location/Qualifiers  
1. 856  
/organism="Homo sapiens"  
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Query Match 32.9%; Score 134.4; DB 6; Length 3701;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

202 ATTCTTCAAGAAAGCAACAGCAGAGTTTGAAGCAATTCACCTGGTTACATTT-CT 260  
3206 ATTCCACAGAAAGCAACAGCAGAGTTTGAAGCAATTCACCTGGTTACATTTACT 3265

Oy 261 TCGTAGCTTTATCATCTTTGGCTATCTTCACTCTGAATCTTCAATGGCGTTATCA 320  
Db 326 TCGTAGCTTTATCATCTTTGGCTATCTTCACTCTGAATCTTCAATGGCGTTATCA 3325  
Oy 321 TTGACAACTTCAACCAAGCAAGAAAAGATTAATGATCTGGTGTCTTGAT 372  
Db 3326 TTGACAACTTCAACCAAGCAAGAAAAGTATGAGTGGCAAGACATTTTAT 3377

RESULT 7  
BD217793 3701 bp DNA linear PAT 17-JUL-2003  
LOCUS Regulation of sodium channel in posterior root ganglion.  
DEFINITION BD217793  
ACCESSION BD217793.1 GI:33027563  
KEYWORDS JP 2002509860-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Hajj, S.D. and Waxman, S.  
TITLE Regulation of sodium channel in posterior root ganglion  
JOURNAL Patent: JP 2002509860-A 3 02-APR-2002;  
YALE UNIVERSITY  
OS Homo sapiens (human)  
PN JP 2002509860-A/3  
PD 02-APR-2002  
PF 23-JAN-1999 JP 2000529355  
PR 29-JAN-1998 US 60/072990, 20-NOV-1998 US 60/109402 PI  
SULAVMAN DIB HAJJ, STEPHEN WAXMAN  
PC C07K14/435, A61K38/00, A61K39/395, A61K45/00, A61P25/04, A61P43/00,  
PC C07K16/18, A61K38/00, A61K39/395, A61K45/00, A61P25/04, A61P43/00,  
PC C12N5/10, C12N15/09, C12P21/02, G01N33/566, G01N33/84, A61K37/02,  
PC C12N5/00,  
PC C12N15/00  
CC partial human NaN cDNA sequence  
CC Y = c or t  
PH key Location/Qualifiers  
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ORIGIN  
Query Match 32.9%; Score 134.4; DB 6; Length 3701;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
Oy 202 ATTTCTACAGAAAGCAAGCCAGAGTTTGAGAGCAATTCCTGGTTACATT-CT 260  
Db 3206 ATTCACAGAAAGCAAGCCAGAGTTTGAGAGCAATTCCTGGTTACATTACT 3265  
Oy 261 TCGTAGCTTTATCATCTTTGGCTATCTTCACTCTGAATCTTCAATGGCGTTATCA 320  
Db 3266 TCGTAGCTTTATCATCTTTGGCTATCTTCACTCTGAATCTTCAATGGCGTTATCA 3325  
Oy 321 TTGACAACTTCAACCAAGCAAGAAAAGATTAATGATCTGGTGTCTTGAT 372  
Db 3326 TTGACAACTTCAACCAAGCAAGAAAAGTATGAGTGGCAAGACATTTTAT 3377

RESULT 8  
HSA417790 5419 bp mRNA linear PRI 09-OCT-2002  
LOCUS Homo sapiens mRNA for voltage-gated sodium channel (NAV1.9 gene).  
DEFINITION HSA417790  
ACCESSION AJ417790.1 GI:22796539  
KEYWORDS NAV1.9 gene; voltage-gated sodium channel.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Blum, R., Kailitz, K.W. and Komerth, A.  
TITLE Neurotrophin-evoked depolarization requires the sodium channel  
Na(V)1.9  
JOURNAL Nature 419 (6908), 687-693 (2002)  
MEDLINE 22272672  
PUBMED 12384589  
REFERENCE  
AUTHORS Blum, R.  
TITLE Direct Submission  
JOURNAL Submitted (25-OCT-2001) Blum R., Institut fuer Neurologie,  
Ludwig-Maximilians-Universitaet, Biedersteiner Strasse 29, Geb.  
608, 80802 Muenchen, GERMANY

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Location/Qualifiers  
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ORIGIN  
Query Match 32.9%; Score 134.4; DB 9; Length 5419;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;

Matches	155;	Conservative	0;	Mismatches	16;	Indels	1;	Gaps	1;
QY	202	ATTCTTAACAGAAAGAACAAACAGCCAGAGTTTGAGAGCAATTCACGCTTACATTT-CT	260						
Db	3803	ATTCCACAGAGAAAGAAACAAACAGCCAGAGTTTGAGAGCAATTCACGCTTACATTTACT	3862						
QY	261	TGTAAGCTTTATCATCTTTGGCTCATCTTCACCTGATCTCTTCATTGAGCGGTATCA	320						
Db	3863	TGTAAGCTTTATCATCTTTGGCTCATCTTCACCTGATCTCTTCATTGAGCGGTATCA	3922						
QY	321	TTGACAACTTCAACCCACAGCAGAAAAAGATAGTATCTGGGTTGTCCTTGAT	372						
Db	3923	TTGACAACTTCAACCCACAGCAGAAAAAGTATGATGGTCCAGACATTTTAT	3974						
RESULT 9									
LOCUS	BD012083								
DEFINITION	Human sodium channel SCN12A and SCN8A.								
ACCESSION	BD012083.1	GI:22092272							
VERSION	WO 0190355-A/2.								
KEYWORDS	WO 0190355-A/2.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	1 (bases 1 to 5728)								
JOURNAL	Kanazawa, I., Goto, J. and Jeong, S. Y. Human sodium channel SCN12A and SCN8A Patent: WO 0190355-A 2 29-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON YONG JEONG								
COMMENT	OS Homo sapiens (human)								
	PN WO 0190355-A/2								
	PD 29-NOV-2001								
	PP 11-JUL-2000 WO 2000JP004629								
	PR 23-MAY-2000 JP 00P 152085								
	PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG								
	PC C12N15/12, C07K14/47, C07K16/18								
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ORIGIN									
Query Match	32.9%; Score 134.4; DB 6; Length 5728;								
Best Local Similarity	90.1%; Pred. No. 1.4e-20;								
Matches	155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;								
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Db	4002	ATTCCACAGAGAAAGAAACAAACAGCCAGAGTTTGAGAGCAATTCACGCTTACATTTACT	4061						
QY	261	TGTAAGCTTTATCATCTTTGGCTCATCTTCACCTGATCTCTTCATTGAGCGGTATCA	320						
Db	4062	TGTAAGCTTTATCATCTTTGGCTCATCTTCACCTGATCTCTTCATTGAGCGGTATCA	4122						
QY	321	TTGACAACTTCAACCCACAGCAGAAAAAGATAGTATCTGGGTTGTCCTTGAT	372						
Db	4122	TTGACAACTTCAACCCACAGCAGAAAAAGTATGATGGTCCAGACATTTTAT	4173						
RESULT 10									
LOCUS	BD082952								
DEFINITION	Human sodium channel SCN12A.								
ACCESSION	BD082952								
VERSION	BD082952.1	GI:22628562							
KEYWORDS	JP 200137294-A/2.								

SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 5728) Kanazawa,I., Goto,J., and Tel,Y. Human sodium channel SCN1A Patent: JP 2001327294-A 2-27-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP
AUTHORS	JOURNAL
TITLE	COMMENT
ORIGIN	OS Homo sapiens (human) PN JP 2001327294-A/2 PD 27-NOV-2001 PF 23-MAY-2000 JP 2000152085 PI ICHIRO KANAZAWA,JUN GOTO,YOSHIIRO TEL PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
FEATURES	FT CDS Location/Qualifiers 1..5728 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
source	Query Match 32.9%; Score 134.4; DB 6; Length 5728; Best Local Similarity 90.1%; Pred. No. 1,4e-20; Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
Oy	202 ATTTCTCAAGAAAGAACAACAGCCAGGATTGGAGCAATTCAGTCACTCGGTACTT-CT 260 Db 4002 ATTCCACAGGAAGAAACAACAGCCAGGATTGGAGCAATTCAGTCACTCGGTACTTACT 4051
Oy	261 TCGTAGTCTTATCATCTTGCGCTCATCTCTCACTGAAATCTCTTCATGGCGGTATCA 320 Db 4062 TCGTAGTCTTATCATCTTGCGCTCATCTCTCACTGAAATCTCTTCATGGCGGTATCA 4121
Oy	321 TTGCAACTTCACCAACAGCAAGAAAAGATAGTATCTGGGTGCTTCAAT 372 Db 4122 TTGCAACTTCACCAACAGCAAGAAAAGTATGGTGCCAACATTTTAT 4173
RESULT 11	
AF150882	
LOCUS	5728 bp mRNA linear PRI 15-JAN-2000
DEFINITION	Homo sapiens voltage-gated sodium channel alpha subunit, alternate splice variant SCN12A-s (SCN12A) mRNA, complete cds.
ACCESSION	AF150882
VERSION	AF150882.1 GI:6693704
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 5728) Jeong,S.Y., Goto,J., Hashida,H., Suzuki,T., Ogata,K., Masuda,N., Hirai,M., Ieshara,K., Uchiyama,Y., and Kanazawa,I. Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A
TITLE	Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
JOURNAL	MEDLINE
PUBMED	20090626
REFERENCE	10623608 2 (bases 1 to 5728)
AUTHORS	Jeong,S.-Y., Suzuki,T., Hashida,H., Ogata,K., Masuda,M., Goto,J. and Kanazawa,I.
TITLE	Direct Submission
JOURNAL	Submitted (12-MAY-1999) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bukeyo-Ku, Tokyo 113-8655, Japan
FEATURES	Location/Qualifiers 1..5728 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"
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ORIGIN

Query Match 32.9%; Score 134.4; DB 9; Length 5728;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTTCTACGAAAGAAACAGCCAGGTTTGAGAGCAATTCATCGGTTACATTT-CT 260  
DB 4002 ATTCACAGAGAAAGAAACAGCCAGGTTTGAGAGCAATTCATCGGTTACATTTACT 4061  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTCTTCAATGGCGTTATCA 320  
DB 4062 TCGTAGCTTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTCTTCAATGGCGTTATCA 4121  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAGATAGTATCTGGGTTGTCTTGAT 372  
DB 4122 TTGACAACTTCAACCAACAGCAAGAAAAGTTAGTGCGCAACATTTTAT 4173

RESULT 12  
AR340678 5860 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340678  
DEFINITION Sequence 41 from patent US 6573067.  
ACCESSION AR340678  
VERSION AR340678.1 GI:33732410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5860)  
AUTHORS Dib-Hajj, S. and Waxman, S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 41 03-JUN-2003;  
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ORIGIN /mol\_type="genomic DNA"

Query Match 32.9%; Score 134.4; DB 6; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTTCTACGAAAGAAACAGCCAGGTTTGAGAGCAATTCATCGGTTACATTT-CT 260  
DB 3833 ATTCACAGAGAAAGAAACAGCCAGGTTTGAGAGCAATTCATCGGTTACATTTACT 3892  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTCTTCAATGGCGTTATCA 320  
DB 3893 TCGTAGCTTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTCTTCAATGGCGTTATCA 3952  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAGATAGTATCTGGGTTGTCTTGAT 372  
DB 3953 TTGACAACTTCAACCAACAGCAAGAAAAGTTAGTGCGCAACATTTTAT 4004

RESULT 13  
AF188679 6237 bp mRNA linear PRI 14-DEC-1999  
LOCUS AF188679  
DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit  
(SCN11A) mRNA, complete cds.  
VERSION AF188679  
KEYWORDS AF188679.1 GI:6572949  
SOURCE  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 6237)  
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A., Wood, P.M. and  
Waxman, S.G.  
TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root  
ganglion neurons  
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)  
MEDLINE 20047838  
PUBMED 10580103  
REFERENCE 2 (bases 1 to 6237)  
AUTHORS Dib-Hajj, S.D., Tyrell, L., Cummins, T.R., Black, J.A. and Waxman, S.G.  
TITLE Direct Submission  
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,  
Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA  
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IAECVFTGITYIFBALIKILARGFLIDERSFLRDMNMIDSIVIGAIYSYIPGTTIKL  
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NLTLAVVTMAVEQNKVVAIEBAEKMGFGAQQLLKEKRALVAMGIDRSLSLSLET



SYTPRRKRLGKRRKSPFLRESKDPGSDSDPDCOKKPOLLEOTRRLSNTLSD  
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SMPLNTLKIIGNSVAGSLVAVLVIIFESVGMQFGRSFGSKPCKNPG  
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KAVYLN.FIALLINSFSEERNGULREBARKYOLALDPRAPCFVRHLEHCHK  
WCKRNL.PQCKEYAGGCAOSKDIIPVMEKRSSETOEBGILITSIPKTLGRHMT  
WLVKLEBDDVEFSGBDNRITIQPEEQAYLHQENKPKTSQVOSVEIDMFSD  
EPHLITODPRKSDVTSILSECSITIDQDGMVLEPVKPKQPERCLPKGFCFPC  
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LNLCTDIIIFTHIFLEMLKMWALFGVFGFSAACDFIIVSVTTLINLMLEKSE  
RTLRALRPLALSGEGRKVVNALGAILALLINVLICIFLMPCLLIVYFESGFE  
GKCLNGDSVINTITITTKSOCSBGSNPMINOKNPNVGNAYIALAQVATKCMNDI  
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QDIEMTEBOKKYVAMKKGSKPKQKPIPRELNCOQIVPDIVSQ.FDI.IIISLIL  
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TEBESDPLGSDDFDIIFYEWKFPDEATQIFKYSALSDPDALEPLRLVAKPNKYQL  
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ORIGIN  
Query Match 32.9%; Score 134.4; DB 9; Length 6237;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATT-CT 260  
DB 383 ATTCCAGAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATTACT 3892  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 320  
DB 3893 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 3952  
QY 321 TTGCAACTTCAACCAAGCAAGAAAGATAGATCTGGGTGCTTGAT 372  
DB 3953 TTGCAACTTCAACCAAGCAAGAAAGATAGATCTGGGTGCTTGAT 4004

RESULT 14  
LOCUS BD012082 6528 bp DNA linear PAT 02-AUG-2002  
DEFINITION Human sodium channel SCN12A and SCN8A.  
ACCESSION BD012082  
VERSION BD012082.1 GI:22092271  
KEYWORDS WO 0190355-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 6528)  
REFERENCE Kanazawa, I., Goto, J. and Jeong, S. Y.  
Human sodium channel SCN12A and SCN8A  
Patent: WO 0190355-A 1 29-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON  
YONG JEONG  
OS Homo sapiens (human)  
PN WO 0190355-A/1  
PD 29-NOV-2001  
PF 11-JUL-2000 WO 2000JP004629  
PR 23-MAY-2000 JP 00P 152085

PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
PC C12N15/12, C07K14/47, C07K16/18  
CC  
FH Key Location/Qualifiers  
FT CDS (200)..(5575).  
source 1..6528  
Location/Qualifiers  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 32.9%; Score 134.4; DB 6; Length 6528;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATT-CT 260  
DB 4002 ATTCCAGAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATTACT 4061  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 320  
DB 4062 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 4121  
QY 321 TTGCAACTTCAACCAAGCAAGAAAGATAGATCTGGGTGCTTGAT 372  
DB 4122 TTGCAACTTCAACCAAGCAAGAAAGATAGATCTGGGTGCTTGAT 4173

## RESULT 15

LOCUS BD082951 6528 bp DNA linear PAT 27-AUG-2002  
DEFINITION Human sodium channel SCN12A.  
ACCESSION BD082951  
VERSION BD082951.1 GI:22628561  
KEYWORDS JP 2001327294-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 6528)  
REFERENCE Kanazawa, I., Goto, J. and Tel, Y.  
Human sodium channel SCN12A  
Patent: JP 2001327294-A 1 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
OS Homo sapiens (human)  
PN JP 2001327294-A/1  
PD 27-NOV-2001  
PF 23-MAY-2000 JP 2000152085  
PI ICHIRO KANAZAWA, JUN GOTO, YOSHIOHRO TEI  
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
CC  
FH Key Location/Qualifiers  
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## ORIGIN

Query Match 32.9%; Score 134.4; DB 6; Length 6528;  
Best Local Similarity 90.1%; Pred. No. 1.4e-20;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATT-CT 260  
DB 4002 ATTCCAGAGAAAGAACAGCAGGAGTTGAGAGCAATTCCTCGGTACATTACT 4061  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 320  
DB 4062 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGGAATCTTCACTTGGCGTTATCA 4121

Wed Mar 24 11:10:39 2004

us-09-646-224a-15.rge

Page 10

[illegible]

Search completed: March 22, 2004, 19:32:44  
Job time : 2179.44 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:33:04 ; Search time 296.047 Seconds  
(without alignments)  
5869.049 Million cell updates/sec

Title: US-09-646-224A-15

Perfect score: 409  
Sequence: 1 atccaccagcgcgcgcga.....gtccccaagaagaatcc 409

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseq19808:\*  
2: geneseq19908:\*  
3: geneseq20008:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq20028:\*  
7: geneseq2003as:\*  
8: geneseq2003bs:\*  
9: geneseq2003cs:\*  
10: geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	100.0	409	AAZ21493	AAZ21493 Human sen
2	134.4	32.9	856	AAZ60242	AAZ60242 CDNA enco
3	134.4	32.9	3638	AAZ87602	AAZ87602 Human sod
4	134.4	32.9	3701	AAZ30104	AAZ30104 Human sod
5	134.4	32.9	5728	AAZ42750	AAZ42750 Human sod
6	134.4	32.9	5860	AAZ30101	AAZ30101 Human sod
7	134.4	32.9	5860	AAZ32193	AAZ32193 Human Na
8	134.4	32.9	5828	AAZ42749	AAZ42749 Human sod
9	88	21.5	5822	AAZ87601	AAZ87601 Mouse sod
10	88	21.5	5822	AAZ30103	AAZ30103 Mouse sod
11	88	21.5	5822	AAZ32195	AAZ32195 Mouse Na
12	85.2	20.8	637	AAZ5851	AAZ5851 Human SCN
13	83.2	20.3	5334	AAZ60244	AAZ60244 Stabillise
14	81.6	20.0	5298	AAZ32209	AAZ32209 Rat Na v
15	81.6	20.0	5875	AAZ87600	AAZ87600 Rat sodiu
16	81.6	20.0	5875	AAZ30102	AAZ30102 Rat sodiu
17	81.6	20.0	5897	AAZ21480	AAZ21480 Rat senso
18	81.6	20.0	5905	AAZ52929	AAZ52929 Primary r
19	81.6	20.0	5905	AAZ32191	AAZ32191 Rat Na v
20	81.6	20.0	5908	AAZ60241	AAZ60241 CDNA enco
21	78.4	19.2	6021	AAZ42420	AAZ42420 Rat volta
22	78.4	19.2	7555	AAZ81328	AAZ81328 Cardiac s
23	77.2	18.9	5977	AAZ58420	AAZ58420 Tetradoto

24	77.2	18.9	6007	AAZ58421	AAZ58421 Tetradoto
25	77.2	18.9	6556	AAZ58419	AAZ58419 PM4 sodiu
26	77.2	18.9	6586	AAZ58423	AAZ58423 PM4 sodiu
27	77.2	18.9	6586	AAZ42021	AAZ42021 Toxicity
28	76.4	18.7	6048	AAZ09029	AAZ09029 Human hhl
29	76.4	18.7	6048	AAZ0825	AAZ0825 Human SCN
30	76.4	18.7	8490	AAZ35506	AAZ35506 Human gen
31	76.4	18.7	8509	AAZ64433	AAZ64433 Human dit
32	74.4	18.2	366	AAZ5819	AAZ5819 Human SCN
33	74.2	18.1	6957	AAZ852723	AAZ852723 Primary r
34	74	18.1	7008	AAZ87645	AAZ87645 Human ion
35	74	18.1	7008	AAZ87639	AAZ87639 Human ion
36	74	18.1	7053	AAZ93791	AAZ93791 Human CDN
37	74	18.1	7053	AAZ42751	AAZ42751 Human sod
38	73.6	18.0	7555	AAZ05831	AAZ05831 Cardiac s
39	72.8	17.8	8553	AAZ14821	AAZ14821 Toxicity
40	72.4	17.7	188	AAZ87657	AAZ87657 Human ion
41	71.2	17.4	6596	AAZ87646	AAZ87646 Human ion
42	71.2	17.4	6599	AAZ87650	AAZ87650 Human ion
43	71.2	17.4	6599	AAZ87648	AAZ87648 Human ion
44	71.2	17.4	6599	AAZ87647	AAZ87647 Human ion
45	71.2	17.4	9112	AAZ58823	AAZ58823 Human adu

## ALIGNMENTS

RESULT 1  
ID AAZ21493 standard; CDNA; 409 BP.  
AAZ21493

AAZ21493;

03-DEC-1999 (first entry)

Human sensory neuron specific 2a nucleotide sequence fragment #13.

Sensory neuron specific 2a; SNS-2a; sodium channel protein; pain;

voltage gated; hypersensitivity; ss.

XX Homo sapiens.

XX OS

XX PN WO9947670-A1.

XX PD 23-SEP-1999.

XX PF 18-MAR-1999; 99WO-GS000838.

XX PR 18-MAR-1998; 98GB-00005793.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Grose DT, Hick CA, Tate SN;

XX DR WPI; 1999-562112/47.

XX PT Mammalian sodium channel protein for treating pain and hypersensitivity.

XX PS Claim 6; Page 67; 73pp; English.

XX CC AAZ21481 to AAZ21495 represent fragments of the human sensory neuron

CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel

CC protein. SNS-2a can be used in a method for the identification of a

CC modulator of a sodium channel, and for assaying for compounds which

CC modulate sodium flux. The sodium channel modulators can be used in a

CC medicament for the treatment of pain or hypersensitivity

XX Sequence 409 BP; 117 A; 90 C; 76 G; 126 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 409; DB 2; Length 409;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-97; Mismatches 0; Gaps 0;

OY 1 ATCCACCCAGGCCCCGCGACATGCCATCACTCAAGGCTGAGCTCGAAAAGTGAAGAC 60  
 DB 1 ATCCACCCAGGCCCCGCGACATGCCATCACTCAAGGCTGAGCTCGAAAAGTGAAGAC 60  
 OY 61 AGGCTCCCAACAGGGGCTATGAGTGTGAGAAAGGCTATGATCAATGTTGCTGCTAA 120  
 DB 61 AGGCTCCCAACAGGGGCTATGAGTGTGAGAAAGGCTATGATCAATGTTGCTGCTAA 120  
 OY 121 GAAACACTTGGTCTTTAGATGAAGTGTGATGATGATGATGATGATGATGATGATG 180  
 DB 121 GAAACACTTGGTCTTTAGATGAAGTGTGATGATGATGATGATGATGATGATGATG 180  
 OY 181 TTTTCTCTCTATTAATAAATAATTTCTAAGAAAGAAACACAGCAGAGTTTGAGACA 240  
 DB 181 TTTTCTCTCTATTAATAAATAATTTCTAAGAAAGAAACACAGCAGAGTTTGAGACA 240  
 OY 241 ATTCACTGGGTACATTTCTGAGTCTTTATCATCTTTGCTCATTTCTCTGAA 300  
 DB 241 ATTCACTGGGTACATTTCTGAGTCTTTATCATCTTTGCTCATTTCTCTGAA 300  
 OY 301 TCTCTTCATGGCGTTATCATTCAGACACTTCAACCAACAGCAAGAAAGATAGTATCTG 360  
 DB 301 TCTCTTCATGGCGTTATCATTCAGACACTTCAACCAACAGCAAGAAAGATAGTATCTG 360  
 OY 361 GGTTGCTTGAATTTGTAATGTATCTCTGCTCCCAAGAAAGAAATCC 409  
 DB 361 GGTTGCTTGAATTTGTAATGTATCTCTCTCCCAAGAAAGAAATCC 409

RESULT 2  
 AAX60242  
 ID AAX60242 standard; cDNA; 856 BP.

AC AAX60242;  
 DT 11-AUG-1999 (first entry)

DE cDNA encoding type 5 sodium channel protein designated PNS.

XX Type 5 sodium channel; PNS; nervous system; plexiform;  
 XX dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
 XX diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
 XX neuropathic pain; migraine; headache; ss.

OS Homo sapiens.

PN FR2771103-A1.

PD 21-MAY-1999.

PF 19-NOV-1998; 98FR-00014551.

PR 20-NOV-1997; 97US-0066225P.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;

DR WPI; 1999-315739/27.

DR P-PSDB; AAY16577.

PT Isolated DNA encoding sodium channel of the nervous system.

PS Claim 1; Fig 3A; 90bp; French.

XX The present sequence encodes a type 5 sodium channel protein designated  
 CC PNS. The protein is a sodium ion channel of the nervous system, and is  
 CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
 CC used to identify inhibitors of sodium channel proteins that are resistant  
 CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
 CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
 CC neuropathy, and especially neuropathic pain, e.g. migraine and headache

SQL Sequence 856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;

Query Match 32.9%; Score 134.4; DB 2; Length 856;  
 Best Local Similarity 90.1%; Pred. No. 2.9e-25;  
 Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

OY 202 ATTTCTAACGAAAGAAACACAGCAGAGTTTGAGAGCAATTCATCTGGTTACATTT-CT 260

DB 603 ATTCACAGGAAAGAAACACAGCAGAGTTTGAGAGCAATTCATCTGGTTACATTTACT 662

OY 261 TCGTAGTCTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTTCAATTTGGCTATCA 320

DB 663 TCGTAGTCTTATCATCTTTGGCTCATTTCTTCACTCTGAAATCTTCAATTTGGCTATCA 722

OY 321 TTGCACTTCAACCAACAGCAGAAAGATAGATCTGGGTTGCTGAT 372

DB 723 TTGCACTTCAACCAACAGCAGAAAGATAGATCTGGGTTGCTGAT 774

RESULT 3

AAX87602  
 ID AAX87602 standard; cDNA; 3638 BP.

AC AAX87602;  
 DT 26-OCT-1999 (first entry)

DE Human sodium channel NaV partial cDNA.

XX NaV; sodium channel; ion transport; human; dorsal root ganglia; pain;  
 XX paraesthesia; hyperexcitability; therapy; SCN1A gene; ss.

OS Homo sapiens.

PN WO938889-A2.

PD 05-AUG-1999.

PF 29-JAN-1999; 99WO-US002008.

PR 29-JAN-1998; 98US-0072990P.

PR 20-NOV-1998; 98US-0109402P.

PA (UYVA) UNIV YALE.

PI Dib-Hajj S, Waxman S;

DR WPI; 1999-479168/40.

DR P-PSDB; AAY06598.

PT New isolated nucleic acids encoding sodium channels, used to develop

PT products for treating acute or chronic pain or hyperexcitability

PT phenomena.

PS Claim 1; Fig 8A1-2; 91pp; English.

XX This is the nucleotide sequence of a partial cDNA clone which codes for a  
 CC portion (see AAY06598) of human NaV, a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The NaV channel cDNA was obtained from human DRG tissue  
 CC cDNA by PCR amplification (see also AAX87620-22). Rat, mouse and human  
 CC NaV nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98)  
 CC are provided. The invention also includes expression vectors and  
 CC transformed host cells, methods for identifying tissues and cells that  
 CC express NaV, methods for identifying agents that modulate NaV channel  
 CC activity or NaV channel mRNA transcription or translation, and a method  
 CC for using such agents to treat acute or chronic pain, paraesthesia and  
 CC hyperexcitability phenomena. The preferential expression of NaV in  
 CC sensory DRG and trigeminal neurons provides a target for selectively  
 CC modifying the behaviour of these nerve cells while not affecting other  
 CC nerve cells in the brain and spinal cord. The gene is named SCN1A

Query Match	32.9%	Score 134.4	DB 2	Length 3638
Best Local Similarity	90.1%	Pred. No. 4.6e-25		
Matches 155	Conservative 0	Mismatches 16	Indels 1	Gaps 1
Qy	202	ATTCTTAACAGAAACAGACGCCAGAGTTTGAGAGCAATTCACGCTTACATTT-CT	260	
Db	3143	ATTCCACAGAGAAACAGACGCCAGAGTTTGAGAGCAATTCACGCTTACATTTACT	3207	
Qy	261	TGCTAGTCTTTATCATCTTTGGCTCATCTTTCACCTGTGAATCTCTTCATTGGCGTTATCA	320	
Db	3203	TGCTAGTCTTTATCATCTTTGGCTCATCTTTCACCTGTGAATCTCTTCATTGGCGTTATCA	326	
Qy	321	TTGACAACTTCAACCAAGCAGCAAGAAAAAGATAGTATCTGGGTCTCTTGAT	372	
Db	3263	TTGACAACTTCAACCAAGCAGCAAGAAAAAGTATGTTGGCCAAACATTTTAT	3314	
RESULT 4				
AAF30104				
ID	AAF30104	standard; cDNA; 3701 BP.		
XX	AAF30104;			
XX	AC			
DT	30-APR-2001	(first entry)		
XX				
DE	Human sodium channel NaV partial cDNA.			
KM	Sodium channel; NaV; human; tetrodotoxin resistant; pain; paraesthesia;			
XX	hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.			
OS	Homo sapiens.			
XX				
FT	Key	Location/Qualifiers		
FT	CDS	1..3699		
FT		/*tag= a		
FT		/partial		
PN	MO200105831-A1.			
XX				
PD	25-JAN-2001.			
XX				
PE	14-JUL-2000; 2000MO-US019342.			
PR	16-JUL-1999; 99US-00354147.			
XX				
PA	(UTYA ) UNIV YALE.			
PI	D1b-HaJj S, Waxman SG;			
DR	WPI: 2001-103147/11.			
DR	P-P8DB; AAB20125.			
XX				
PT	Nucleic acid molecules encoding human tetrodotoxin resistant sodium			
PT	channels, useful for preventing, diagnosing and treating pain,			
PT	paraesthesia and/or hyperexcitability phenomena.			
XX				
PS	Example 4; Fig 8A; 162bp; English.			
CC	The present sequence is that of a partial cDNA for a novel human			
CC	tetrodotoxin resistant sodium channel, termed NaN (see AAB20125). The			
CC	cDNA was isolated from a human dorsal root ganglia tissue cDNA library by			
CC	PCR amplification (see also AAF30122-23). A full-length sequence is given			
CC	in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium			
CC	channel protein family and produces a TTX-R sodium current. Such channels			
CC	underlie the generation and propagation of impulses in excitable cells			
CC	such as neurons and muscle fibres. Preferential expression of NaN on			
CC	sensory neurons innervating the body (dorsal root ganglia) and the face			
CC	(trigeminal ganglia), but not on other neurons, makes it a very useful			
CC	target for diagnostic and/or therapeutic uses in relation to acute and/or			
CC	chronic pain pathologies. A claimed method of treating pain, paraesthesia			
CC	and/or hyperexcitability phenomena in a human or animal subject involves			

CC	administering an agent that alters sodium current flow through Na <sup>v</sup> channels, or which modulates transcription or translation of Na <sup>v</sup> mRNA, in
CC	channels, or which modulates transcription or translation of Na <sup>v</sup> mRNA, in
CC	dorsal root ganglia or trigeminal neurons. Na <sup>v</sup> nucleic acids are used in
CC	gene therapy to correct disorders associated with decreased sodium
CC	channel expression or (antisense) to down-regulate Na <sup>v</sup> expression, in the
CC	diagnosis of disease, and in the recombinant production of Na <sup>v</sup>
CC	polypeptides
XX	
XX	Sequence 3701 BP, 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;
XX	
Qy	Query Match 32.9%; Score 134.4; DB 4; Length 3701;
Db	Best Local Similarity 90.1%; Pred. No. 4.7e-25;
Db	Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1
Qy	202 ATTTCTAACAGAAAGAACACAGCCAGAGTTTGAGAGCAATTCACCTGGATTACCTT-CT 266
Db	3206 ATTCCACAGAGAAAGAACACAGCCAGAGTTTGAGAGCAATTCACCTGGATTACCTTACT 326
Qy	261 TCGTATCTTTTATCATCTTGGCTCATCTTCACCTGGAATCTCTTCAATGGCGATTACA 326
Db	3266 TCGTATCTTTTATCATCTTGGCTCATCTTCACCTGGAATCTCTTCAATGGCGATTACA 333
Qy	321 TTGACAACTTCAACCAACGACGAGAAAAGATAGATGATCTGGGTTGCTTGAT 372
Db	3326 TTGACAACTTCAACCAACGACGAGAAAAGATAGATGATGCTGGCAAGACATTTTAT 3377
RESULT 5	
AAI42750	AAI42750 standard; cDNA; 5728 BP.
XX	AAI42750;
AC	
XX	19-JUL-2002 (first entry)
DT	
XX	
DE	Human sodium channel subunit SCN12A-s coding sequence.
XX	
KX	Human, gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;
KW	human nervous system; chromosome 3p23-21.3; excitatory cell;
KM	drug development; familial hyperglycaemia; QT extending syndrome type 3;
XX	motor endplate disease.
XX	
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FT	CDS 200..4534
FT	/*tag= a
FT	/product= "human sodium channel subunit SCN12A-s"
XX	
XX	WO200190355-A1.
PN	
XX	29-NOV-2001.
PD	
XX	11-JUL-2000; 2000WO-JP004629.
PE	
XX	23-MAY-2000; 2000JP-00152085.
PR	
XX	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA	
XX	Kanazawa I, Goto J, Jeong S;
PI	
XX	WPI; 2002-393394/42.
DR	P-PSDB; AAO14926.
XX	
PT	Sodium channel alpha subunits SCN12A and SCN8A of human nervous system
XX	together with splicing variants, useful in studying physiological
XX	mechanism relating to excitatory cells and in drug development.
XX	
PS	Claim 7; Page 55-70; 118pp; Japanese.
XX	
CC	The invention comprises the amino acid and coding sequence of three
CC	sodium channel subunits from the human nervous system (SCN12A, SCN12A-s
CC	and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and

CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel  
CC subunit proteins are useful in studying physiological mechanisms relating  
CC to excitatory cells and in drug development. The sodium ion channel  
CC subunit proteins are useful for treating diseases such as familial  
CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.  
CC The present cDNA sequence encodes the human SCN12A-s sodium channel  
CC subunit  
XX  
SQ Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;  
Query Match 32.9%; Score 134.4; DB 6; Length 5728;  
Best Local Similarity 90.1%; Pred. No. 5.4e-25;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
XX  
QY 202 ATTCTACAGAAAGAACACAGCCAGAGTTGAGAGCAATTCGCTTACATT-CT 260  
DB 4002 ATTCACAGAGAAAGAACACAGCCAGAGTTGAGAGCAATTCGCTTACATTCT 4061  
QY 261 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGAACTCTTCAATTGGCGTTATCA 320  
DB 4062 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGAACTCTTCAATTGGCGTTATCA 4121  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAAGATTAATATCTGGTGTCTTGAT 372  
DB 4122 TTGACAACTTCAACCAACAGCAAGAAAAAGTATGAGTGGCCAGACATTTTAT 4173  
XX  
RESULT 6  
AAF30101  
ID AAF30101 standard; cDNA; 5860 BP.  
XX  
AC AAF30101;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human sodium channel NaN cDNA.  
XX  
KW Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia;  
XX hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 31..5406  
FT /tag= a  
FT  
XX  
PN WO200105831-A1.  
XX  
PD 25-JAN-2001.  
XX  
PP 14-JUL-2000; 2000WO-US019342.  
XX  
PR 16-JUL-1999; 99US-00354147.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI DiB-Hajj S, Waxman SG;  
XX  
XX WPI; 2001-103147/11.  
XX P-PSDB; AAB20121.  
XX  
PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
PT channels, useful for preventing, diagnosing and treating pain,  
PT paraesthesia and/or hyperexcitability phenomena.  
XX  
PS Claim 1; Fig 11A; 162pp; English.  
XX  
XX The present sequence is that of cDNA encoding a novel human tetrodotoxin  
XX resistant sodium channel, termed NaN (see AAB20121). The cDNA was  
XX isolated from a human dorsal root ganglia tissue cDNA library by PCR  
XX amplification (see also AAF30122-23). NaN belongs to the a-subunit  
XX voltage-gated sodium channel protein family and produces a TTX-R sodium  
XX current. Such channels underlie the generation and propagation of

CC impulses in excitable cells such as neurons and muscle fibres.  
CC Preferential expression of NaN on sensory neurons innervating the body  
CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
CC neurons, makes it a very useful target for diagnostic and/or therapeutic  
CC uses in relation to acute and/or chronic pain pathologies. A claimed  
CC method of treating pain, paraesthesia and/or hyperexcitability phenomena  
CC in a human or animal subject involves administering an agent that alters  
CC sodium current flow through NaN channels, or which modulates  
CC transcription or translation of NaN mRNA, in dorsal root ganglia or  
CC trigeminal neurons. NaN nucleic acids are used in gene therapy to correct  
CC disorders associated with decreased sodium channel expression or  
CC (antisense) to down-regulate NaN expression, in the diagnosis of disease,  
CC and in the recombinant production of NaN polypeptides  
XX  
SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
Query Match 32.9%; Score 134.4; DB 4; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 5.4e-25;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
XX  
QY 202 ATTCTACAGAAAGAACACAGCCAGAGTTGAGAGCAATTCGCTTACATT-CT 260  
DB 3893 ATTCACAGAGAAAGAACACAGCCAGAGTTGAGAGCAATTCGCTTACATTACT 3892  
QY 261 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGAACTCTTCAATTGGCGTTATCA 320  
DB 3893 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGAACTCTTCAATTGGCGTTATCA 3952  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAAGATTAATATCTGGTGTCTTGAT 372  
DB 3953 TTGACAACTTCAACCAACAGCAAGAAAAAGTATGAGTGGCCAGACATTTTAT 4004  
XX  
RESULT 7  
ADD32193  
ID ADD32193 standard; cDNA; 5860 BP.  
XX  
AC ADD32193;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
XX  
XX expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 31..5406  
FT /tag= a  
FT /product= "Na v 1.9 sodium channel protein"  
FT  
XX  
PN WO2003080570-A2.  
XX  
PD 02-OCT-2003.  
XX  
PP 20-MAR-2003; 2003WO-US008611.  
XX  
PR 20-MAR-2002; 2002US-036550P.  
XX  
PA (TRAN-) TRANSMOLECULAR INC.  
XX  
PI Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
XX P-PSDB; ADD32194.  
XX  
PT Expression vector useful for stable cloning and expression of Nav1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
PT fragment.  
XX

PS Disclosure; SEQ ID NO 3; 125pp; English.

CC The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell.

CC Also described: (1) a recombinant cell comprising the plasmid selected from pRAN, pCMV-rNAN-GFP, pEG338XN-rNAN and the plasmid described above;

CC (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a human Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.

CC XX

SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;

Query Match 32.9%; Score 134.4; DB 9; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 5.4e-25;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTTACAGAAAGAACACAGCCAGATTGAGAGCAATTCCTGGTTACATTT-CT 260  
DB ATTCACAGAGAAAGAACACAGCCAGATTGAGAGCAATTCCTGGTTACATTTACT 3892

QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGGAATCTCTCATTTGGCGTTATCA 320  
DB TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGGAATCTCTCATTTGGCGTTATCA 3952

QY 321 TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCTGGGTGCTTGAT 372  
DB TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCTGGGTGCTTGAT 4004

RESULT 8  
AAL42749 ID AAL42749 standard; cDNA; 6528 BP.

AC AAL42749;

XX 19-JUL-2002 (first entry)

DE Human sodium channel subunit SCN12A coding sequence.

XX

KW Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCNA8;

KM human nervous system; chromosome 3p23-21.3; excitatory cell;

KM drug development; familial hyperglycaemia; QT extending syndrome type 3;

KM motor endplate disease.

OS Homo sapiens.

XX

XX Key Location/Qualifiers  
FH 200..5575  
FT /\*tag= a  
FT /product= "Human sodium channel subunit SCN12A"

XX MO200190355-A1.

XX 29-NOV-2001.

XX 11-JUL-2000; 2000MO-JP004629.

XX PF 23-MAY-2000; 2000JP-00152085.

XX PR

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Kanazawa I, Goto J, Jeong S;

XX WPI; 2002-393394/42.

DR P-PSDB; AAO14925.

XX

PT Sodium channel alpha subunits SCN12A and SCNA8 of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.

PT

PS Claim 6; Page 29-46; 118pp; Japanese.

XX

CC The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCNA8). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCNA8 gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate disease. The present cDNA sequence encodes the human SCN12A sodium channel subunit

CC XX

SQ Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;

Query Match 32.9%; Score 134.4; DB 6; Length 6528;  
Best Local Similarity 90.1%; Pred. No. 5.6e-25;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTTACAGAAAGAACACAGCCAGATTGAGAGCAATTCCTGGTTACATTT-CT 260  
DB ATTCACAGAGAAAGAACACAGCCAGATTGAGAGCAATTCCTGGTTACATTTACT 4061

QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGGAATCTCTCATTTGGCGTTATCA 320  
DB TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGGAATCTCTCATTTGGCGTTATCA 4121

QY 4062 TCGTAGCTTTATCATCTTTGGCTCATCTCTCACTGGAATCTCTCATTTGGCGTTATCA 4121

QY 321 TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCTGGGTGCTTGAT 372  
DB TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCTGGGTGCTTGAT 4173

RESULT 9  
AAX87601 ID AAX87601 standard; cDNA; 5822 BP.

AC AAX87601;

XX 26-OCT-1999 (first entry)

DE Mouse sodium channel NaN cDNA.

XX

KW NaN; sodium channel; ion transport; mouse; dorsal root ganglia; pain;

KM paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

XX

OS Mus musculus.

XX

XX Key Location/Qualifiers  
FH 19..5316  
FT /\*tag= a  
FT /\*tag= b  
FT /note= "these bases represent nucleotides missing from the sequence given in Fig 7 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

FT 5789..5794  
FT /\*tag= c

XX polyA\_signal

XX WO9938889-A2.

XX 05-AUG-1999.

XX

XX 29-JAN-1999; 99WO-US002008.  
 PF 29-JAN-1998; 98US-0072990P.  
 PR 20-NOV-1998; 98US-0109402P.  
 XX (UYVA ) UNIV YALE.  
 XX DiB-Hajj S, Waxman S;  
 XX WPI; 1999-479168/40.  
 DR P-PSDB; AAY06597.  
 XX New isolated nucleic acids encoding sodium channels, used to develop  
 PT products for treating acute or chronic pain or hyperexcitability  
 PT phenomena.  
 PS Claim 1; Fig 7A1-3; 91pp; English.  
 XX This is the nucleotide sequence of an isolated nucleic acid which encodes  
 CC the mouse Nan channel (see AAY06597), a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The Nan channel cDNA was obtained from mouse trigeminal  
 CC ganglia cDNA by PCR amplification using rat Nan-based primers (see  
 CC AAX87618-19). Rat, mouse and human Nan nucleic acids (see AAX87600-02)  
 CC and polypeptides (see AAY06596-98) are provided. The invention also  
 CC includes expression vectors and transformed host cells, methods for  
 CC identifying tissues and cells that express Nan, methods for identifying  
 CC agents that modulate Nan channel activity or Nan channel mRNA  
 CC transcription or translation, and a method for using such agents to treat  
 CC acute or chronic pain, paresthesia and hyperexcitability phenomena. The  
 CC preferential expression of Nan in sensory DRG and trigeminal neurons  
 CC provides a target for selectively modifying the behaviour of these nerve  
 CC cells while not affecting other nerve cells in the brain and spinal cord.  
 CC The gene encoding Nan has been named Scnlla  
 CC XX  
 SQ Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 0 U; 61 Other;  
 Query Match 21.5%; Score 88; DB 2; Length 5822;  
 Best Local Similarity 73.3%; Pred. No. 8e-13;  
 Matches 126; Conservative 0; Mismatches 45; Indels 1; Gaps 1;  
 QY 202 ATTTCTACAGAAAGAACACAGCCAGATTGAGAGCAATTCACCTCGGTTACATT-CT 260  
 DB 3764 ATTCAGAGGAGAAAGATGAGCGCGCTTGAGGCGATCTATACGATACCTTTACT 3823  
 QY 261 TCGTAGCTTTATCATCTTGGCTCATCTCTCACTGTGAATCTCTTCATTGGCGTTATCA 320  
 DB 3824 TCGTGGTTTTTATCATCTTCGGCTCATCTTTACCTGAACCTCTTTATCGGTTATTA 3883  
 QY 321 TTGACAACTTCAACCAAGCAGAAAAAGATAGTATCTGGGTGCTTGAT 372  
 DB 3884 TTGACAACTTCAATCAGCAGCAAAAAAGTTAGTGGCCAGACATTTTAT 3935  
 RESULT 10  
 AAF30103  
 ID AAF30103 standard; cDNA; 5822 BP.  
 XX AAF30103;  
 AC 30-APR-2001 (first entry)  
 DT Mouse sodium channel Nan cDNA.  
 DE Sodium channel; Nan; Scnlla; mouse; tetrodotoxin resistant; pain;  
 KW paresthesia; hyperexcitability; analgesic; vaccine; gene therapy;  
 KM diagnosis; ss.  
 XX Mus musculus.  
 OS  
 XX  
 FH Key Location/Qualifiers

FT CDS 19..5316  
 FT /\*tag= a  
 FT polyA\_signal 5789..5794  
 FT /\*tag= b  
 FT polyA\_site 5800..5822  
 FT /\*tag= c  
 PN WO200105831-A1.  
 XX 25-JAN-2001.  
 XX 14-JUN-2000; 2000WO-US019342.  
 XX 16-JUL-1999; 99US-00354147.  
 XX (UYVA ) UNIV YALE.  
 XX DiB-Hajj S, Waxman SG;  
 XX WPI; 2001-103147/11.  
 DR P-PSDB; AAB20124.  
 XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 PT channels, useful for preventing, diagnosing and treating pain,  
 PT paresthesia and/or hyperexcitability phenomena.  
 PS Example 3; Fig 7A; 162pp; English.  
 XX The present sequence is that of cDNA encoding a novel mouse tetrodotoxin  
 CC resistant sodium channel, termed Nan (see AAB20124). The cDNA was  
 CC isolated from trigeminal ganglia cDNA using primers (see AAF30120-21)  
 CC based on rat Nan sequences. Mouse Nan shows 68% similarity to human Nan  
 CC (see AAB20121). The gene encoding Nan, termed Scnlla, is located on mouse  
 CC chromosome 9. Nan belongs to the  $\alpha$ -subunit voltage-gated sodium channel  
 CC protein family and produces a TTX-R sodium current. Such channels  
 CC underlie the generation and propagation of impulses in excitable cells  
 CC such as neurons and muscle fibres. Preferential expression of Nan on  
 CC sensory neurons innervating the body (dorsal root ganglia) and the face  
 CC (trigeminal ganglia), but not on other neurons, makes it a very useful  
 CC target for diagnostic and/or therapeutic uses in relation to acute and/or  
 CC chronic pain pathologies. A claimed method of treating pain, paresthesia  
 CC and/or hyperexcitability phenomena in a human or animal subject involves  
 CC administering an agent that alters sodium current flow through Nan  
 CC channels, or which modulates transcription or translation of Nan mRNA, in  
 CC dorsal root ganglia or trigeminal neurons. Nan nucleic acids are used in  
 CC gene therapy to correct disorders associated with decreased sodium  
 CC channel expression or (antisense) to down-regulate Nan expression, in the  
 CC diagnosis of disease, and in the recombinant production of Nan  
 CC polypeptides  
 CC XX  
 SQ Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;  
 Query Match 21.5%; Score 88; DB 4; Length 5822;  
 Best Local Similarity 73.3%; Pred. No. 8e-13;  
 Matches 126; Conservative 0; Mismatches 45; Indels 1; Gaps 1;  
 QY 202 ATTTCTACAGAAAGAACACAGCCAGATTGAGAGCAATTCACCTCGGTTACATT-CT 260  
 DB 3764 ATTCAGAGGAGAAAGATGAGCGCGCTTGAGGCGATCTATACGATACCTTTACT 3823  
 QY 261 TCGTAGCTTTATCATCTTGGCTCATCTCTCACTGTGAATCTCTTCATTGGCGTTATCA 320  
 DB 3824 TCGTGGTTTTTATCATCTTCGGCTCATCTTTACCTGAACCTCTTTATCGGTTATTA 3883  
 QY 321 TTGACAACTTCAACCAAGCAGAAAAAGATAGTATCTGGGTGCTTGAT 372  
 DB 3884 TTGACAACTTCAATCAGCAGCAAAAAAGTTAGTGGCCAGACATTTTAT 3935  
 RESULT 11  
 ADD32195  
 ID ADD32195 standard; cDNA; 5822 BP.



AC	ADD32195,	
XX	15-JAN-2004 (first entry)	
DT		
XX		
DE	Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:5.	
XX		
KW	expression vector; Na v 1.9 sodium channel protein;	
KM	sodium channel protein; dorsal root ganglion neuron; mouse; gene; ss.	
XX		
OS	Mus musculus.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	19..5316
FT		/*tag= a
FT		/product= "Na v 1.9 sodium channel protein"
PN	MO2003080570-A2.	
XX		
PD	02-OCT-2003.	
XX		
PP	20-MAR-2003; 2003WO-US008611.	
XX		
PR	20-MAR-2002; 2002US-0365550P.	
XX		
PA	(TRAN-) TRANSMOLECULAR INC.	
XX		
PI	Gonda MA, Greenwood JD;	
XX		
DR	WPI; 2003-876895/81.	
XX	P-P8DB; ADD32196.	
PT	Expression vector useful for stable cloning and expression of Nav1.9	
PT	sodium channel at the mRNA and protein levels comprises a nucleic acid	
PT	sequence that encodes a mammalian Nav1.9 sodium channel protein or its	
PT	fragment.	
XX		
XX	Disclosure; SEQ ID NO 5; 125pp; English.	
XX		
CC	The present invention describes an expression vector comprising a nucleic	
CC	acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or	
CC	its fragment, and producing a sodium current when transfected in a cell.	
CC	Also described: (1) a recombinant cell comprising the plasmid selected	
CC	from pNan, pCMV-rNan-GFP, pLG338XM-rNan and the plasmid described above;	
CC	(2) a method of making a cell or cell line that produces a Na v 1.9	
CC	sodium channel-dependent sodium current by: (a) providing a cell that has	
CC	been transfected with the expression vector; and (b) culturing the cell	
CC	under conditions that allow expression of Na v 1.9 sodium channel protein	
CC	to produce a sodium current into the transfected cell; (3) a method of	
CC	screening for an agent that modulates sodium current in a cell by: (a)	
CC	exposing the cell or cell line produced by the method to the agent; and	
CC	(b) measuring sodium current following exposure to the agent, where an	
CC	alteration in the level of sodium current is indicative of an agent	
CC	capable of modulating sodium current in a cell; and (4) a recombinant	
CC	cell comprising the expression vector. The expression vectors are useful	
CC	for the stable cloning and expression of the Na v 1.9 sodium channel at	
CC	the mRNA and protein levels, and for producing sodium channel currents	
CC	characteristic of native currents in dorsal root ganglion neurons. The	
CC	present sequence encodes a mouse Na v 1.9 sodium channel protein, which	
CC	is used in the exemplification of the present invention.	
XX		
XX	Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;	
XX		
Query Match	21.5%; Score 88; DB 9; Length 5822;	
Best Local Similarity	73.3%; Pred. NO. Be-13;	
Matches	126; Conservative 0; Mismatches 45; Indels 1; Gaps 1	
QY	202 ATTCTTAACAGAAAGACAACAGCCAGATTGGAGAGCAATTCCTCGTTACATTT-CT 260	
DB	3764 ATTCCAGAGGGGAAGATGAGCAGCCGGCCTTGAAGGCGCATGTATACGATATCCTTTACT 3822	
QY	261 TCGTAGTCTTATCATCTTTGGCTCATTTCTTCATCTGTGATCTTTCATGGCGTTATCA 320	
DB	3824 TCGTAGTCTTATCATCTTTGGCTCATTTCTTCATCTGTGATCTTTCATGGCGTTATTA 3882	

Gy	321	TTCGCACTTCAACCAAGCACAATAAAGTAGTATCGGGTGTCTGCAT	372
D6	3884	TTGCAACTTCAATTCCAGACGAGAAAAAGTTAGTGCCCAAGCATTTTTAT	3935
<hr/>			
RESULT 12			
ID	AAH55851		
ID	AAH55851	standard; DNA; 637 BP.	
XX	AAH55851;		
AC			
XX			
DT	04-SEP-2001	(first entry)	
XX			
DE	Human SCN3A genomic DNA fragment SEQ ID NO:95.		
XX			
KW	Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;		
RW	diagnosis; mutation; chromosome 2q23-q31; neurological disorder;		
KW	anticonvulsant; neuroprotective; de.		
XX			
OS	Homo sapiens.		
PX	MO200138564-A2.		
PN			
XX			
PD	31-MAY-2001.		
PF	24-NOV-2000; 2000MO-CAN001404.		
PR	26-NOV-1999; 99US-0167623P.		
PA	(UYMC-) UNIV MCGILL.		
XX			
PL	Rouleau GA, Latremiere RG, Rochefort D, Cossette P, Ragsdale D;		
DR	WPI; 2001-355945/37.		
PT	Determining a predisposition to epilepsy and/or development of epilepsy		
PT	comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA		
PT	variant, equivalent, or mutation which shows a linkage disequilibrium.		
XX			
PS	Disclosure; Page 183; 268pp; English.		
XX			
XX	The present invention describes a method (M1) of determining an		
CC	individual's predisposition to epilepsy and/or development of epilepsy,		
CC	as well as predicting the individual's response to medication. The method		
CC	comprises determining the genotype of at least one gene selected from		
CC	SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which		
CC	shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium		
CC	channel genes located on chromosome 2. The idiopathic generalised		
CC	epilepsy (IGE) gene is more specifically localised on chromosome 2q23-		
CC	q31. Compounds identified as modulators of the biological activity of		
CC	SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy		
CC	or other neurological disorders. They have anticonvulsant and		
CC	neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679		
CC	represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,		
CC	oligonucleotides and proteins given in the exemplification of the present		
CC	invention		
SQ	Sequence 637 BP; 194 A; 117 C; 102 G; 224 T; 0 U; 0 Other;		
XX			
XX			
Query Match	20.8%; Score 85.2; DB 5; Length 637;		
Best Local Similarity	66.5%; Pred. No.2,1e-12;		
Matches 137;	Conservative 0; Mismatches 68; Indels 1; Gaps 1;		
Gy	153	GAATGCTATATTTTTCGCCAGTAATGTGTTTTCTCTTATTAATAAATTTCTAACG	212
Db	161	GATTTAGTGAAGTATTTATAGATTTTTCATATTTTAAATATTTTCAATTCATTTAG	220
Gy	213	AAGAACAACAGCCAGAGTGTGAGACATTCACTCGGTTACAT-TTCCTCGAATCTTT	271
D6	221	GTTAACTTCAAGCTGTATATGAGAAAATCTGTATACATGATTTTATCTTGTACATCTT	280
Gy	272	ATCATCTTTGGCTCATCTTTCATCTGATCTCTTCATTCGAGGTTATCATCTTACACATTC	331

Db 281 ATCATCTTTGGGTGATCTTCTGACTGTAATCTATTCATTTGGTGATCATAGATACTTC 340  
 QY 332 AACCAACGACAGAAAAAGATAAGTAT 357  
 Db 341 AACCGACAGAAAAAGAGATAAGTAT 366

## RESULT 13

AA60244  
 ID AA60244 standard; cDNA; 5334 BP.

XX AC AA60244;

XX XX 11-AUG-1999 (first entry)

DE Stabilised cDNA encoding type 5 sodium channel protein designated PNS.

XX KM Type 5 sodium channel; PNS; nervous system; plexiform;  
 KM dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
 KM diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
 KM neuropathic pain; migraine; headache; ss.

OS Synthetic.  
 OS Rattus sp.

XX PN FR2771103-A1.

XX PD 21-MAY-1999.

XX PF 19-NOV-1998; 98FR-00014551.

XX PR 20-NOV-1997; 97US-0066225P.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Dierrich PS, Fish LM, Khare R, Robert DK, Sangameswaran L;

XX DR WPI; 1999-315739/27.

XX XX Isolated DNA encoding sodium channel of the nervous system.

XX PS Example 7; Fig 5A-E; 90pp; French.

XX XX The present sequence encodes a type 5 sodium channel protein designated  
 CC PNS. The protein is a sodium ion channel of the nervous system, and is  
 CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
 CC used to identify inhibitors of sodium channel proteins that are resistant  
 CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
 CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
 CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
 CC XX

XX SQ Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;

XX Query Match 20.3%; Score 83.2; DB 2; Length 5334;

XX Best Local Similarity 71.5%; Pred. No. 1.4e-11;

XX Matches 123; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

XX QY 202 ATTTCTAACAGAAAGAACAGCCAGAGTTTGA-GAGCAATTCACCTCGTTACATTCT 260

XX Db 3766 ATTCGAGAGAGAAAGACGAGCCGAGCTTTGAGCGCAACCTTACGGGTATCTCTACT 3825

XX QY 261 TCGTAGTCTTTATCATCTTTGGCTCATTTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320

XX Db 3826 TTGTGGTTTTTATCATCTTCGGCTCTCTCTTACCTGAACCTTTATCGGGTATATTA 3885

XX QY 321 TTGACAACTTCAACCAACGACAGAAAAAGATAAGTATCTGGGTCTTGAT 372

XX Db 3886 TTGACAACTTCAATCAGACAGAAAAAGTTAGTGGCCCAAGACATCTTCAT 3937

## RESULT 14

ADD32209

ID ADD32209 standard; cDNA; 5298 BP.

XX AC ADD32209;

XX XX 15-JAN-2004 (first entry)

DE Rat Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:19.

XX KM expression vector; Na v 1.9 sodium channel protein;  
 KM sodium channel protein; dorsal root ganglion neuron; rat; gene; ss.

XX OS Rattus norvegicus.

XX FH Key Location/Qualifiers

XX FT 1-5298

XX FT CDS /tag= a /product= "Na v 1.9 sodium channel protein"

XX PN MO2003080570-A2.

XX PD 02-OCT-2003.

XX PF 20-MAR-2003; 2003WO-US008611.

XX PR 20-MAR-2002; 2002US-036550P.

XX PA (TRAN-) TRANSMOLECULAR INC.

XX PI Gonda MA, Greenwood JD;

XX XX WPI; 2003-876895/81.

XX DR P-PSDB; ADD32210.

XX PT Expression vector useful for stable cloning and expression of Nav1.9  
 PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
 PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
 XX fragment.

XX PS Claim 13; SEQ ID NO 19; 1255P; English.

XX XX The present invention describes an expression vector comprising a nucleic  
 CC acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
 CC its fragment, and producing a sodium current when transfected in a cell.  
 CC Also described: (1) a recombinant cell comprising the plasmid selected  
 CC from pRAN, pCMV-rRAN-GFP, pEG338XN-rRAN and the plasmid described above;  
 CC (2) a method of making a cell or cell line that produces a Na v 1.9  
 CC sodium channel-dependent sodium current by: (a) providing a cell that has  
 CC been transfected with the expression vector; and (b) culturing the cell  
 CC under conditions that allow expression of Na v 1.9 sodium channel protein  
 CC to produce a sodium current into the transfected cell; (3) a method of  
 CC screening for an agent that modulates sodium current in a cell by: (a)  
 CC exposing the cell or cell line produced by the method to the agent; and  
 CC (b) measuring sodium current following exposure to the agent, where an  
 CC alteration in the level of sodium current is indicative of an agent  
 CC capable of modulating sodium current in a cell; and (4) a recombinant  
 CC cell comprising the expression vector. The expression vectors are useful  
 CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
 CC the mRNA and protein levels, and for producing sodium channel currents  
 CC characteristic of native currents in dorsal root ganglion neurons. The  
 CC present sequence encodes a rat Na v 1.9 sodium channel protein, which is  
 XX used in the exemplification of the present invention.

XX SQ Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other;

XX Query Match 20.0%; Score 81.6; DB 9; Length 5298;

XX Best Local Similarity 70.9%; Pred. No. 3.7e-11;

XX Matches 122; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

XX QY 202 ATTTCTAACAGAAAGAACAGCCAGAGTTTGA-GAGCAATTCACCTCGGTACATTCT 260

XX Db 3743 ATTCGAGAGAGAAAGACGAGCCGAGCTTTGAGCGCAACCTTACGGGTATCTCTACT 3802

XX QY 261 TCGTAGTCTTTATCATCTTTGGCTCATTTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320

Db 3803 TTGGGTTTATATATCTTGGCTCTCTTACCTCGAACCTTTATCGGTATTA 3862  
 QY 321 TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCGGTGTTCTTGAT 372  
 Db 3863 TTGACAACTTCAATCAGACAGAGAAAAAGTTAGTGCCCAAGACATTTTAT 3914

RESULT 15  
 ID AAX87600 standard; cDNA; 5875 BP.  
 XX AAX87600;  
 AC AAX87600;  
 XX 26-OCT-1999 (first entry)  
 DT 26-OCT-1999 (first entry)  
 XX Rat sodium channel Nan cDNA.  
 DE Rat sodium channel Nan cDNA.  
 XX NAN; sodium channel; ion transport; rat; dorsal root ganglia; pain;  
 KM paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.  
 XX Rattus sp.  
 OS Rattus sp.  
 XX Key Location/Qualifiers  
 FH 41..5338  
 FT /\*tag= a  
 FT CDS 5551..5600  
 FT /\*tag= b  
 FT misc\_feature /note= "these bases represent nucleotides missing from  
 the sequence given in Fig 1 of the specification. The  
 FT nucleotides are included to maintain the nucleotide  
 FT numbering given in the specification for this DNA  
 FT sequence"

XX MO938889-A2.  
 XX  
 XX PD 05-AUG-1999.  
 XX  
 XX PF 29-JAN-1999; 99WO-US002008.  
 XX  
 XX PR 29-JAN-1998; 98US-0072990P.  
 XX 20-NOV-1998; 98US-0109402P.  
 XX (UYTA ) UNIV YALE.  
 XX PA  
 XX PI Dib-Hadj S, Waxman S;  
 XX WPI: 1999-479168/40.  
 XX DR P-PSDB; AAY06596.  
 XX  
 XX PT New isolated nucleic acids encoding sodium channels, used to develop  
 PT products for treating acute or chronic pain or hyperexcitability  
 PT phenomena.  
 XX  
 XX PS Claim 1; Fig 1A-D; 91pp; English.  
 XX  
 XX CC This is the nucleotide sequence of an isolated nucleic acid which encodes  
 CC the rat Nan channel (see AAY06596), a previously unidentified voltage  
 CC gated sodium channel protein that is preferentially expressed in dorsal  
 CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R  
 CC sodium current. The Nan channel cDNA was obtained from Sprague-Dawley rat  
 CC DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse  
 CC and human Nan nucleic acids (see AAX87600-02) and polypeptides (see  
 CC AAY06596-98) are provided. The invention also includes expression vectors  
 CC and transformed host cells, methods for identifying tissues and cells  
 CC that express Nan, methods for identifying agents that modulate Nan  
 CC channel activity or Nan channel mRNA transcription or translation, and a  
 CC method for using such agents to treat acute or chronic pain, paraesthesia  
 CC and hyperexcitability phenomena. The preferential expression of Nan in  
 CC sensory DRG and trigeminal neurons provides a target for selectively  
 CC modifying the behaviour of these nerve cells while not affecting other  
 CC nerve cells in the brain and spinal cord. The Nan gene has been named  
 CC Scn1a

XX SQ Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;  
 Query Match 20.0%; Score 81.6; DB 2; Length 5875;  
 Best Local Similarity 70.9%; Pred. No. 3.8e-11;  
 Matches 122; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 202 ATTTCTAAGAGAAAGAACACAGCCAGAGTTGA-GAGCAATTCACGCGTTACATTCT 260  
 Db 3783 ATTCAGAGAGAAAGACAGACGACCGACTTGAAGCGAACTCTACGCGTATCTTACT 3842  
 QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCACTGATCTGATCTTCATTGCGGTTATCA 320  
 Db 3843 TTGTGTTTATCATCTTGGCTCTCTTACCTCGAACCTTTATCGGTATTA 3902  
 QY 321 TTGACAACTTCAACCAACAGAGAAAAAGATAGATATCGGTGTTCTTGAT 372  
 Db 3903 TTGACAACTTCAATCAGACAGAGAAAAAGTTAGTGCCCAAGACATTTTAT 3954

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 Job time : 297.047 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 19:33:04 ; Search time 250.501 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-15

Perfect score: 409 1 atccaccgccgcgcgcga.....gtccctcaagaagaatcc 409

Sequence: 1 atccaccgccgcgcgcga.....gtccctcaagaagaatcc 409

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134.4	32.9	3701	US-10-388-470-6	Sequence 6, Appl1
2	134.4	32.9	5860	US-10-388-470-41	Sequence 41, Appl1
3	88	21.5	5822	US-10-388-470-4	Sequence 4, Appl1
4	81.6	20.0	5875	US-10-388-470-1	Sequence 1, Appl1
5	76.4	18.7	6048	US-09-840-125-3	Sequence 3, Appl1
6	76.4	18.7	6048	US-09-896-994-1	Sequence 1, Appl1
7	76.4	18.7	6090	US-10-077-054-1	Sequence 1, Appl1
8	76.4	18.7	8491	US-10-101-510-617	Sequence 617, App
9	76.4	18.7	8491	US-10-333-191-1	Sequence 1, Appl1
10	76.4	18.7	8491	US-10-333-191-3	Sequence 3, Appl1
11	70.4	17.2	6344	US-10-209-776-1	Sequence 1, Appl1
12	70.4	17.2	6524	US-10-202-824-1	Sequence 1, Appl1
13	70.4	17.2	6527	US-10-202-824-7	Sequence 7, Appl1
14	70.4	17.2	7052	US-10-202-824-5	Sequence 5, Appl1
15	69.6	17.0	6822	US-09-917-800A-1604	Sequence 1604, Ap

16	69	16.9	3033	US-09-457-571-1	Sequence 1, Appl1
17	69	16.9	6452	US-09-457-571-9	Sequence 9, Appl1
18	68.8	16.8	1122	US-09-864-761-20706	Sequence 20706, A
19	68.8	16.8	473	US-09-864-761-3944	Sequence 3944, Ap
20	68.8	16.8	473	US-09-864-761-13959	Sequence 13959, A
21	68	16.6	142	US-09-864-761-30523	Sequence 30523, A
22	68	16.6	8530	US-10-220-120-104	Sequence 104, App
23	67.4	16.5	6348	US-09-919-039-366	Sequence 366, App
24	67.4	16.5	6361	US-10-161-803-61	Sequence 61, Appl
25	67.4	16.5	6371	US-09-457-571-13	Sequence 13, Appl
26	67.4	16.5	6404	US-09-457-571-14	Sequence 14, Appl
27	66.2	16.2	6328	US-10-161-803-60	Sequence 60, Appl
28	66.2	16.2	7028	US-10-101-510-630	Sequence 630, App
29	60.8	14.9	6027	US-10-297-022-40	Sequence 40, Appl
30	60.8	14.9	6315	US-09-428-371-2	Sequence 2, Appl1
31	60.6	14.8	5889	US-09-930-871-3	Sequence 3, Appl1
32	60.6	14.8	5922	US-09-930-871-13	Sequence 13, Appl
33	60.6	14.8	5997	US-09-930-871-1	Sequence 1, Appl1
34	60.6	14.8	6030	US-09-930-871-11	Sequence 11, Appl
35	60.2	14.7	6318	US-09-428-371-1	Sequence 1, Appl1
36	46.2	11.3	5482	US-10-429-681-2	Sequence 2, Appl1
37	43.2	10.6	19734	US-10-311-455-1906	Sequence 1906, Ap
38	43.2	10.6	3673778	US-10-312-841-2	Sequence 2, Appl1
39	43	10.5	6639	US-09-917-800A-1586	Sequence 1586, Ap
40	40	9.8	550	US-09-814-353-5098	Sequence 5098, Ap
41	40	9.8	550	US-09-814-353-11390	Sequence 11390, A
42	39.8	9.7	3596	US-10-435-804-5	Sequence 5, Appl1
43	39.8	9.7	3632	US-10-435-804-3	Sequence 3, Appl1
44	39.8	9.7	3632	US-10-435-804-4	Sequence 4, Appl1
45	39.8	9.7	7791	US-10-375-253-35	Sequence 35, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-388-470-6  
Sequence 6, Application US/10388470  
Publication No. US2003028662A1  
GENERAL INFORMATION:  
APPLICANT: Didi-Hajj, Sulayman  
TITLE OR INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
FEATURE:  
NAME/KEY: unanure  
LOCATION: (922)  
OTHER INFORMATION: Y = C or T. Xaa at amino acid position 308 is  
OTHER INFORMATION: Leu.  
US-10-388-470-6  
Query Match 32.9%; Score 134.4; DB 15; Length 3701;  
Best Local Similarity 90.1%; Pred. NO. 1.8e-25;

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Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
QY 202 ATTCTAACAAGAAACAGACGAGTTGAGAGCAATTCAGTGGTTACATTT-CT 260
Db 3206 ATTCACAGAGAAAGAAACAGACGAGTTGAGAGCAATTCAGTGGTTACATTTACT 3265
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320
Db 3266 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3325
QY 321 TTGACAACCTTCAACCAAGCAGCAAAAAAGATAGATCTGGGTGTTGAT 372
Db 3326 TTGACAACCTTCAACCAAGCAGCAAAAAAGTATGAGTGGCCAGACATTTTAT 3377

RESULT 2
US-10-388-470-41
; Sequence 41, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 41
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human Nan
US-10-388-470-41

Query Match 32.9%; Score 134.4; DB 15; Length 5860;
Best Local Similarity 90.1%; Pred. No. 2.3e-25;
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
QY 202 ATTCTAACAAGAAACAGACGAGTTGAGAGCAATTCAGTGGTTACATTT-CT 260
Db 3833 ATTCACAGAGAAAGAAACAGACGAGTTGAGAGCAATTCAGTGGTTACATTTACT 3892
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320
Db 3893 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3952
QY 321 TTGACAACCTTCAACCAAGCAGCAAAAAAGATAGATCTGGGTGTTGAT 372
Db 3953 TTGACAACCTTCAACCAAGCAGCAAAAAAGTATGAGTGGCCAGACATTTTAT 4004

RESULT 3
US-10-388-470-4
; Sequence 4, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
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; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; NAME/KEY: unsure
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-10-388-470-4

Query Match 21.5%; Score 88; DB 15; Length 5822;
Best Local Similarity 73.3%; Pred. No. 6.6e-13;
Matches 126; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 202 ATTCTAACAAGAAACAGACGAGTTGAGAGCAATTCAGTGGTTACATTT-CT 260
Db 3764 ATTCACAGAGAAAGATAGAGCGCGCTTGAAGCGCAATCTTACGATACCTTTACT 3823
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320
Db 3824 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3883
QY 321 TTGACAACCTTCAACCAAGCAGCAAAAAAGATAGATCTGGGTGTTGAT 372
Db 3884 TTGACAACCTTCAACCAAGCAGCAAAAAAGTATGAGTGGCCAGACATTTTAT 3935

RESULT 4
US-10-388-470-1
; Sequence 1, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/10/388,470
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; NAME/KEY: unsure
; LOCATION: (1996)..(4042)
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OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position  
; OTHER INFORMATION: 652 is Leu, Xaa at amino acid position 1334 is Asn  
; OTHER INFORMATION: or Lys.  
US-10-388-470-1

Query Match	20.0%;	Score 81.6;	DB 15;	Length 5875;
Best Local Similarity	70.9%;	Pred. No. 3.5e-11;		
Matches 122;	Conservative	0;	Mismatches 49;	Indels 1;
				Gaps 1;

QY 202 ATTCTTAACAGAAACAAACAGCCAGAGTTGA -GAGCAATTCACTCGGTACATTTCT 260

Db 3783 ATTCAGAGAGAAACACGACGCCGAGCTTGGAGCAACTTACGGGTAATCTCTACT 3844

QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTTCACTGTGATCTCTTCAATGGCGTTATCA 320

Db 3843 TTGTGGTTTTTATCATCTTGGCTCTTCTTTACCTGAACTCTTTATGGATGTTATTA 3902

QY 321 TTGACAACTTCAACCAACGACAGAAAAAGATAGTATCTGGGTGTCCTGAT 372

Db 3903 TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGTGGCCAAACATTTTAT 3954

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RESULT 5
US-09-840-125-3
: Sequence 13, Application US/09840125
: Patent No. US20020061524A1
: GENERAL INFORMATION:
: APPLICANT: Splawski, Igor
: TITLE OF INVENTION: Keating, Mark T.
: TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
: FILE REFERENCE: 2323-155
: CURRENT APPLICATION NUMBER: US/09/840,125
: CURRENT FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/634,920
: PRIOR FILING DATE: 2000-08-09
: PRIOR APPLICATION NUMBER: 60/147,488
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 6048
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(6048)
: US-09-840-125-3

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Query Match	18.7%	Score 76.4	DB 9	Length 6048
Best Local Similarity	71.0%	Pred. No. 8.8e-10		
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DB	4299	GTATGAGAGCAGCCTCAGTGGGAAATACAACCTCAGATGATCATCTATTGTGATTTT	4358	
QY	271	TATCATCTTGGCTAATTTTCACTCTGAATCTTTTCATTTGGCGTTATATTGAACATT	330	
DB	4358	CATCATCTTTGGGTCTTTCTTCAACCTGAACTCTTTATTTGGTGTGATCATATTGAACATT	4418	
QY	331	CACCAACAGCAGAAAAGATAGTATCTGGGGTTGCTTGAT	372	
DB	4419	CAACCAACAGAAAGAAAGTTTGGGGGCCAGAGCATCTTTTCAT	4460	

RESULT 6  
US-09-896-994-1  
; Sequence 1, Application US/09896994  
; Publication No. US2003007424A1  
; GENERAL INFORMATION:  
; APPLICANT: Ken Stokes  
; Jos e Morissette

1 TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
2 SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATMENT  
3  
4 NUMBER OF SEQUENCE ADDRESSES: 12  
5  
6 CORRESPONDENCE ADDRESS:  
7  
8 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1.r1s  
9  
10 STREET: One Liberty Place - 46th Floor  
11  
12 CITY: Philadelphia  
13  
14 STATE: PA  
15  
16 COUNTRY: U.S.A.  
17  
18 STD. NO. 16102

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Wordperfect 6.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/896,994
? FILING DATE: 02-Jul-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/514,907
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Paul K. Legaard
? REGISTRATION NUMBER: 38,534
? REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
? TELECOMMUNICATIONS INFORMATION:
? TELEPHONE: (215) 568-3100
? TELEFAX: (215) 568-3439
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 6048 bases
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-896-994-1

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Query Match	Best Local Similarity	18.7%;	Score 76.4;	DB 10;	Length 6048;	
Matches	Conservative	0;	Mismatches 46;	Indels 1;	Gaps 1;	
Qy	212	GAAGAA	CAACAGC	AGATTG	AGCAATCTACTGGTTACAT-TTCTTGTA	CTT 270
Db	4299	GTATGAAG	AGAGCGCTCAGTGG	AATCAACCTCTACATGTACATCTATTTGTTCATTTT		4358
Qy	271	TATCATCTTTGGC	CTATTCTTCACTCTG	AATCTCTTCACTTTGGCGT	ATCATTTGACAATT	330
Db	4359	CATCATCTTTGGG	CTTTCTTCTTCAACCCGTAA	CCCTTTTATTTGGTGTCA	TCATTTGACAACTT	4418
Qy	331	CAACCAACAG	CAAAAAAGATTA	GTATCTGGGTTGTCTTGAT		372
Db	4419	CAACCAACGA	AAAAAAGATTAGGGGGC	CAGACATCTTTCAAT		4460

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RESULT 7
US-10-077-054-1
: Sequence 1, Application US/10077054
: Publication No. US20030157660A1
: GENERAL INFORMATION:
: APPLICANT: Maklelski, Jonathan C
: APPLICANT: Ye, Bin
: TITLE OF INVENTION: Sodium Channel Alpha Subunits
: FILE REFERENCE: 960296, 98032
: CURRENT APPLICATION NUMBER: US/10/077,054
: CURRENT FILING DATE: 2002-02-12
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 6091
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

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NAME/KEY: CDS  
LOCATION: (10)..(6054)  
US-10-077-054-1

Query Match 18.7%; Score 76.4; DB 14; Length 6091;  
Best Local Similarity 71.0%; Pred. No. 8.9e-10;  
Matches 115; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

212 GAAAGAACAAACAGCAGGAGTTGAGCAATTCACGCTGATCAT-TTCTTCGTAGTCTT 270  
DB 4305 GTATGAAGAGAGCCTCAGTGGGAATACACCTCACTACATCTATTTTGTGATTTT 4364

271 TATCATCTTTGGCTCATCTTCTCACTGATCTCTTCAATGGCGTTATCATTCACAATT 330  
DB 4365 CATCATCTTTGGGCTTTCTTCACTGATCTCTTATTTGGTGCATCATTCAGCAACTT 4424

331 CAACCAACAGCAGAAAAGATATGATCTGAGTGTCTTGAT 372  
DB 4425 CAACCAACAGAAAAGATTAAGGGGCGCAGGACATCTTCAT 4466

RESULT 8  
US-10-101-510-617  
Sequence 617, Application US/10101510  
Publication No. US20030148295A1  
GENERAL INFORMATION:  
APPLICANT: WAN, JACKSON  
APPLICANT: WANG, YIXIN  
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
FILE REFERENCE: 15117.0012  
CURRENT APPLICATION NUMBER: US/10/101,510  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: 60/276,947  
PRIOR FILING DATE: 2001-03-20  
NUMBER OF SEQ ID NOS: 805  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 617  
LENGTH: 8490  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (6774)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7021)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7227)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7286)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7300)..(7301)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7477)..(7478)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (7538)  
OTHER INFORMATION: a, t, c, g, other or unknown  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (8167)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-101-510-617

Query Match 18.7%; Score 76.4; DB 14; Length 8490;  
Best Local Similarity 71.0%; Pred. No. 1.1e-09;  
Matches 115; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

212 GAAAGAACAAACAGCAGGAGTTGAGCAATTCACGCTGATCAT-TTCTTCGTAGTCTT 270  
DB 4449 GTATGAAGAGAGCCTCAGTGGGAATACACCTCACTACATCTATTTTGTGATTTT 4508

271 TATCATCTTTGGCTCATCTTCTCACTGATCTCTTCAATGGCGTTATCATTCACAATT 330  
DB 4509 CATCATCTTTGGGCTTTCTTCACTGATCTCTTATTTGGTGCATCATTCAGCAACTT 4568

331 CAACCAACAGCAGAAAAGATATGATCTGAGTGTCTTGAT 372  
DB 4569 CAACCAACAGAAAAGATTAAGGGGCGCAGGACATCTTCAT 4610

RESULT 9  
US-10-333-191-1  
Sequence 1, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
APPLICANT: Splawski, Igor  
TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
TITLE OF INVENTION: Arrhythmia  
FILE REFERENCE: 2323-154-II  
CURRENT APPLICATION NUMBER: US/10/333,191  
PRIOR FILING DATE: 2003-01-17  
CURRENT APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 8491  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 18.7%; Score 76.4; DB 15; Length 8491;  
Best Local Similarity 71.0%; Pred. No. 1.1e-09;  
Matches 115; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

212 GAAAGAACAAACAGCAGGAGTTGAGCAATTCACGCTGATCAT-TTCTTCGTAGTCTT 270  
DB 4449 GTATGAAGAGAGCCTCAGTGGGAATACACCTCACTACATCTATTTTGTGATTTT 4508

271 TATCATCTTTGGCTCATCTTCTCACTGATCTCTTCAATGGCGTTATCATTCACAATT 330  
DB 4509 CATCATCTTTGGGCTTTCTTCACTGATCTCTTATTTGGTGCATCATTCAGCAACTT 4568

331 CAACCAACAGCAGAAAAGATATGATCTGAGTGTCTTGAT 372  
DB 4569 CAACCAACAGAAAAGATTAAGGGGCGCAGGACATCTTCAT 4610

RESULT 10  
US-10-333-191-3  
Sequence 3, Application US/10333191  
Publication No. US20030235838A1  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
APPLICANT: Splawski, Igor



TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in Drug-induced Cardiac  
TITLE OF INVENTION: Arrhythmia  
FILE REFERENCE: 2323-154-II  
CURRENT APPLICATION NUMBER: US/10/333,191  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: PCT/US01/22639  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 60/219,738  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 3  
LENGTH: 8491  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(6198)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(8491)  
OTHER INFORMATION: n may be any base  
US-10-333-191-3

Query Match 18.7%; Score 76.4; DB 15; Length 8491;  
Best Local Similarity 71.0%; Fred. No. 1.1e-09;  
Matches 115; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

Qy 212 GAAAGACACAGCAGCAGGTTGAGAGCAATTCACGCTGATACAT-TTCTTCGTAGCTT 270  
Db 4449 GTAAGAGAGAGCAGCCTCAGTGGAGATACACCTACATGATCATCTTTTTCATTTT 4508  
Qy 271 TATCATCTTGGCTCATCTTCTCCTGATCTCTTCAATGCGCTTATCATGACAACTT 330  
Db 4509 CATCATCTTGGCTTCTTCTTCACTGACCTGATCTTATGCTGATCATGACAACTT 4568  
Qy 331 CAACCAACAGCAAAAGATATGATGTGGTGTCTTGAT 372  
Db 4569 CAACCAACAGCAAAAGATGAGGGCCAGGACATCTTCAT 4610

## RESULT 11

US-10-209-776-1  
Sequence 1, Application US/10209776  
Publication No. US20030096360A1  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
Delgado, Stephen G  
Fish, Linda M  
Sangameswaran, Lakshmi  
TITLE OF INVENTION: CLONED PERIPHERAL NERVE  
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Synex Corporation, Patent Department A2-200  
STREET: 3401 Hillview Avenue P.O. Box 10850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/209,776  
FILING DATE: 01-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,828  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Perles, Rohan  
REGISTRATION NUMBER: 35,752  
REFERENCE/DOCKET NUMBER: 28340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-852-1698  
TELEFAX: (415)-496-3529  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6344 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: Dorsal root ganglia  
CELL TYPE: Peripheral nerve  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-209-776-1

Query Match 17.2%; Score 70.4; DB 14; Length 6344;  
Best Local Similarity 66.9%; Fred. No. 3.7e-08;  
Matches 115; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Qy 202 ATTCTACAGAAAGAACACAGCCAGGTTGAGACCAATTCACGCTTACAT-TTCT 260  
Db 4158 ATTCGGAGAGATCAACAGTCAGCTTAACGAGGAGAACAACTTGATATGATCCTGATCT 4217  
Qy 261 TCGTACGCTTATCATCTTGGCTCATCTTCTCCTGATCTGATCTTCAATGGCGTTATCA 320  
Db 4218 TCGCGTTTCATCATTTTGGTGGCTTCTTCAAGCTGAATCTTTTGGGGCTCAATA 4277  
Qy 321 TTGCAACTTCAACCAACAGCAGAAAGATATCTGGGTGTCTTAT 372  
Db 4278 TCGCAACTTCAACCAACAGAAAGAAAGCTAGAGGCGCAGATCTTCAT 4329

## RESULT 12

US-10-202-824-1  
Sequence 1, Application US/10202824  
Publication No. US20030176648A1  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6524 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-202-824-1

Query Match 17.2%; Score 70.4; DB 14; Length 6524;  
Best Local Similarity 66.9%; Pred. No. 3.8e-08;  
Matches 115; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Db 202 ATTCTAAGAAAGAACAGCAGAGTTGAGAGCAATTCATCGGTTACAT-TTCT 260  
4342 ATTCGGAGAGATCAACAGTCAAGCTTAAGTGGAGAACACTGTACATGTAAGTACT 4401

Qy 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTGATCTGATCTCTTCAATGGCGTTATCA 320  
4402 TCGTGGTTTTCATCATTTTGGGCTTCTTCAAGCTGATCTTTGTTGGGGTCATTA 4461

Qy 321 TTGACAACTTCAACCAAGCAGGAAAAAGATAGTATCGGTTGCTTGAT 372  
Db 4462 TCGAACACTTCAACCAAGCAGGAAAAAGCTAGAGGCCAGGACATCTTCAT 4513

## RESULT 13

US-10-202-824-7

Sequence 7, Application US/10202824

Publication No. US20030176648A1

GENERAL INFORMATION:

APPLICANT: Wood, John N.

Akopian, Armen N.

TITLE OF INVENTION: Ion Channel

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: ZENECA Pharmaceuticals

STREET: 1800 Concord Pike, P.O. Box 15437

CITY: Wilmington

STATE: Delaware

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/202,824

FILING DATE: 26-Jul-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/669,656

FILING DATE: 24-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschultz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: PHM.70086

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-7466

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6527 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 204..6077  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-202-824-7

Query Match 17.2%; Score 70.4; DB 14; Length 6527;  
Best Local Similarity 66.9%; Pred. No. 3.8e-08;  
Matches 115; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Qy 202 ATTCTAAGAAAGAACAGCAGAGTTGAGAGCAATTCATCGGTTACAT-TTCT 260  
Db 4342 ATTCGGAGAGATCAACAGTCAAGCTTAAGTGGAGAACACTGTACATGTAAGTACT 4401

Qy 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTGATCTGATCTCTTCAATGGCGTTATCA 320  
Db 4402 TCGTGGTTTTCATCATTTTGGGCTTCTTCAAGCTGATCTTTGTTGGGGTCATTA 4461

Qy 321 TTGACAACTTCAACCAAGCAGGAAAAAGATAGTATCGGTTGCTTGAT 372  
Db 4462 TCGAACACTTCAACCAAGCAGGAAAAAGCTAGAGGCCAGGACATCTTCAT 4513

## RESULT 14

US-10-202-824-5

Sequence 5, Application US/10202824

Publication No. US20030176648A1

GENERAL INFORMATION:

APPLICANT: Wood, John N.

Akopian, Armen N.

TITLE OF INVENTION: Ion Channel

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: ZENECA Pharmaceuticals

STREET: 1800 Concord Pike, P.O. Box 15437

CITY: Wilmington

STATE: Delaware

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/202,824

FILING DATE: 26-Jul-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/669,656

FILING DATE: 24-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschultz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: PHM.70086

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-7466

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7052 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 204..6602

SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-202-824-5

Query Match 17.2%; Score 70.4; DB 14; Length 7052;  
Best Local Similarity 66.9%; Pred. No. 3.9e-08;  
Matches 115; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Qy 202 ATTCTAAGAAAGAACAGCAGAGTTGAGAGCAATTCATCGGTTACAT-TTCT 260

Job time : 280.501 secs

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Db 4927 TCGTCGTTTCATCATTTTGGTGGCTTCTTCACTGGAATCTTTGTTGGGCTCATTA 4986  
QY 321 TTGACAACTTCAACCAACGACGAAAAAGATAGATATCTGGGTTGCTTGAT 372  
Db 4987 TCGACAACTTCAACCAACGAAAAAGATAGAGGCGACGACATCTTCA 5038

RESULT 15

US-09-917-800A-1604  
; Sequence 1604, Application US/09917800A  
; Patent No. US20020119462A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5038-US  
; CURRENT APPLICATION NUMBER: US/09/917, 800A  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,040  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,880  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/290,029  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/290,645  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: US 60/292,336  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/295,798  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/297,457  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,884  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,459  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 1740  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1604  
; LENGTH: 6822  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_013119  
US-09-917-800A-1604

Query Match 17.0%; Score 69.6; DB 9; Length 6822;  
Best Local Similarity 66.9%; Pred. No. 6.3e-08;  
Matches 99; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 225 CCAAGTTTGAGCAATTCACGCTTACATTTCTCGTAGCTTTATCATCTTTGGCT 284  
Db 4573 CCAATATAGAAAGAACTGTACATGTACCTGTACTTGTCACTTCAATCTTGGCT 4632  
QY 285 CATTCTTCACTCTGAAATCTTTCATTTGGCGTTATCATGACACTTCAACCAAGCAGA 344  
Db 4633 CGTTCTTCACTCTAAATCTTATTCATCGGTTCATCATATGACACTTCAACCAAGCAGA 4692  
QY 345 AAAAGATAGATCTGGGTTGCTTGAT 372  
Db 4693 AGAAGTTTGAGGTCACAGACATCTTAT 4720

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## OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:45:54 ; Search time 3081.98 Seconds

(Without alignments)  
4669.435 Million cell updates/sec

Title: US-09-646-224A-15

Perfect score: 409  
Sequence: 1 atccaccgccgcgcgcga.....gtccctccaagaagaatcc 409Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 37577330 segs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Pending Patents NA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	100.0	409	27	US-09-646-224A-15
2	366	89.5	115159	103	US-60-466-412-84151
3	209.4	51.2	651	73	US-60-178-306-658
4	209.4	51.2	651	73	US-60-178-309-337
5	137.6	33.6	3163	77	US-60-213-846-1412
6	134.4	32.9	856	15	US-09-195-851-3
7	134.4	32.9	3701	1	PCT-US00-19342-6
8	134.4	32.9	3701	1	PCT-US99-02008-6
9	134.4	32.9	3701	50	US-10-388-470-6
10	134.4	32.9	5728	48	US-10-219-0518-910
11	134.4	32.9	5728	48	US-10-296-130-3
12	134.4	32.9	5860	1	PCT-US00-19342-41
13	134.4	32.9	5860	1	PCT-US03-08611-3
14	134.4	32.9	5860	50	US-10-388-470-41
15	134.4	32.9	5860	93	US-60-365-550-3
16	134.4	32.9	6237	108	US-60-516-609-317
17	134.4	32.9	6499	32	US-09-770-175-8399
18	134.4	32.9	6528	48	US-10-296-130-1
19	134.4	32.9	6528	105	US-60-485-101-251
20	126.6	31.0	201	103	US-60-466-412-152254
21	91.2	22.3	5833	45	US-10-144-771-19000
22	91.2	22.3	5833	93	US-60-360-207-19000
23	91	22.2	6925	76	US-60-207-214-72
24	88	21.5	5822	1	PCT-US00-19342-4
25	88	21.5	5822	1	PCT-US03-08611-5
26	88	21.5	5822	1	PCT-US99-02008-4
27	88	21.5	5822	50	US-10-388-470-4
28	88	21.5	5822	93	US-60-365-550-5
29	88	21.5	5858	46	US-10-180-934-1
30	88	21.5	5858	50	US-10-377-139-15
31	88	21.5	5858	105	US-60-485-101-345
32	86.8	21.2	5763	45	US-10-144-771-153
33	86.8	21.2	5763	93	US-60-360-207-153
34	85.2	20.8	637	30	US-09-718-355D-95
35	85.2	20.8	637	53	US-10-664-422-95
36	85.2	20.8	637	53	US-10-664-423-95
37	85.2	20.8	637	53	US-10-664-603-95
38	85.2	20.8	21347	79	US-60-230-445-440
39	84.2	20.6	567	73	US-60-173-463-161
40	84.2	20.6	788	77	US-60-213-177-25
41	84.2	20.6	788	79	US-60-230-445-136
42	84.2	20.6	1403	77	US-60-213-177-48
43	84.2	20.6	2358	79	US-60-233-937-245
44	84.2	20.6	13084	79	US-60-230-445-562
45	84.2	20.6	32768	76	US-60-207-583-274

## ALIGNMENTS

RESULT 1  
US-09-646-224A-15  
; Sequence 15, Application US/09646224A  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Wellcome PLC  
; APPLICANT: Tate, Simon N  
; APPLICANT: Grose, David T  
; APPLICANT: Hicks, Caroline A  
; TITLE OF INVENTION: Ion Channels  
; FILE REFERENCE: PG3432  
; CURRENT APPLICATION NUMBER: US/09/646, 224A  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: GB 9805793.8  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 409  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-646-224A-15

Query Match 100.0%; Score 409; DB 27; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1,1e-86;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCACCCAGGCCCCGCGCATGCACTCCCAAGCTGAGTGCAGAACTGAAAGAC 60  
DB 1 ATCCACCCAGGCCCCGCGCATGCACTCCCAAGCTGAGTGCAGAACTGAAAGAC 60  
QY 61 AGGCTCCCAAGGCGGCTATGCTGTAGAGAGGCTATGATCAATGTTGCTCTAA 120  
DB 61 AGGCTCCCAAGGCGGCTATGCTGTAGAGAGGCTATGATCAATGTTGCTCTAA 120  
QY 121 GAACACCTTGCTCTAGATGAATGATGATGATGATGATGATGATGATGATGATG 180  
DB 121 GAACACCTTGCTCTAGATGAATGATGATGATGATGATGATGATGATGATGATG 180  
QY 181 TTTTCTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 240  
DB 181 TTTTCTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 240  
QY 241 ATTCACCTGTTACATTTCTGATGCTTATCATCTTTGCTCATCTCTGAA 300  
DB 241 ATTCACCTGTTACATTTCTGATGCTTATCATCTTTGCTCATCTCTGAA 300  
QY 301 TCTCTCATGCGCTTATCATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 360  
DB 301 TCTCTCATGCGCTTATCATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 360  
QY 361 GGTGCTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 409  
DB 361 GGTGCTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 409

RESULT 2  
US-60-466-412-84151  
; Sequence 84151, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARILL, Michele  
; APPLICANT: IAKUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CLO01466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; PRIOR FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 429241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84151  
; LENGTH: 115159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1) ..(115159)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-466-412-84151

Query Match 89.5%; Score 366; DB 103; Length 115159;  
Best Local Similarity 97.8%; Pred. No. 1,1e-75;  
Matches 391; Conservative 1; Mismatches 6; Indels 2; Gaps 2;

QY 1 ATCCACCCAGGCCCCGCGCATGCACTCCCAAGCTGAGTGCAGAACTGAAAGAC 60  
DB 88428 ATCCACCCAGGCCCCGCGCATGCACTCCCAAGCTGAGTGCAGAACTGAAAGAC 88486  
QY 61 AGGCTCCCAAGGCGGCTATGCTGTAGAGAGGCTATGATCAATGTTGCTCTAA 120  
DB 88487 AGGCTCCCAAGGCGGCTATGCTGTAGAGAGGCTATGATCAATGTTGCTCTAA 88546  
QY 121 GAACACCTTGCTCTAGATGAATGATGATGATGATGATGATGATGATGATGATG 180  
DB 121 GAACACCTTGCTCTAGATGAATGATGATGATGATGATGATGATGATGATGATG 180

Db 88547 GAAACCTTGTCTTGTAGTAAGTAGTAGTATATTTTCTCCAGTATG 88606  
QY 181 TTTTCTTCTTATTAATAAATTTCTAACGAAAGACACAGCCGAGTTGAGCA 240  
Db 88607 TTTTCTTCTTATTAATAAATTTCTAACGAAAGACACAGCCGAGTTGAGCA 88666  
QY 241 ATTACAGGGTATCATTT-CTTGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGA 299  
Db 88667 ATTACAGGGTATCATTTCTTGTAGTCTTATCATCTTTGGCTCATCTTCACTCTGA 88726  
QY 300 ATCTCTTATTCGCGTATCATTCAGCAACTTCAACGACGAGAAAGATAGTATCT 359  
Db 88727 ATCTCTTATTCGCGTATCATTCAGCAACTTCAACGACGAGAAAGATAGTATCT 88786  
QY 360 GGGTGTCTTGAATTTGGTAAATGATCTCTGCTCCAAA 399  
Db 88787 GGGTGTCTTGAATTTGGTAAATGATCTCTGCTCCAAA 88826

RESULT 3  
US-60-178-306-658  
; Sequence 658, Application US/60178306  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,  
; FILE REFERENCE: CL000202  
; CURRENT APPLICATION NUMBER: US/60/178,306  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 1726  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 658  
; LENGTH: 651  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-178-306-658

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Matches 233; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 146 GTAGTTGAATGCTTATATTTTCTCCAGTATGTTTTTCTCTTATTAATAAATTT 205  
Db 1 GTAGTTGAATGCTTATATTTTCTCCAGTATGTTTTTCTCTTATTAATAAATTTCT 60  
QY 206 CTAAAGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGCT 264  
Db 61 AACGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGCT 120  
QY 265 AGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCATGTA 324  
Db 121 AGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCATGTA 180  
QY 325 CAACCTTAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 384  
Db 181 CAACCTTAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 240  
QY 385 TCTCTGCTCTCCAAA 399  
Db 241 TCTCTGCTCTCCAAA 255

RESULT 4  
US-60-178-309-337  
; Sequence 337, Application US/60178309  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000208  
; CURRENT APPLICATION NUMBER: US/60/178,309

; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 1012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 337  
; LENGTH: 651  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-178-309-337

Query Match 51.2%; Score 209.4; DB 73; Length 651;  
Best Local Similarity 91.4%; Pred. No. 3.5e-39;  
Matches 233; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 146 GTAGTTGAATGCTTATATTTTCTCCAGTATGTTTTTCTCTTATTAATAAATTT 205  
Db 1 GTAGTTGAATGCTTATATTTTCTCCAGTATGTTTTTCTCTTATTAATAAATTTCT 60  
QY 206 CTAAAGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGCT 264  
Db 61 AACGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGCT 120  
QY 265 AGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCATGTA 324  
Db 121 AGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCATGTA 180  
QY 325 CAACCTTAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 384  
Db 181 CAACCTTAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 240  
QY 385 TCTCTGCTCTCCAAA 399  
Db 241 TCTCTGCTCTCCAAA 255

RESULT 5  
US-60-213-846-1412  
; Sequence 1412, Application US/60213846  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1412  
; LENGTH: 3163  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-213-846-1412

Query Match 33.6%; Score 137.6; DB 77; Length 3163;  
Best Local Similarity 91.3%; Pred. No. 6.9e-22;  
Matches 157; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 202 ATTTCTAAGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGTTATCATTT-CT 260  
Db 2640 ATTTCTAAGAAAGACAGCAGGAGTTGAGCAATTCAGTTCGTTATCATTTACT 2699  
QY 261 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCA 320  
Db 2700 TCGTAGTCTTATCATCTTTGGCTCATCTTCACTGAACTCTTCAATGGCGTTATCA 2759  
QY 321 TTGCAACTTCAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 372  
Db 2760 TTGCAACTTCAACCAACAGCAAGAAAGATAGTATCTGGGTCTCTTGAATTTGGTATGTA 2811

RESULT 6  
US-09-195-851-3  
; Sequence 3, Application US/09195851

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 ; PRIOR FILING DATE: 1998-01-29  
 ; PRIOR APPLICATION NUMBER: US 60/109,402



PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 3701  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3699)  
OTHER INFORMATION: partial human Nan cDNA sequence  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (922)  
OTHER INFORMATION: Y = c or t. Xaa at amino acid position 308 is  
OTHER INFORMATION: Leu.  
US-10-388-470-6

Query Match 32.9%; Score 134.4; DB 50; Length 3701;  
Best Local Similarity 90.1%; Pred. No. 4.2e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACATT-CT 260  
DB 3206 ATTCCACAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACATTACT 3265

QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 320  
DB 3266 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 3325

QY 321 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 372  
DB 3326 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 3377

RESULT 10  
US-10-219-051B-910  
Sequence 910, Application US/10219051B  
GENERAL INFORMATION:  
APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
APPLICANT: Hospital / Bayer AG  
TITLE OR INVENTION: Nucleotide sequences involved in pain  
FILE REFERENCE: Lea 35693 Foreign Countries  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US/10/219,051B  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 60/312,147  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 60/346,382  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 60/333,347  
PRIOR FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 14715  
SOFTWARE: Perl script  
SEQ ID NO 910  
LENGTH: 5728  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(5728)  
OTHER INFORMATION: n=a, c, g or t  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: EMBL / AF150882  
DATABASE ENTRY DATE: 2000-01-16  
US-10-219-051B-910

Query Match 32.9%; Score 134.4; DB 47; Length 5728;  
Best Local Similarity 90.1%; Pred. No. 4.8e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
QY 202 ATTCTAAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACATT-CT 260

DB 4002 ATTCCACAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACTACT 4061  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 320  
DB 4062 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 4121

QY 321 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 372  
DB 4122 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 4173

RESULT 11  
US-10-296-130-3  
Sequence 3, Application US/10296130  
GENERAL INFORMATION:  
APPLICANT: KANAZAWA, Ichiro  
APPLICANT: GOTO, Jun  
APPLICANT: JEONG, Seon-Yong  
TITLE OR INVENTION: Human Sodium Channel SCN12A and SCN8A  
FILE REFERENCE: 2002-1512A/WMC/00653  
CURRENT APPLICATION NUMBER: US/10/296,130  
CURRENT FILING DATE: 2003-07-30  
PRIOR APPLICATION NUMBER: PCT/JP00/04629  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: JP2000-152085  
PRIOR FILING DATE: 2000-05-23  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 5728  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (200)..(4534)  
FEATURE:  
NAME/KEY: modified base  
LOCATION: 5632  
OTHER INFORMATION: n = a, g, c or t  
PUBLICATION INFORMATION:  
AUTHORS: Seon-Yong Jeong et al.  
TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel a Subunit  
JOURNAL: Biochem. Biophys. Res. Commun.  
VOLUME: 267  
ISSUE: 1  
PAGES: 262-270  
DATE: 2000-01-15  
DATABASE ACCESSION NUMBER: GenBank AF150882  
DATABASE ENTRY DATE: 2000-01-15  
US-10-296-130-3

Query Match 32.9%; Score 134.4; DB 48; Length 5728;  
Best Local Similarity 90.1%; Pred. No. 4.8e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACTACT 260  
DB 4002 ATTCCACAGAAAGAAACAGCCAGATTGAGCAATTCTCGGTTACTACT 4061

QY 261 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 320  
DB 4062 TCGTAGCTTTATCATCTTTGGCTCATCTTCTGAATCTCTGATGGCGTTATCA 4121

QY 321 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 372  
DB 4122 TTGACAACTTCAACCAACAGCAAGAAAGATAGTATCTGGCTTGTAT 4173

RESULT 12  
PCT-US00-19342-41  
Sequence 41, Application PC/TU0019342

GENERAL INFORMATION:  
APPLICANT: Yale University  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-02-WO  
CURRENT APPLICATION NUMBER: PCT/US00/19342  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/354,147  
PRIOR FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: full length cDNA sequence for human Nan  
PCT-US00-19342-41

Query Match 32.9%; Score 134.4; DB 1; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 4.9e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

DB 202 ATTTCTAACAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATT-CT 260  
DB 3833 ATTCACAGAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATTACT 3892  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320  
DB 3893 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3952  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 372  
DB 3953 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 4004

RESULT 13  
PCT-US03-08611-3  
Sequence 3, Application PC/TUS0308611  
GENERAL INFORMATION:  
APPLICANT: Transmolecular, Inc.  
APPLICANT: GONDA, Matthew A  
APPLICANT: GREENWOOD, John D  
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Chan  
FILE REFERENCE: 51530-5007-WO  
CURRENT APPLICATION NUMBER: PCT/US03/08611  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: US 60/365,550  
PRIOR FILING DATE: 2002-03-20  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION:  
PCT-US03-08611-3

Query Match 32.9%; Score 134.4; DB 1; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 4.9e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTTCTAACAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATT-CT 260  
DB 3833 ATTCACAGAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATTACT 3892  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320

DB 3893 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3952  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 372  
DB 3953 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 4004

RESULT 14  
US-10-388-470-41  
Sequence 41, Application US/10388470  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: full length cDNA sequence for human Nan  
US-10-388-470-41

Query Match 32.9%; Score 134.4; DB 50; Length 5860;  
Best Local Similarity 90.1%; Pred. No. 4.9e-21;  
Matches 155; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 202 ATTTCTAACAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATT-CT 260  
DB 3833 ATTCACAGAGAAAGAACAGCCAGAGTTGAGAGCAATTCACGCTTACATTACT 3892  
QY 261 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 320  
DB 3893 TCGTAGCTTTATCATCTTTGGCTCATTTCTCACTCTGAATCTCTTCAATGGCGTTATCA 3952  
QY 321 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 372  
DB 3953 TTGACAACTTCAACCAACAGCAAGAAAAGATATGATCTGGGTGCTTGAAT 4004

RESULT 15  
US-60-365-550-3  
Sequence 3, Application US/60365550  
GENERAL INFORMATION:  
APPLICANT: Transmolecular, Inc.  
APPLICANT: GONDA, Matthew A  
APPLICANT: GREENWOOD, John D  
APPLICANT: DIB-HAJJ, Sulayman D  
APPLICANT: WAXMAN, Steven G  
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Chan  
FILE REFERENCE: 51530-5007-PR  
CURRENT APPLICATION NUMBER: US/60/365,550  
CURRENT FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: 09/354,147  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/072,990



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NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 266  
LENGTH: 4855  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-266

Query Match 19.1%; Score 78; DB 7; Length 4855;  
Best Local Similarity 71.6%; Pred. No. 1.4e-11;  
Matches 116; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 212 GAAAGAACACAGCAGGATTGAGACAAATTCCTCGGTACAT-TTCTTCGTAGTCTT 270  
DB 3194 GATAGAAAGAGCCTCTGATGGAGATACACCTCTACATGATCATCTATTTTGTCAATTT 3253  
QY 271 TATCATCTTTGGCTCATTTCTTCACTCTGAATCTTTTCATTTGGCGTTATTCATGACAACTT 330  
DB 3254 CATCATCTTTGGGCTTTCTTCTTCACTGAACTTTTATTTGGTGTCAATGACAACTT 3313  
QY 331 CAACCAACAGCAAGAAAGATATGATCTGGGTGCTTGAT 372  
DB 3314 CAACCAACAGCAAGAAAGATACGGGGCCAGGACATCTTCAT 3355

RESULT 3  
US-60-548-091-268  
Sequence 268, Application US/60548091  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CLO01506  
CURRENT FILING DATE: 2004-02-27  
CURRENT APPLICATION NUMBER: US/60/548,091  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 268  
LENGTH: 4855  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-268

Query Match 19.1%; Score 78; DB 7; Length 4855;  
Best Local Similarity 71.6%; Pred. No. 1.4e-11;  
Matches 116; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 212 GAAAGAACACAGCAGGATTGAGACAAATTCCTCGGTACAT-TTCTTCGTAGTCTT 270  
DB 3194 GATAGAAAGAGCCTCTGATGGAGATACACCTCTACATGATCATCTATTTTGTCAATTT 3253  
QY 271 TATCATCTTTGGCTCATTTCTTCACTCTGAATCTTTTCATTTGGCGTTATTCATGACAACTT 330  
DB 3254 CATCATCTTTGGGCTTTCTTCTTCACTGAACTTTTATTTGGTGTCAATGACAACTT 3313  
QY 331 CAACCAACAGCAAGAAAGATATGATCTGGGTGCTTGAT 372  
DB 3314 CAACCAACAGCAAGAAAGATACGGGGCCAGGACATCTTCAT 3355

RESULT 4  
US-60-548-091-267  
Sequence 267, Application US/60548091  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CLO01506  
CURRENT FILING DATE: 2004-02-27  
CURRENT APPLICATION NUMBER: US/60/548,091  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 267

LENGTH: 4852  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-267

Query Match 18.7%; Score 76.4; DB 7; Length 4852;  
Best Local Similarity 71.0%; Pred. No. 3.7e-11;  
Matches 115; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 212 GAAAGAACACAGCAGGATTGAGACAAATTCCTCGGTACAT-TTCTTCGTAGTCTT 270  
DB 3191 GATAGAAAGAGCCTCTGATGGAGATACACCTCTACATGATCATCTATTTTGTCAATTT 3250  
QY 271 TATCATCTTTGGCTCATTTCTTCACTCTGAATCTTTTCATTTGGCGTTATTCATGACAACTT 330  
DB 3251 CATCATCTTTGGGCTTTCTTCTTCACTGAACTTTTATTTGGTGTCAATGACAACTT 3310  
QY 331 CAACCAACAGCAAGAAAGATATGATCTGGGTGCTTGAT 372  
DB 3311 CAACCAACAGCAAGAAAGATACGGGGCCAGGACATCTTCAT 3352

RESULT 5  
US-60-548-091-5535  
Sequence 5535, Application US/60548091  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CLO01506  
CURRENT FILING DATE: 2004-02-27  
CURRENT APPLICATION NUMBER: US/60/548,091  
NUMBER OF SEQ ID NOS: 24433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5535  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-548-091-5535

Query Match 17.7%; Score 72.4; DB 7; Length 201;  
Best Local Similarity 73.9%; Pred. No. 1.6e-10;  
Matches 105; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 212 GAAAGAACACAGCAGGATTGAGACAAATTCCTCGGTACAT-TTCTTCGTAGTCTT 270  
DB 59 GATAGAAAGAGCCTCTGATGGAGATACACCTCTACATGATCATCTATTTTGTCAATTT 118  
QY 271 TATCATCTTTGGCTCATTTCTTCACTCTGAATCTTTTCATTTGGCGTTATTCATGACAACTT 330  
DB 119 CATCATCTTTGGGCTTTCTTCTTCACTGAACTTTTATTTGGTGTCAATGACAACTT 178  
QY 331 CAACCAACAGCAAGAAAGATATGATCTGGGTGCTTGAT 372  
DB 179 CAACCAACAGCAAGAAAGATATGATCTGGGTGCTTGAT 372

RESULT 6  
US-10-487-337-1  
Sequence 1, Application US/10487337  
GENERAL INFORMATION:  
APPLICANT: Kenji OKUSE  
APPLICANT: Mark BAKER  
APPLICANT: Louis POON  
APPLICANT: John Nicholas WOOD  
APPLICANT: Mubashir Malik-HALL  
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS  
FILE REFERENCE: 117-492 / N.86242A GCW  
CURRENT FILING DATE: 2004-02-20  
CURRENT APPLICATION NUMBER: US/10/487,337  
PRIOR FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: PCT/GB02/03852  
PRIOR APPLICATION NUMBER: GB 0120238.1

PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 6524  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (204)..(6074)  
OTHER INFORMATION:  
US-10-487-337-1

Query Match 17.2%; Score 70.4; DB 6; Length 6524;  
Best Local Similarity 66.9%; Pred. No. 1.7e-09;  
Matches 115; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

QY 202 ATTCTAAGAAAGAACAGCAGAGTTGAGACAAATTCATCGGTACT-TTCT 260  
DB 4342 ATTCCGAGAGATCAACAGTACCTTAAGGAGAACTTGATGATGATCTACT 4401  
QY 261 TCGAGCTTTATCATCTTTGGCTCATTTCTCACTGAAATCTTCATTGGCGTTATCA 320  
DB 4402 TCGTCGTTTCATATTTTGGGTCTTTCACGCTGAATCTTTGTTGGGTCTATA 4461  
QY 321 TTGACAACTTCAACCAACAGCAAAAAAGATAGTATCTGGGTGCTTGAAT 372  
DB 4462 TCGCAACTTCAACCAACAGCAAAAAAGATAGTATCTGGGTGCTTGAAT 4513

RESULT 7  
US-10-487-337-5

Sequence 5, Application US/10487337  
GENERAL INFORMATION:  
APPLICANT: Kenji OKUSE  
APPLICANT: Mark BAKER  
APPLICANT: Louis POON  
APPLICANT: John Nicholas WOOD  
APPLICANT: Mubashir Malik-HALL  
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS  
FILE REFERENCE: 117-492 / N 86242A GCW  
CURRENT APPLICATION NUMBER: US/10/487,337  
CURRENT FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: PCT/GB02/03852  
PRIOR FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: GB 0120238.1  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 5874  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(5874)  
OTHER INFORMATION:  
US-10-487-337-5

Query Match 16.6%; Score 68; DB 6; Length 5874;  
Best Local Similarity 74.1%; Pred. No. 7.4e-09;  
Matches 86; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 257 TTCTTCGAGCTTTATCATCTTTGGCTCATTTCTCACTGAAATCTTCATTTGGCGTT 316  
DB 4189 TACTTTGATCTTCATATTTTGGAGGCTTTTCACACTGAATCTTTGTTGGGCTC 4248  
QY 317 ATCAATGCAACTTCAACCAACAGCAGAAAAAGATAGTATCTGGGTGCTTGAAT 372  
DB 4249 ATAAATGCAACTTCAACCAACAGAAAAAGATAGTATCTGGGTGCTTGAAT 4304

RESULT 8

US-60-545-213-3899  
Sequence 3899, Application US/60545213  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounes, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
TITLE OF INVENTION: Target Genes  
FILE REFERENCE: AM101083 (031896-042099)  
CURRENT APPLICATION NUMBER: US/60/545,213  
CURRENT FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3899  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-545-213-3899

Query Match 14.8%; Score 60.6; DB 7; Length 600;  
Best Local Similarity 68.3%; Pred. No. 3.5e-07;  
Matches 84; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 250 GTTACATTTCTTGTGATCTTTATCATCTTTGGCTCATTTCTCACTGAAATCTTCAT 309  
DB 396 GTATCTTACTTTGTTATTTTTCATCATCTTTGGGTCTTTTACCTTGAACCTGTTAT 455  
QY 310 TGGCGTTATCATTTGACAACTTCAACCAACAGCAAAAAAGATAGTATCTGGGTGCTT 369  
DB 456 TGGGTGATCATGATGATATTTTCAACGACAGAAAAAGATTTGAGGTCAAGACATCTT 515  
QY 370 GAT 372  
DB 516 TAT 518

RESULT 9

US-60-545-213-8171  
Sequence 8171, Application US/60545213  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounes, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042099)  
CURRENT APPLICATION NUMBER: US/60/545,213  
CURRENT FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8171  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-545-213-8171

Query Match 14.8%; Score 60.6; DB 7; Length 600;  
Best Local Similarity 68.3%; Pred. No. 3.5e-07;  
Matches 84; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 250 GTTACATTTCTTGTGATCTTTATCATCTTTGGCTCATTTCTCACTGAAATCTTCAT 309  
DB 396 GTATCTTACTTTGTTATTTTTCATCATCTTTGGGTCTTTTACCTTGAACCTGTTAT 455  
QY 310 TGGCGTTATCATTTGACAACTTCAACCAACAGCAAAAAAGATAGTATCTGGGTGCTT 369  
DB 456 TGGGTGATCATGATGATATTTTCAACGACAGAAAAAGATTTGAGGTCAAGACATCTT 515  
QY 370 GAT 372  
DB 516 TAT 518

RESULT 10  
US-60-548-091-5558

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; Sequence 5558, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001506
; CURRENT FILING DATE: 2004-02-27
; CURRENT APPLICATION NUMBER: US/60/548,091
; NUMBER OF SEQ ID NOS: 2443
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-5558

Query Match          11.6%; Score 47.6; DB 7; Length 201;
Best Local Similarity 80.0%; Pred. No. 0.0008;
Matches 56; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 303 TCTTATGGCGCTTATCATCTTGACCACTTCAACCAACAGAGAAAAGTAACTATCTGGG 362
DB 1 TCTTATGGCGCTTATCATCTTGACCACTTCAACCAACAGAGAAAAGTAACTATCTGGG 60
QY 363 TTGCTTGAT 372
DB 61 ACATCTTCAAT 70

RESULT 11
US-60-545-213-2996
; Sequence 2996, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2996
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-2996

Query Match          9.7%; Score 39.8; DB 7; Length 1400;
Best Local Similarity 67.5%; Pred. No. 0.19;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 256 TTCTTCGTAGCTTTATCATCTTGGCTCATCTTCACTGGAATCTTCTGATGGCGT 315
DB 38 TTACTTTGTTCTTCATCTTCTGCTGCTTTTGATGATGATCTTTGTGCGCGT 97
QY 316 TATCATTGACAACCTTCAACCAAC 338
DB 98 CATCATGACAACTTTGAGTACC 120

RESULT 12
US-60-545-213-2997
; Sequence 2997, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2997
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-2997

Query Match          9.7%; Score 39.8; DB 7; Length 1400;
Best Local Similarity 67.5%; Pred. No. 0.19;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 256 TTCTTCGTAGCTTTATCATCTTGGCTCATCTTCACTGGAATCTTCTGATGGCGT 315
DB 38 TTACTTTGTTCTTCATCTTCTGCTGCTTTTGATGATGATCTTTGTGCGCGT 97
QY 316 TATCATTGACAACCTTCAACCAAC 338
DB 98 CATCATGACAACTTTGAGTACC 120

RESULT 13
US-60-545-213-7268
; Sequence 7268, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7268
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-7268

Query Match          9.7%; Score 39.8; DB 7; Length 1400;
Best Local Similarity 67.5%; Pred. No. 0.19;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 256 TTCTTCGTAGCTTTATCATCTTGGCTCATCTTCACTGGAATCTTCTGATGGCGT 315
DB 38 TTACTTTGTTCTTCATCTTCTGCTGCTTTTGATGATGATCTTTGTGCGCGT 97
QY 316 TATCATTGACAACCTTCAACCAAC 338
DB 98 CATCATGACAACTTTGAGTACC 120

RESULT 14
US-60-545-213-7269
; Sequence 7269, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7269
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-7269

Query Match          9.7%; Score 39.8; DB 7; Length 1400;
Best Local Similarity 67.5%; Pred. No. 0.19;
```



Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 256 TTTCCTTGCTGCTCTTATCATCTTGGCTCATCTTCACTGTAATCTCTTCATTGGCGT 315  
DB 38 TTACTTGTTCCTTCATCTTCCTGCTGCTGCTTCTGATGCTGAATCTCTTGTGCGCGT 97

QY 316 TATCATGACACTTCAACCAAC 338  
DB 98 CATCATGACACTTGAATGATACC 120

## RESULT 15

US-10-021-698A-3499

; Sequence 3499, Application US/10021698A

; GENERAL INFORMATION:

; APPLICANT: KEITH, TIM

; APPLICANT: LITTLE, RANDALL

; APPLICANT: VAN EERDEWEGH, PAUL

; APPLICANT: DUPUIS, JOSEF

; APPLICANT: DEL MASTRO, RICHARD

; APPLICANT: SIMON, JASON

; APPLICANT: ALLEN, KRISTINA

; APPLICANT: PANDIT, SUNIL

; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO

; FILE REFERENCE: 2976-4044US1

; CURRENT APPLICATION NUMBER: US/10/021,698A

; CURRENT FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: 60/211,749

; PRIOR FILING DATE: 2000-06-14

; NUMBER OF SEQ ID NOS: 6160

; SOFTWARE: PatentIn 2.1

; SEQ ID NO 3499

; LENGTH: 8654

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-021-698A-3499

Query Match 9.7%; Score 39.8; DB 6; Length 8654;

Best Local Similarity 67.5%; Pred. No. 0.35;

Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 256 TTTCCTTGCTGCTCTTATCATCTTGGCTCATCTTCACTGTAATCTCTTCATTGGCGT 315  
DB 5621 TTACTTGTTCCTTCATCTTCCTGCTGCTGCTTCTGATGCTGAATCTCTTGTGCGCGT 5680

QY 316 TATCATGACACTTCAACCAAC 338  
DB 5681 CATCATGACACTTGAATGATACC 5703

Search completed: March 23, 2004, 04:50:36

Job time : 528.31 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 2399.71 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-15

Perfect score: 409  
Sequence: 1 atccaccgaagccgcgca.....gtccccaagaagaatcc 409

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1\_0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vic:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vil:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	91.2	22.3	1151	28	CC310778	TAM32-14H
2	83.8	20.5	518	28	B2141710	CH230-257
3	82.6	20.2	1079	28	CC313020	TAM32-16F
4	79.6	19.5	533	28	BH040362	RPT-24-3

5	79.2	19.4	633	14	CB457889	MA
6	79.2	19.4	692	13	BM385338	MA
7	78.4	19.2	480	12	BM494034	IPCBRT.1
8	75.6	18.5	908	13	BQ946179	AGENCOURT
9	75.6	18.5	4675	11	AK083220	Mus muscu
10	75.6	18.5	5666	29	AY416501	Mus muscu
11	75.6	18.5	5710	29	AY416500	Pan trogl
12	75.6	18.5	470	13	BQ359333	RC1-HN003
13	74.4	18.2	366	28	AQ037968	CIT-HSP-2
14	74.4	18.1	5943	29	AY416499	Homo sapi
15	72.8	17.8	763	14	CA358980	631834 NC
16	72.4	17.3	401	9	AL723537	AL723537
17	70.8	17.3	997	29	CNS0311D	Tetradon
18	70.4	17.2	521	14	CB720975	CB720975
19	70.4	17.2	574	14	CB608527	AMGNNUC:N
20	70.2	17.2	778	9	AU035605	AU035605
21	69.8	17.1	519	14	CB534807	768167 MA
22	69.8	16.9	655	14	CB110238	CB110238 K-EST0151
23	68.6	16.8	442	14	CB789718	AMGNNUC:C
24	68.2	16.7	688	12	BM650999	BM650999 170006873
25	68.2	16.7	754	13	BU877740	BU877740 603861203
26	68.2	16.6	689	10	BF347024	BF347024 602021819
27	67.6	16.5	502	12	BM633126	BM633126 170006875
28	67.6	16.4	615	12	AM133907	AM133907 f113c05.Y
29	62.6	15.3	421	13	BQ338035	BQ338035 CM4-NN008
30	59.2	14.5	283	10	BB387422	BB387422 BB387422
31	55.4	13.5	592	13	BM28334	BM28334 BM28334
32	55.4	13.5	651	13	BM252385	BM252385 BM252385
33	55.4	13.5	224	10	BM455509	BM455509 BM455509
34	53.8	13.2	751	13	BU226444	BU226444 603946353
35	51.4	12.6	840	28	CC075336	CC075336 CSU-K337
36	51.4	12.6	810	10	BB458095	BB458095 BB458095
37	50.6	12.4	311	10	CE171395	CE171395 t19t-988
38	48.6	11.9	737	29	CB761310	AMGNNUC:N
39	48.2	11.8	658	13	BE501378	BE501378 DKFZ07797
40	48.2	11.8	573	29	CE531906	CE531906 t19t-988
41	45.8	11.2	593	13	BM228855	BM228855 BM228855
42	45.2	11.1	901	29	CNS0760F	AL430789 clone XBA
43	44.8	11.0	708	29	CE293601	CE293601 t19t-988
44	44.8	11.0	775	29	CNS00A2L	AL054745 Drosophila
45	44.8	11.0	775	29	CNS00A2L	

## ALIGNMENTS

RESULT 1  
CC310778/c  
LOCUS  
DEFINITION  
TAM32-14H9, ECL.1 TAM32 gallus genomic clone TAM32-14H9,  
genomic survey sequence.  
ACCESSION  
CC310778  
VERSION  
CC310778.1 GI:30703926  
KEYWORDS  
GSS.  
SOURCE  
Gallus gallus (chicken)  
ORGANISM  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE  
1 (bases 1 to 1151)  
Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 152000 Std Error: 0.00  
Seq primer: ECL1 TACGACTCACTATAGGCGC  
Class: BAC ends  
High quality sequence start: 252  
High quality sequence stop: 872.

## FEATURES

source

Location/Qualifiers

1. .1151  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/strain="Red Jungle Fowl"  
/db\_xref="taxon:9031"  
/clone="TAM32-14H9"  
/sex="female"  
/cell\_line="UCD001, inbred 256"  
/note="Vector: pSCBAC1, Site 1: EcoRI, Site 2: EcoRI;  
TAM32 Female Chicken library - for library and clone  
ordering information: <http://www.hbz.tamu.edu>"

## ORIGIN

Query Match 22.3%; Score 91.2; DB 28; Length 1151;  
Best Local Similarity 58.7%; Pred. No. 4.3e-09;  
Matches 176; Conservative 0; Mismatches 123; Indels 1; Gaps 1;

QY 82 GCTGTAGGAGAGGCTATGTATGTCATGCTGCTAGAAACACCTTGCTCTTCTAGA 141  
DB 737 GCATTTACATTAAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 678  
QY 142 TAAGTACTAGATGCTATATTTTCTCCAGTAATTTTCTCTTATTAATAAAA 201  
DB 677 TAATTAATTAACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 618  
QY 202 ATTTCTAACAGAAAGAACACAGCCAGGTTGAGAGCAATTCAGTTCATTTCTT 261  
DB 617 ATATTTTCTAGATGATCAATCACTTAAGTATGAGACAACTGTACATGATCTTAT 558  
QY 262 C-GTAGCTTATCATCTTTGGCTCATCTCTGATCTGATCTCTTCAATGCGCTTACA 320  
DB 557 TTGTCTATCTTATCAATTTGGATCATCTTTTACATTTGACCTTTTCAATGCTGATTA 498  
QY 321 TTGACACTTCAACCAACAGCAGAAAGATATGATCTGGGCTCTTGTATTTGATAT 380  
DB 497 TAGACACTTCAACCAACAGCAGAAAGATATGATATTAATAATTTCTATATTTGCAT 438

RESULT 2  
B2141710 518 bp DNA linear GSS 11-OCT-2002  
LOCUS CH230-257H1.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone  
DEFINITION CH230-257H1, genomic survey sequence.  
ACCESSION B2141710.1 GI:23782657  
VERSION B2141710.1  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 518)  
Zhang, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K.,  
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D.,  
Riggs, P., de Jong, P., and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 MboI segment  
Unpublished (1999)  
Other GSSs: CH230-257H1.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [szhao@tigr.org](mailto:szhao@tigr.org)  
Clones are derived from the rat BAC library CHORI-230  
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@mail.choi.org](mailto:pdejong@mail.choi.org)).  
Clones may be purchased from BACPAC Resources  
(<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end  
page: [http://www.tigr.org/cdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html)

## FEATURES

source

Plate: 257 row: H column: 1  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers

1. .518  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SanHad/MCM"  
/db\_xref="taxon:10116"  
/clone="CH230-257H1"  
/sex="female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: pTARBAC1.3; Site 1: MboI, Site 2: MboI;  
CHORI-230 Rat (BN/SanHad/MCM) BAC library produced by  
Pieter de Jong"

## ORIGIN

Query Match 20.5%; Score 83.8; DB 28; Length 518;  
Best Local Similarity 66.5%; Pred. No. 1.8e-07;  
Matches 135; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

QY 203 TTCTAACAGAAAGAACACAGCCAGGTTGAGAGCAATTCAGTTCATTTCTT 261  
DB 215 TTTCTGACGTAATATGAACAGCCGAATACGAATACAGTCTTACATGATTCATTTCT 274  
QY 262 CGTAGCTTATCATCTTTGGCTCATCTCTGATCTGATCTCTTCAATGCGTATCAT 321  
DB 275 TGTCTTCTTCAATCTTGGCTCATCTTCTTCACTGTAACCTGTCATGAGTGATCAT 334  
QY 332 TGACAACTTCAACCAACAGCAGAAAGATATGATCTGGGCTCTTGTATTTGATAT 381  
DB 335 AGATATTTTCAACCAACAGCAGAAAGATATGATATCTTAGTTTCTTCAATGACGCA 394  
QY 382 GTATCTTGTCTCTCCAAAGAG 404  
DB 395 GAAAAAATGACATTCATGTAGG 417

RESULT 3  
CC313020/c 1079 bp DNA linear GSS 14-MAY-2003  
LOCUS TAM32-16F3 Sp6.1 TAM32 Gallus gallus genomic clone TAM32-16F3,  
DEFINITION genomic survey sequence.  
ACCESSION CC313020  
VERSION CC313020.1 GI:30707075  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 1079)  
Kremetzki, C., Hignobocham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E., and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
Insert Length: 152000 Std Error: 0.00  
Seq primer: Sp6 ATTTAGGTGACACTATAG  
Class: BAC ends  
High quality sequence start: 7  
High quality sequence stop: 775.  
Location/Qualifiers

## FEATURES

source

1. .1079  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/strain="Red Jungle Fowl"  
/db\_xref="taxon:9031"  
/clone="TAM32-16F3"



QY 259 CTGCTAGCTTTATCATCTTGGCTCATTCTGCAATCTCTTCAATGGCGTTAT 318  
DB 402 CTTTGTCATCTTCAATCATCTTGGCTCATTCTTCAATCTCTGCAATCTCTTCAATGGCGTTAT 461  
QY 319 CATTGACACTTCAACCAACAGCAGAAAAAGTAAATGATC 358  
DB 462 CATTGATACTTCAATCAACCAACAGAAAAAGTAAATGATC 501

RESULT 6  
B0385338 692 bp mRNA linear EST 28-NOV-2002  
LOCUS 6038587671 CSEQCHN75 Gallus gallus CDNA clone CHEST866g20 5', mRNA  
DEFINITION  
ACCESSION B0385338  
VERSION B0385338.1 GI:25893339  
KEYWORDS EST  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 692)  
Boardman, P.E., Sanz-Ezquerro, D., Overton, I.M., Burt, D.W., Bosch, E.,  
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
2235532  
12445392

TITLE  
JOURNAL  
MEDLINE  
PUBMED

COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
source  
1..692  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST866g20"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_1ib="CSEQCHN75"  
/note="Organ: trunks; Vector: Bluescript II KS(+);  
Site 1: EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following the first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
Bluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 19.4%; Score 79.2; DB 13; Length 692;  
Best Local Similarity 62.8%; Pred. No. 1.5e-06;  
Matches 123; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 177 ATTGTTTCTTCTTATTAATAAATTTCTAAGAAAGACACAGCCAGAGTTGAG 236  
DB 217 ATGGATATATATATATGCTGCAAGTTGATTCAGAGATGTAAGATCAACCTAAGATATGAG 276  
QY 237 AGCAATTCACCTGGTTACATTTCTTGATGCTTATATCATCTTGGCTCATCTTCACATC 296

DB 277 GACAACCTGATCANGATATCTTATTTGATCATATATATTTGATCATCTTTACAT 336  
QY 297 TGAATCTCTTATGAGGTTATCATCTTGAACCTCAACCAACAGCAAGAAAGTAAGTA 356  
DB 337 TGAACCTTTTATGAGGTTCTATTAAGCACTTCAACCAACCAAGAAAGTTGAG 396  
QY 357 TCTGGTTGCTTGTAT 372  
DB 397 GTCAGATATATTTAT 412

RESULT 7  
BM494034 480 bp mRNA linear EST 11-FEB-2002  
LOCUS BM494034  
DEFINITION  
ACCESSION BM494034  
VERSION BM494034.1 GI:18645215  
KEYWORDS EST  
SOURCE Ictalurus punctatus (channel catfish)  
ORGANISM Ictalurus punctatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
Ictaluridae; Ictalurus.  
1 (bases 1 to 480)  
Nonneman, D.J. and Waldbieser, G.C.  
Characterization of a brain cDNA library from adult channel catfish  
(Ictalurus punctatus)  
Unpublished (2002)  
Contact: Waldbieser GC  
Catfish Genetics Research Unit  
USDA-Agricultural Research Service  
141 Experiment Station Road, Stoneville, MS 38776, USA  
Tel: 662 686 3593  
Fax: 662 686 3567  
Email: gwaldbieser@ars.usda.gov  
Single pass sequencing. Bases called with Phred v0.000925.c. Low  
quality bases and vector trimmed with Lucy vl.16.  
Plate: Brl\_10 row: C column: 1  
Seq primer: M13 Reverse.

FEATURES  
source  
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Location/Qualifiers  
/organism="Ictalurus punctatus"  
/mol\_type="mRNA"  
/strain="USDAl03"  
/db\_xref="taxon:7998"  
/clone="IPGBrl\_10\_C01\_21\_06Mar00\_006"  
/sex="female and male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_1ib="Ictalurus punctatus Brain primary library"  
/note="Organ: brain; Vector: pSport1; Site\_1: Sal I;  
Site\_2: Not I; Primary library"

ORIGIN

Query Match 19.2%; Score 78.4; DB 12; Length 480;  
Best Local Similarity 69.8%; Pred. No. 2.4e-06;  
Matches 120; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

QY 202 ATTTTACAGAAAGAACACAGCAGAGTTGAGAGCAATTCACCTCGGTTACAT-TTCT 260  
DB 198 ATTCAGAGAGGTTAAGATCAACCGAAGTATGAAGATATCTCAATGATCATCTAT 257  
QY 261 TCGTAGTCTTATCATCTTGGCTCATCTTCACTTGAATCTCTTCAATGGCGTTATCA 320  
DB 258 TCGTATCTTATCATCTTGGCTCATCTTCACTTGAATCTCTTCAATGGCGTTATCA 317  
QY 321 TTGAACATTCACCAACAGCAAGCAAGAAAGATTAAGTATCTGGGTTCTTGAAT 372  
DB 318 TCAGCAATTCACCAACAGCAAGCAAGAAAGTTGAGGTCAGATATCTTCAAT 369

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BO946179	AGENCOURT_8926526 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5469275 5', mRNA sequence.	BO946179				Mus musculus (house mouse)
BO946179	EST	BO946179.1 GI:22361657				Mus musculus (house mouse)
REFERENCE	1. (bases 1 to 908) NIH-MGC http://mgs.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: http://image.llnl.gov Plate: L16ML1398 row: C column: 04 High quality sequence stop: 596. Location/Qualifiers					
FEATURES	source					
ORIGIN						
Query Match	18.5%; Score 75.6; DB 13; Length 908;					
Beet Local Similarity	68.4%; Pred.No. 7.9e-06;					
Matches	119; Conservative 0; Mismatches 54; Indels 1; Gaps 1					
Dy	200 AATTTCTTAACGAAAGAACAACACCGAAGTTTGAGAGCAATTCACTGGTTACAT-TT 258					
Dd	155 AGATTCGCCGAAGCCGGAACGACACGCTGATTATAGAGGCCAACATCTCATATACATCA 214					
Dy	259 CTTCGTAGCTTTATTCATTTTGGCTCATTTCTTCACTCTGAATCTCTTCATTCGGGTTAT 318					
Dd	215 CTTGCTCATTCTTCATCATCTTGGCTCTCTTCTTCAACCCTCAACTGTTTCATCGTGTCAT 274					
Dy	319 CATGCAACCTTCAACCAACAGCAGAAAAAGATAGTATCTGGGTTCCTTGAT 372					
Dd	275 CATCGCAATTTCAATCAACAGAAAGAAAGTTGGAGCTCAGACATCTTAT 328					
RESULT 9	AK083220	4675 bp	mRNA	linear	HTC 20-SEP-2000	
LOCUS						
DEFINITION	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C65002C19 product:sodium channel, voltage-gated, type VIII, alpha polypeptide, full insert sequence.					
ACCESSION	AK083220					
VERSION	AK083220.1 GI:26101130					
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Niishi, K., Kitanai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Iwawa, M., Obara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
MEDLINE	
PUBMED	5
REFERENCE	
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 4675)
PUBMED	Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hoshizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuhrara, C., Matsumura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahita, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Shuhiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, url: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details.
SOURCE	URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ location/Qualifiers 1. 4675 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J"

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/db\_xref="MGI:2417601"  
/db\_xref="taxon:10090"  
/clone="C630029C19"  
/sex="male"  
/tissue\_type="hippocampus"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
1..3589  
/note="putative sodium channel, voltage-gated, type VIII, alpha polypeptide [MGI:103169, GB|NM\_011323, evidence: BLASTN, 99%, match=3589]"

## ORIGIN

Query Match 18.5%; Score 75.6; DB 11; Length 4675;  
Best Local Similarity 68.4%; Pred. No. 5.2e-06;  
Matches 119; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 200 AAATTTCTAAGAGAAAGCAACAGCAGAGTTTGAGAGCAATTCACCTGGTTACAT-TT 258  
DB 1914 AGATTTCCGAAAGCCGAGACGACCTGATTTATAGGCGCAACATCTACATGATACATCTA 1973  
QY 259 CTTGCTAGCTTTTATCATCTTGGCTCATCTTTCATCTGATCTCTTCATTTGGCGTTAT 318  
DB 1974 CTTGCTATCTTTCATCATCTTGGCTCTCTTCTTCACTCACTGATCTGATGTCAT 2033  
QY 319 CATTGACAATTTCAACCAAGAGAGAAAAAGATAGTATCTGGGTGTTCTTGAT 372  
DB 2034 CATGCAATTTTCATCAACAGAGAAAAAGTTTGAGGTGACGACATCTTCAT 2087

RESULT 10  
LOCUS

AY416501 5666 bp DNA linear GSS 17-DEC-2003  
DEFINITION Mus musculus SCN8A gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION AY416501  
VERSION AY416501.1 GI:39772461  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 5666)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 5666)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

## TITLE

JOURNAL This sequence was made by sequencing genomic exons and ordering  
COMMENT them based on alignment.

## FEATURES

source  
1..5666  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
1..5666  
/gene="SCN8A"  
/locus\_tag="HMC5911"

## ORIGIN

Query Match 18.5%; Score 75.6; DB 29; Length 5666;  
Best Local Similarity 68.4%; Pred. No. 4.9e-06;  
Matches 119; Conservative 0; Mismatches 54; Indels 1; Gaps 1;  
QY 200 AAATTTCTAAGAGAAAGCAACAGCAGAGTTTGAGAGCAATTCACCTGGTTACAT-TT 258  
DB 3992 AGATTTCCGAAAGCCGAGACGACCTGATTTATAGGCGCAACATCTACATGATACATCTA 4051  
QY 259 CTTGCTAGCTTTTATCATCTTGGCTCATCTTTCATCTGATCTCTTCATTTGGCGTTAT 318  
DB 4052 CTTGCTATCTTTCATCATCTTGGCTCTCTTCTTCACTCACTGATCTGATGTCAT 4111  
QY 319 CATTGACAATTTCAACCAAGAGAGAAAAAGATAGTATCTGGGTGTTCTTGAT 372  
DB 4112 CATGCAATTTTCATCAACAGAGAAAAAGTTTGAGGTGACGACATCTTCAT 4165

RESULT 11  
LOCUS

AY416500 5710 bp DNA linear GSS 17-DEC-2003  
DEFINITION Pan troglodytes SCN8A gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION AY416500  
VERSION AY416500.1 GI:39772460  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1 (bases 1 to 5710)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 5710)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

JOURNAL This sequence was made by sequencing genomic exons and ordering  
COMMENT them based on alignment.

FEATURES  
source  
1..5710  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
1..5710  
/gene="SCN8A"  
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## TITLE

JOURNAL This sequence was made by sequencing genomic exons and ordering  
COMMENT them based on alignment.

## ORIGIN

Query Match 18.5%; Score 75.6; DB 29; Length 5710;  
Best Local Similarity 68.4%; Pred. No. 4.9e-06;  
Matches 119; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 200 AAATTTCTAAGAGAAAGCAACAGCAGAGTTTGAGAGCAATTCACCTGGTTACAT-TT 258  
DB 4269 AGATTTCCGAAAGCCGAGACGACCTGATTTATAGGCGCAACATCTACATGATACATCTA 4328  
QY 259 CTTGCTAGCTTTTATCATCTTGGCTCATCTTTCATCTGATCTCTTCATTTGGCGTTAT 318  
DB 4329 CTTGCTATCTTTCATCATCTTGGCTCTCTTCTTCACTCACTGATCTGATGTCAT 4388  
QY 319 CATTGACAATTTCAACCAAGAGAGAAAAAGATAGTATCTGGGTGTTCTTGAT 372  
DB 4389 CATGATAATTTTCATCAACAGAGAAAAAGTTTGAGGTGACGACATCTTCAT 4442



LOCUS	BO359333	470 bp	mRNA	linear	EST 20-MAY-2000
RESULT 12					
BO359333					
DEFINITION	RC1-HN0031-221100-012-f02 HN0031 Homo sapiens CDNA, mRNA sequence.				
ACCESSION	BO359333				
VERSION	BO359333.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 470) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, P.S., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, J.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202663				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?el=RC1ef2=RC1-HN0031 221100-012-f02ef3=2000-11-22ef4=1) Seq. primer: puc 18 forward High quality sequence stop: 470. Location/Qualifiers 1. 470 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_11b="HN0031" /note="Organ: head normal; Vector: puc18; Site: 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
FEATURES					
source					
ORIGIN					
Query Match	18.3%;	Score 75;	DB 13;	Length 470;	
Best Local Similarity	75.6%;	Pred. No. 1.2e-05;			
Matches	93;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;
250	GTACATTTCTCGTAGTCTTATCATCTTTGGCTCATCTTCACTGCAATCTCTTCAT	309			
266	GTACCTTACCTTTGTCATCTTCATCATCTTTGGCTCTCTTCACCTCAACCTCTTCAT	325			
310	TGGCTTATCATTTGACCACTTCAACCAACAGCAAGAAAAAGAAATGATCTGGCTGCTCT	369			
326	TGGCTTCATCATTTGACCACTTCAACCAACAGCAAGAAAGTTAGGGGGGAAAGACATCTT	385			
370	GAT 372				
386	TAT 388				
RESULT 13					

LOCUS	A0037988/c	366 bp	DNA	linear	GSS 11-JUL-1998
DEFINITION	CIT-HSP-2320K3.TF CIT-HSP Homo sapiens genomic clone 2320K3.				
ACCESSION	A0037988				
VERSION	A0037988.1 GI:303820				
KEYWORDS	GSS.				
ORGANISM	Homo sapiens (human)				
SOURCE	Homo sapiens				
REFERENCE	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Homnidae, Homo.				
AUTHORS	1 (bases 1 to 366) Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.				
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)				
JOURNAL	Unpublished (1998)				
COMMENT	Other GSSs: CIT-HSP-2320K3.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@reagen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends				
FEATURES	Location/Qualifiers				
SOURCE	1..366 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="2320K3" /sex="Male" /cell_type="Sperm" /clone_id="CIT-HSP" /note="Vector: pBelobAC11; site_1: HindIII; site_2: HindIII"				
ORIGIN	Query Match 18.2%; Score 74.4; DB 28; Length 366; Best Local Similarity 67.3%; Pred. No. 1.8e-05; Matches 105; Conservative 0; Mismatches 51; Indels 0; Gaps 0;				
OY	204	TTCTTACGAAAGAACACACAGCCGAGACTTGGAGAGCAATTCATCCGCTTACATTTCTCG	263		
Db	283	TTCTTTTAGTGAATTCACACCCAGTATGAGACCACTGTACATCATTTTATTTTG	224		
OY	264	TAGCTTTATCATCTTTGGGCTCATTTCTTCACTCGATGATCTTTCATTTGGCGTTATCAT	323		
Db	223	TCATCTTTATTTATTTTGGTTCATCTTTTACCTTGAATCTTTTTCATTTGATGATCATAG	164		
OY	324	ACAACTTCAACCAACAGACAGAAAAAGATAATCT	359		
Db	163	ATAACTCAACCAACGAAAAAGAAATAGTATAT	128		
RESULT 14					
LOCUS	AY416499				
DEFINITION	AY416499 5943 bp DNA linear GSS 17-DEC-2003				
ACCESSION	AY416499				
VERSION	AY416499.1 GI:39772459				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Homnidae, Homo.				

REFERENCE 1 (bases 1 to 5943)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civiello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.O., Snihsy,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 5943)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civiello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source location/Qualifiers  
1..5943  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>5943  
/gene="SCN8A"  
/locus\_tag="HCM5911"  
ORIGIN  
Query Match 18.1%; Score 74; DB 29; Length 5943;  
Best Local Similarity 67.8%; Pred. No. 1.1e-05;  
Matches 118; Conservative 0; Mismatches 55; Indels 1; Gaps 1;  
QY 200 AAATTCTTAAGAAAGCAACAGACAGAGTTTGAAGCAATTACTCGTTAAT-TT 258  
DB 4269 AGATTCCCGGAAGCCTGATGAGACAGCTTAAGTATAGAGCAATATCTACATGATCATCTA 4328  
QY 259 CTTCGAGCTCTTATCATCTTGGCTCATCTTCTGACTGATCTCTTCAATTTGGCTTAT 318  
DB 4329 TTTTGTCACTCTTCATCATCTTGGCTCTCTTCTTCACTGACCTGTAACCTGTTGATGTCAT 4388  
QY 319 CATTGACAACTTCAACCAAGACAGAAAAAGATTAAGTATCTGGTGTCTTGAT 372  
DB 4389 CATTGATTAATCTTCAATCAACAAAGAAAAAGTTGAGGTGATGACATCTTCAT 4442  
RESULT 15  
CA358980 763 bp mRNA linear EST 05-NOV-2002  
LOCUS 631834 NCCOWA 1RT Oncorhynchus mykiss cDNA clone 1RTSD21\_B\_B11 5',  
DEFINITION mRNA sequence.  
ACCESSION CA358980  
VERSION CA358980.1 GI:24604167  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)  
ORGANISM Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 763)  
Rexroad,C.E. and Keele,J.W.  
Sequence analysis of a rainbow trout normalized cDNA library  
Unpublished (2002)  
COMMENT Contact: Rexroad CE  
USDA, ARS, National Center for Cool and Cold Water Aquaculture  
11876 Leetown Road, Kearneysville, WV 25430, USA  
Tel: 304 724 8340 x2129  
Fax: 304 725 0351  
Email: crexroad@nccwa.ars.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified by  
cross match v0.990329.  
Seq primer: ACGGATACAAATTCACACAGGA.

FEATURES  
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/db\_xref="taxon:8022"  
/clone="1RTSD21\_B\_B11"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled tissue from brain, gill, liver,  
spleen, muscle, and kidney."  
ORIGIN  
Query Match 17.8%; Score 72.8; DB 14; Length 763;  
Best Local Similarity 68.2%; Pred. No. 3.2e-05;  
Matches 101; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 225 CCAGAGTTTGAGCAATTCACCTGCTTACATTTCTTGTAGTCTTTATTCATCTTGGCT 284  
DB 467 CCATCTATGAAGACAACTTACATGATACATCTTCTGATCTTCACTTTCATCTTGGAT 526  
QY 285 CATTCTTCACTCTGAATCTTCTTCAATTTGGCGTTATCATTTGACAACTTCAACCAAGCAGA 344  
DB 527 CTTCTTCACTCCCTCAACCTCTTCAATTTGGTGCATCATTTGACAACTTCAACCAAGAGAAA 586  
QY 345 AAAAGATTAATATCTGGGTGCTTGAT 372  
DB 587 AAAAGTTTGAGGTGACGAGCATCTTCAT 614  
Search completed: March 22, 2004, 23:13:10  
Job time : 2407.71 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 311.57 seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-16

Perfect score: 585  
Sequence: 1 tttccagaacaatacaagtc.....tgtgtgtgtgataaatttc 585

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_ov: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pln: \*  
35: em\_hcg\_rod: \*  
36: em\_hcg\_man: \*  
37: em\_hcg\_vtc: \*  
38: em\_ey: \*  
39: em\_hugo\_hum: \*  
40: em\_hugo\_mus: \*  
41: em\_hugo\_other: \*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585	100.0	585	6 AX017232	AX017232 Sequence
2	585	100.0	585	6 BD138454	BD138454 Mammalian
3	425.8	72.8	5728	6 BD012083	BD012083 Human sod
4	425.8	72.8	5728	6 BD082952	BD082952 Human sod
5	425.8	72.8	5728	6 AF150882	AF150882 Homo sapi
6	425.8	72.8	167476	9 AC116038	AC116038 Homo sapi
7	163.4	27.9	5419	9 HSA417790	AJ417790 Homo sapi
8	163.4	27.9	5860	6 AR340678	AR340678 Sequence
9	163.4	27.9	6237	9 AF186679	AF186679 Homo sapi
10	163.4	27.9	6528	6 BD012082	BD012082 Human sod
11	163.4	27.9	6528	6 BD082951	BD082951 Human sod
12	163.4	27.9	6528	9 AF109737	AF109737 Homo sapi
13	163.4	23.0	203255	2 AC117294	AC117294 Rattus no
14	134.8	23.0	210800	2 AC127824	AC127824 Rattus no
15	134.8	23.0	243048	2 AC127215	AC127215 Rattus no
16	131.4	22.5	3701	6 AR340648	AR340648 Sequence
17	131.4	22.5	3701	6 BD217793	BD217793 Regulatio
18	128.2	21.9	241289	2 AC124662	AC124662 Mus muscu
19	113	19.3	5822	6 AR340647	AR340647 Sequence
20	113	19.3	5822	6 BD217792	BD217792 Regulatio
21	113	19.3	5858	10 AF118044	AF118044 Mus muscu
22	112.8	19.3	5334	6 E36125	E36125 Nucleic aci
23	112.8	19.3	5849	10 RNO237852	RJ237852 Rattus no
24	112.8	19.3	5875	6 AR340646	AR340646 Sequence
25	112.8	19.3	5875	6 BD217791	BD217791 Regulatio
26	112.8	19.3	5897	6 AX017217	AX017217 Sequence
27	112.8	19.3	5897	6 BD138440	BD138440 Mammalian
28	112.8	19.3	5905	10 AF059030	AF059030 Rattus no
29	112.8	19.3	5908	6 E36122	E36122 Nucleic aci
30	112.6	19.2	5921	10 AB031389	AB031389 Mus muscu
31	86.6	14.8	103065	9 AC137625	AC137625 Homo sapi
32	84.2	14.4	8530	6 AX552195	AX552195 Sequence
33	82.2	14.1	227768	2 AC095653	AC095653 Rattus no
34	82.2	14.1	232042	2 AC128144	AC128144 Rattus no
35	82.2	14.1	247254	2 AC114844	AC114844 Rattus no
36	81.6	13.9	5874	6 AR253325	AR253325 Sequence
37	81.6	13.9	5874	6 AX252393	AX252393 Sequence
38	81.6	13.9	5874	6 AX710162	AX710162 Sequence
39	81.6	13.9	5874	9 AF117907	AF117907 Homo sapi
40	80.2	13.7	215113	10 AC104834	AC104834 Mus Muscu
41	80	13.7	192202	2 AC134315	AC134315 Lemur cat
42	79.4	13.6	193311	2 AC134403	AC134403 Mus muscu
43	78.8	13.5	291	9 HSSCN8A25	AF050735 Homo sapi
44	78.8	13.5	6826	6 AR181339	AR181339 Sequence
45	78.8	13.5	6826	10 RATSCEPA	L39018 Rattus norv

# ALIGNMENTS

RESULT 1	AX017232	585 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX017232				
DEFINITION	Sequence 16 from Patent WO947670.				
ACCESSION	AX017232				
VERSION	AX017232.1	GI:10042152			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Tate, S.N., Grose, D.T. and Hick, C.A.				
TITLE	Mammalian sodium channel proteins				
JOURNAL	Patent: WO 947670-A 16 23-SEP-1999;				

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS (GB) ; HICK CAROLINE ANNE (GB)  
Location/Qualifiers  
1. .585  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 585; DB 6; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.9e-131;  
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTTCCAGACAAATACAGAGTCTGCGTCCATAGCCAGGAGCTTTGACATCATC 60
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DB 61 ATAAAGCTCATACCTTAACCATGATGGCTTGATGGCTTAATATACAAACCAACCCCAAG 120
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DB 121 CCATGGAATCCATCCTTGACCATCTCCAACTGGGCTTTGGTGTATCTTTACGTTAGAA 180
OY 181 TGCTCATCAAAATCTTTGCTTTGAGGCAATCACTCTCAACCAATGGCGGAATTTATTT 240
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DB 541 AAAATTAAATGACTCAGAGTTTGTGGGTGTGAAAAATTTTC 585

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RESULT 2  
BD138454 585 bp DNA linear PAT 18-SEP-2002

DEFINITION Mammalian sodium channel protein.  
ACCESSION BD138454  
VERSION BD138454.1 GI:23233399  
KEYWORDS JP 2002508941-A/15.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Grose, D.T., Hick, C.A. and Tate, S.N.  
TITLE Mammalian sodium channel protein.  
JOURNAL Patent: JP 2002508941-A 15 26-MAR-2002;  
GLAXO GROUP LTD

COMMENT OS Homo sapiens (human)  
PN JP 2002508941-A/15  
PD 26-MAR-2002

PF 18-MAR-1999 JP 2000536853  
PR 18-MAR-1998 GB 9805793.8  
PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC  
C12N1/15,  
PC

C12N1/19, C12N1/21, C12N5/10, C12Q1/02, G01N33/15, G01N33/50, G01N33/PC  
68,  
PC C12N15/00, C12N5/00  
CC Mammalian sodium channel protein  
FH Key Location/Qualifiers  
FT source 1. .585  
/organism="Homo sapiens (human)".

FEATURES  
source 1. .585  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 585; DB 6; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.9e-131;  
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTTCCAGACAAATACAGAGTCTGCGTCCATAGCCAGGAGCTTTGACATCATC 60
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DB 61 ATAAAGCTCATACCTTAACCATGATGGCTTGATGGCTTAATATACAAACCAACCCCAAG 120
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DB 121 CCATGGAATCCATCCTTGACCATCTCCAACTGGGCTTTGGTGTATCTTTACGTTAGAA 180
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DB 301 TAAAGACCAAGATGATTTGTAATCTTATCATTTTGAAGTTGTTCAACATATCA 360
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DB 361 CAAAGCAGAAAACCTGGGCAAGTACTCTTGAAGAATAGACAGGGGTACTAATGCA 420
OY 421 TTCTCTACTGGGAAGTTGCTAGAGATAGAGCGGTAAATTTCTGTTCCCTTAATCTC 480
DB 421 TTCTCTACTGGGAAGTTGCTAGAGATAGAGCGGTAAATTTCTGTTCCCTTAATCTC 480
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DB 541 AAAATTAAATGACTCAGAGTTTGTGGGTGTGAAAAATTTTC 585

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RESULT 3  
BD012083 5728 bp DNA linear PAT 02-AUG-2002

DEFINITION Human sodium channel SCN12A and SCN8A.  
ACCESSION BD012083  
VERSION BD012083.1 GI:22092272  
KEYWORDS WO 0190355-A/2.  
SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 5728)
AUTHORS	Kanazawa, I., Goto, J., and Jeong, S.Y.
TITLE	Human sodium channel SCN12A and SCN4A
JOURNAL	Patent: WO 0190355-A 2 29-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON YONG JEONG
COMMENT	OS Homo sapiens (human) PN WO 0190355-A/2 PD 29-NOV-2001 PF 11-JUL-2000 WO 2000JP004629 PI 23-MAY-2000 JP 00P 152085 PC ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG C12N15/12, C07K14/47, C07K16/18
FEATURES	FT CDS Key Location/Qualifiers 1..5728 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
ORIGIN	Query Match 72.8%; Score 425.8; DB 6; Length 5728; Best Local Similarity 93.2%; Pred. No. 1.1e-92; Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;
Qy	70 TACCTAACCATTGTCCTGATGCGCTAAATATACCAACCAACCCAAAGCCATGAT 129
Db	4327 TATCTTAAACATGATGATGATGATGATGATGATGATGATGATGATGAT 4385
Qy	130 CCATCCTTGACCACTCCCACTGGGCTTTGGTGCATCTTATGATGATGATGAT 189
Db	4386 CCATCCTTGACCACTCCCACTGGGCTTTGGTGCATCTTATGATGATGATGAT 4444
Qy	190 AAAATCTTTGCTTTGAGGCAATACCTTCAACCAATGGCTGGAATTTATTTGACTGTG 249
Db	4445 AAAATCTTTGCTTTGAGGCAATACCTTCAACCAATGGCTGGAATTTATTTGACTGTG 4504
Qy	250 GTCGTGCTTTCTTCATTTGATGATGATGATGATGATGATGATGATGATGAT 309
Db	4505 GTCGTGCTTTCTTCATTTGATGATGATGATGATGATGATGATGATGATGAT 4564
Qy	310 GAATTAAGTTTGAATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 369
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Qy	370 AAATCTGGCCCAAGTATCTTCTGAAAGATGACAGGGGTACTAATGCAATCTCTACT 429
Db	4625 AAATCTGGCCCAAGTATCTTCTGAAAGATGACAGGGGTACTAATGCAATCTCTACT 4684
Qy	430 GGGAGTTGCTAGAGATGAGAGCGGTAATTTCTGTTCTCCCTTAATCACTACACAA 489
Db	4685 GGGAGTTGCTAGAGATGAGAGCGGTAATTTCTGTTCTCCCTTAATCACTACACAA 4738
Qy	490 CTGAATATGATGATCAATATCATGAGCTAATGATGATGATGATGATGATGATGAT 549
Db	4739 CTGAATATGATGATCAATATCATGAGCTAATGATGATGATGATGATGATGATGAT 4798
Qy	550 ATGACTCAGAAAGTTTGTGTGTGTGTAAGAAATTT 584
Db	4799 ATGACTCAGAAAGTTTGTGTGTGTGTAAGAAATTT 4833
RESULT 4	BD082952 5728 bp DNA linear PAT 27-AUG-2002
LOCUS	BD082952 Human sodium channel SCN12A.
DEFINITION	BD082952
ACCESSION	BD082952.1 GI:22628562

KEYWORDS	JP 2001327294-A/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 5728)
AUTHORS	Kanazawa, I., Goto, J., and Tei, Y.
TITLE	Human sodium channel SCN12A
JOURNAL	Patent: JP 2001327294-A 2 27-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT	OS Homo sapiens (human) PN JP 2001327294-A/2 PD 27-NOV-2001 PF 23-MAY-2000 JP 2000152085 PI ICHIRO KANAZAWA, JUN GOTO, YOSHITAKA TEI PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
FEATURES	FT CDS Key Location/Qualifiers 1..5728 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
ORIGIN	Query Match 72.8%; Score 425.8; DB 6; Length 5728; Best Local Similarity 93.2%; Pred. No. 1.1e-92; Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;
Qy	70 TACCTAACCATTGTCCTGATGCGCTAAATATACCAACCAACCCAAAGCCATGAT 129
Db	4327 TATCTTAAACATGATGATGATGATGATGATGATGATGATGATGATGAT 4385
Qy	130 CCATCCTTGACCACTCCCACTGGGCTTTGGTGCATCTTATGATGATGATGAT 189
Db	4386 CCATCCTTGACCACTCCCACTGGGCTTTGGTGCATCTTATGATGATGATGAT 4444
Qy	190 AAAATCTTTGCTTTGAGGCAATACCTTCAACCAATGGCTGGAATTTATTTGACTGTG 249
Db	4445 AAAATCTTTGCTTTGAGGCAATACCTTCAACCAATGGCTGGAATTTATTTGACTGTG 4504
Qy	250 GTCGTGCTTTCTTCATTTGATGATGATGATGATGATGATGATGATGATGAT 309
Db	4505 GTCGTGCTTTCTTCATTTGATGATGATGATGATGATGATGATGATGATGAT 4564
Qy	310 GAATTAAGTTTGAATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 369
Db	4565 GAATTAAGTTTGAATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 4624
Qy	370 AAATCTGGCCCAAGTATCTTCTGAAAGATGACAGGGGTACTAATGCAATCTCTACT 429
Db	4625 AAATCTGGCCCAAGTATCTTCTGAAAGATGACAGGGGTACTAATGCAATCTCTACT 4684
Qy	430 GGGAGTTGCTAGAGATGAGAGCGGTAATTTCTGTTCTCCCTTAATCACTACACAA 489
Db	4685 GGGAGTTGCTAGAGATGAGAGCGGTAATTTCTGTTCTCCCTTAATCACTACACAA 4738
Qy	490 CTGAATATGATGATCAATATCATGAGCTAATGATGATGATGATGATGATGATGAT 549
Db	4739 CTGAATATGATGATCAATATCATGAGCTAATGATGATGATGATGATGATGATGAT 4798
Qy	550 ATGACTCAGAAAGTTTGTGTGTGTGTAAGAAATTT 584
Db	4799 ATGACTCAGAAAGTTTGTGTGTGTGTAAGAAATTT 4833
RESULT 5	AF150882 5728 bp mRNA linear PRI 15-JAN-2000
LOCUS	AF150882 Homo sapiens voltage-gated sodium channel alpha subunit, alternate splice variant SCN12A-s (SCN12A) mRNA, complete cds.
DEFINITION	AF150882
ACCESSION	AF150882

VERSION AF150882.1 GI:6693704  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 AUTHORS Jeong, S.-Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,  
 Hirai, M., Ishihara, K., Uchiyama, Y. and Kanazawa, I.  
 TITLE Identification of a novel human voltage-gated sodium channel alpha  
 subunit gene, SCN12A  
 JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
 MEDLINE 20090626  
 PUBMED 10623608  
 REFERENCE 2 (bases 1 to 5728)  
 AUTHORS Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, J.  
 and Kanazawa, I.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,  
 Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan  
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 LOCUS Homo sapiens chromosome 3 clone RP11-134J21, complete sequence.  
 DEFINITION AC116038  
 ACCESSION AC116038.3 GI:37537604  
 VERSION HTG.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
 Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
 Haugen, E.D.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 167476)  
 AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 3 (bases 1 to 167476)  
 AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
 Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.  
 and Haugen, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 4 (bases 1 to 167476)  
 AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
 Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
 Haugen, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-OCT-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 COMMENT On Oct 7, 2003 this sequence version replaced gi:21622736.  
 ----- Genome Center  
 Center: University of Washington Genome Center  
 Center Code: UMG  
 Web site: http://www.genome.washington.edu

ORIGIN

Query Match 72.8%; Score 425.8; DB 9; Length 5728;  
 Best Local Similarity 93.2%; Pred. No. 1.le-92;  
 Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;

Qy 70 TACCTAAACCATGATGGCTTATGATGCTTAATATATACCAACCAACCAAGCATGAT 129  
 Db 4327 TATCTTAAACCATGATGATATGCTTAATATATACCAACCAACCAAGCATGAT 4385  
 Qy 130 CCATCTTGACCACTCAACTGGGCTTTGTGTGATCTTACGTAGATGTCATC 189

Contact: uwgchgs@u.washington.edu  
Project Information

Center project name: Chr-3  
Center clone name: Rpl1-13421 (bc0780)

Summary Statistics

Sequencing vector: plasmid; 100% of reads  
Chemistry: Dye-terminator RT; 45% of reads  
Chemistry: Dye-terminator Big Dye; 55% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 167467 bases at least Q40  
Consensus quality: 167476 bases at least Q30  
Consensus quality: 167476 bases at least Q20  
Insert size: 167476; sum-of-coverage  
Quality coverage: 18.9x in Q20 bases; sum-of-coverage

Overlapping Sequences:

5': Rpl1-114A3 AC137625, 2001-bp overlap  
3': Rpl1-182A24 (UMGC:bc0782) AC123903, 41341-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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-----	-----	-----	-----	-----	-----
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-----	-----	-----	-----	-----	-----
72	<800	1364	1346	4036	3992
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4175	4167	999	990	2583	2550
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72	<800	3014	3028	8136	8039

6640	6560	4721	4667	2738	2744
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4770	4771	727	745	4704	4629
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3468	3447	179	<800	2649	2744
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687	<800	7123	7158	2550	2550
-----	-----	-----	-----	-----	-----
3049	3091	2078	2040	5020	4862
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762	<800	1891	1888	6949	6960
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553	<800	8072	8171	4636	4629
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5080	5088	92	<800	3588	3544
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6613	6560	3674	3639	604	<800
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331	<800	240	<800	953	943
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2328	2299	5050	4878	4728	4629
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2038	2003	1053	1068	178	<800
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1368	1370	86	<800	694	<800
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182	<800	5444	5397	3022	3007
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1620	1560	1265	1228	4079	3992
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775	<800	438	<800	1294	1220
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19834	19753	475	<800	790	<800
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8729	8629	2310	2271	4232	4223
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2264	2299	5177	5089	336	<800
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651	<800	391	<800	4714	4629
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LOCUS Human sodium channel SCN12A and SCN8A.  
DEFINITION BD012082  
ACCESSION BD012082.1 GI:22092271  
VERSION WO 0190355-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Kanazawa, I., Goto, J. and Jeong, S. Y.  
AUTHORS Human sodium channel SCN12A and SCN8A  
TITLE Patent: WO 0190355-A 1 29-NOV-2001;  
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON YONG JEONG  
COMMENT OS Homo sapiens (human)  
PN WO 0190355-A/1  
PD 29-NOV-2001  
PF 11-JUL-2000 WO 2000JP004629  
PI 23-MAY-2000 JP 00P 152085  
PC ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG  
CC C12N15/12, C07K14/47, C07K16/18  
FH Key Location/Qualifiers  
FT CDS 1..6528  
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FEATURES  
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Best Local Similarity 93.7%; Pred. No. 3.6e-29;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 70 TACCTAAACCATGATGCTTGGCTTAATATATACCAACCCCAAGCCATGGAAT 129  
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DB 4386 CCATCCTGACCACT-CACTGGGCTTGTGGTCACTTAGAAGTCTCATC 4444  
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DB 4445 AAAATCTTGGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTGTG 4504  
QY 250 GTCGTGCTTCTTTCATTTAGTA 274  
DB 4505 GTCGTGCTTCTTTCATTTAGTA 4529

RESULT 11  
BD082951 6528 bp DNA linear PAT 27-AUG-2002  
LOCUS Human sodium channel SCN12A.  
DEFINITION

ACCESSION BD082951  
VERSION BD082951.1 GI:22628561  
KEYWORDS JP 2001327294-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Kanazawa, I., Goto, J. and Jeong, S. Y.  
AUTHORS Human sodium channel SCN12A  
TITLE Patent: JP 2001327294-A 1 27-NOV-2001;  
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001327294-A/1  
PD 27-NOV-2001  
PF 23-MAY-2000 JP 2000152085  
PI ICHIRO KANAZAWA, JUN GOTO, YOSHIOHITO TEI  
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
CC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00  
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FEATURES  
source  
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Best Local Similarity 93.7%; Pred. No. 3.6e-29;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 70 TACCTAAACCATGATGCTTGGCTTAATATATACCAACCCCAAGCCATGGAAT 129  
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QY 130 CCATCCTGACCACTGAGTCTTGGTGCATCTTAGCTGAATGCTCATC 189  
DB 4386 CCATCCTGACCACT-CACTGGGCTTGTGGTCACTTAGAAGTCTCATC 4444  
QY 190 AAAATCTTGGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTGTG 249  
DB 4445 AAAATCTTGGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTGTG 4504  
QY 250 GTCGTGCTTCTTTCATTTAGTA 274  
DB 4505 GTCGTGCTTCTTTCATTTAGTA 4529

RESULT 12  
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LOCUS Homo sapiens voltage-gated sodium channel alpha subunit SCN12A  
DEFINITION (SCN12A) mRNA, complete cds.  
ACCESSION AF109737  
VERSION AF109737.1 GI:6693696  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Kanazawa, I., Goto, J. and Jeong, S. Y.  
AUTHORS Human sodium channel SCN12A  
TITLE Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A  
JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
MEDLINE 20090626  
PUBMED 10623608  
REFERENCE 2 (bases 1 to 6528)  
AUTHORS Jeong, S. Y., Suzuki, T., Hashida, H., Masuda, N., Goto, J. and Kanazawa, I.  
TITLE Direct Submission

## JOURNAL

Submitted (27-NOV-1998) Neurology, Graduate School of Medicine,  
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

## FEATURES

## Source

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## ORIGIN

Query Match 27.9%; Score 163.4; DB 9; Length 6528;  
Best Local Similarity 93.7%; Pred. No. 3.6e-29;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
70 TACCTAAACATGATGGCTGATGGCTTAATATACACCAACCCCAAGCAT 129  
Db TACCTAAACATGATGGCTGATGGCTGATGATCTACACCAACCCCAAGCAT 4385  
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130 CCATCTTGAACATCTCCACTGGGCTCTTGTGTGATCTTTAGCTGAAGTGTCTATC 189  
Db CCATCTTGAACATCTCCACTGGGCTCTTGTGTGATCTTTAGCTGAAGTGTCTATC 4444  
4386 CCATCTTGAACATCTCCACTGGGCTCTTGTGTGATCTTTAGCTGAAGTGTCTATC 4444  
190 AAAATCTTGTGAGGCAATCTACTTCCCAATGGCTGGATTTATTTGATCTGTG 249  
Db AAAATCTTGTGAGGCAATCTACTTCCCAATGGCTGGATTTATTTGATCTGTG 4504  
4445 AAAATCTTGTGAGGCAATCTACTTCCCAATGGCTGGATTTATTTGATCTGTG 4504  
250 GTGCGCTCTCTTCCATGTTAGTA 274  
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## RESULT 13

## AC117294

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

AC117294 203255 bp DNA linear HTG 11-OCT-2002  
Rattus norvegicus clone CH230-251M17, WORKING DRAFT SEQUENCE, 2  
unordered pieces.

AC117294.5 GI:23681496  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 203255)

Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,  
Ayalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
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Devila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,  
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Niederhausen, A., Welts, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
Weinstock, G. and Gibbs, R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 203255)  
Worley, K.C.  
Direct Submission  
Submitted (10-APR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 203255)

## REFERENCE







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RESULT 2  
ID AAL42750 standard; cDNA; 5728 BP.

AC AAL42750;

DT 19-JUL-2002 (first entry)

DE Human sodium channel subunit SCN12A-s coding sequence.

Human, gene; ss, sodium channel subunit; SCN12A; SCN12A-s; SCN8A;  
human nervous system; chromosome 3p23-21.3; excitatory cell;  
drug development; familial hyperglycaemia; QT extending syndrome type 3;  
motor endplate disease.

OS Homo sapiens.

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/product= "Human sodium channel subunit SCN12A-s"

WO200190355-A1.

PD 29-NOV-2001.

PF 11-JUL-2000; 2000WO-JP004629.

PR 23-MAY-2000; 2000JP-00152085.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

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PI Kanazawa I, Goto J, Jeong S;
XX MPI: 2002-393394/42.
DR P-PSDB; AAO14926.
XX
XX Sodium channel alpha subunits SCN12A and SCN8A of human nervous system
XX together with splicing variants, useful in studying physiological
XX mechanism relating to excitatory cells and in drug development.
XX Claim 7; Page 55-70; 118bp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of three
XX sodium channel subunits from the human nervous system (SCN12A, SCN12A-s
XX and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and
XX the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel
XX subunit proteins are useful in studying physiological mechanisms relating
XX to excitatory cells and in drug development. The sodium ion channel
XX subunit proteins are useful for treating diseases such as familial
XX hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.
XX The present cDNA sequence encodes the human SCN12A-s sodium channel
XX subunit
XX
XX Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T; 0 U; 1 Other;
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XX Query Match 72.8%; Score 425.8; DB 6; Length 5728;
XX Best Local Similarity 93.2%; Pred. No. 3.4e-107;
XX Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;

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Db 4327 TATCTTAAACATGATGGCTGATGGCTTAATATACACCAACCCCAAGCCATGANT 4385
Oy 130 CCATCCTTGACATCTCCAACTGGGCTTTGGTGTATCTTTAGCTTAATGATGATC 189
Db 4386 CCATCCTTGACATCTCCAACTGGGCTTTGGTGTATCTTTAGCTTAATGATGATC 4444
Oy 190 AAAATCTTTGCTTGAAGCAATACTACTTCAACATGGCTGAATTTATTTGATGTGTG 249
Db 4445 AAAATCTTTGCTTGAAGCAATACTACTTCAACATGGCTGAATTTATTTGATGTGTG 4504
Oy 250 GTCGTGCTTTCTTCCATGTTAGTAATTAATAGCAGTCAAGGACCTTTAAGAACCA 309
Db 4505 GTCGTGCTTTCTTCCATGTTAGTAATTAATAGCAGTCAAGGACCTTTAAGAACCA 4564
Oy 310 GAAGTAATTTGTAATCTTATCAATTTTGAAGTTGTTCAACTATCCCAAGACAGA 369
Db 4565 GAAGTAATTTGTAATCTTATCAATTTTGAAGTTGTTCAACTATCCCAAGACAGA 4624
Oy 370 AAATCTGGCCAAAGTACTTCTGAAGAATAGACAGGGTACTAATGCCATTTCTTACT 429
Db 4625 AAATCTGGCCAAAGTACTTCTGAAGAATAGACAGGGTACTAATGCCATTTCTTACT 4684
Oy 430 GGGAAATTTGCTAGAGATAGAGCGGTAAATTTCTGTGTTCCCTTAATCTCACTACACA 489
Db 4685 GGGAAATTTGCTAGAGATAGAGCGGTAAATTTCTGTGTTCCCTTAATCTCACTACACA 4738
Oy 490 CTGAATATGATGATCAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 549
Db 4739 CTGAATATGATGATCAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 4798
Oy 550 ATGACTCAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
Db 4799 ATGACTCAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4833

```

RESULT 3  
ID AAF30101 standard; cDNA; 5860 BP.

AC AAF30101;

DT 30-APR-2001 (first entry)

XX

DE Human sodium channel Na<sub>v</sub> CDNA.  
XX Sodium channel; Na<sub>v</sub>; human; tetrodotoxin resistant; pain; paraesthesia;  
KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 31..5402  
FT /\*tag= a  
XX  
XX MO200105831-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 14-JUL-2000; 2000MO-US019342.  
XX  
XX 16-JUL-1999; 99US-00354147.  
XX  
XX (UYVA ) UNIV YALE.  
XX  
XX Dib-Hajj S, Waxman SG;  
XX  
XX WPI; 2001-103147/11.  
XX  
XX P-PSDB; AAB20121.  
XX  
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
PT channels, useful for preventing, diagnosing and treating pain,  
PT paraesthesia and/or hyperexcitability phenomena.  
XX  
XX  
XX Claim 1, Fig 11A, 162pp; English.  
XX  
XX The present sequence is that of cDNA encoding a novel human tetrodotoxin  
CC resistant sodium channel, termed Na<sub>v</sub> (see AAB20121). The cDNA was  
CC isolated from a human dorsal root ganglia tissue cDNA library by PCR  
CC amplification (see also AAF30122-23). Na<sub>v</sub> belongs to the a-subunit  
CC voltage-gated sodium channel protein family and produces a TTX-R sodium  
CC current. Such channels underlie the generation and propagation of  
CC impulses in excitable cells such as neurons and muscle fibres.  
CC Preferential expression of Na<sub>v</sub> on sensory neurons innervating the body  
CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
CC neurons, makes it a very useful target for diagnostic and/or therapeutic  
CC uses in relation to acute and/or chronic pain pathologies. A claimed  
CC method of treating pain, paraesthesia and/or hyperexcitability phenomena  
CC in a human or animal subject involves administering an agent that alters  
CC sodium current flow through Na<sub>v</sub> channels, or which modulates  
CC transcription or translation of Na<sub>v</sub> mRNA, in dorsal root ganglia or  
CC trigeminal neurons. Na<sub>v</sub> nucleic acids are used in gene therapy to correct  
CC disorders associated with decreased sodium channel expression or  
CC (antisense) to down-regulate Na<sub>v</sub> expression, in the diagnosis of disease,  
CC and in the recombinant production of Na<sub>v</sub> polypeptides  
XX  
XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
SQ  
Query Match 27.9%; Score 163.4; DB 4; Length 5860;  
Best Local Similarity 93.7%; Pred. No. 1.1e-34;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
XX  
XX 70 TACTTAACATGATGGCTTGAATGAGCTTAATATACACCAACCCCAAGCCATGGAAT 129  
DB 4158 TATCTTAACATGATGGCTTGAATGAGCTTATACACCA-CCCAAGCCATGGAAT 4216  
XX  
XX 130 CCATCTTGAACATCTCCAACTGGGCTTTGTGTCATCTTTAGTTAGAAATGTCATC 189  
DB 4217 CCATCTTGAACATCT-CAACTGGGCTTTGTGTCATCTTTAGTTAGAAATGTCATC 4275  
XX  
XX 190 AAAATCTTGTGTTGAGGCATATCTATCTCCCAATGGCTGGAATTTATTTGATGTGTG 249  
DB 4276 AAAATCTTGTGTTGAGGCATATCTATCTCCCAATGGCTGGAATTTATTTGATGTGTG 4335  
XX  
XX 250 GTGCTGCTCTTTCATCTGTTAGTA 274  
DB 4336 GTGCTGCTCTTTCATCTGTTAGTA 4360

RESULT 4  
ADD32193  
ID ADD32193 standard; cDNA; 5860 BP.  
XX  
XX  
XX ADD32193;  
AC  
XX  
XX 15-JAN-2004 (first entry)  
DT  
XX  
XX Human Na<sub>v</sub> 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
DE  
XX  
XX expression vector; Na<sub>v</sub> 1.9 sodium channel protein;  
KW sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH CDS 31..5406  
FH /\*tag= a  
FT /product= "Na<sub>v</sub> 1.9 sodium channel protein"  
XX  
XX MO2003080570-A2.  
XX  
XX 02-OCT-2003.  
XX  
XX 20-MAR-2003; 2003MO-US008611.  
XX  
XX 20-MAR-2002; 2002US-0365550P.  
XX  
XX (TRAN-) TRANSMOLECULAR INC.  
XX  
XX Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
XX  
XX P-PSDB; ADD32194.  
XX  
XX Expression vector useful for stable cloning and expression of Na<sub>v</sub> 1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Na<sub>v</sub> 1.9 sodium channel protein or its  
PT fragment.  
XX  
XX  
XX Disclosure; SEQ ID NO 3; 125pp; English.  
XX  
XX The present invention describes an expression vector comprising a nucleic  
CC acid sequence that encodes a mammalian Na<sub>v</sub> 1.9 sodium channel protein or  
CC its fragment, and producing a sodium current when transfected in a cell.  
CC Also described: (1) a recombinant cell comprising the plasmid selected  
CC from pRAN, pCMV-rAN-GFP, pLG338XM-rAN and the plasmid described above;  
CC (2) a method of making a cell or cell line that produces a Na<sub>v</sub> 1.9  
CC sodium channel-dependent sodium current by: (a) providing a cell that has  
CC been transfected with the expression vector; and (b) culturing the cell  
CC under conditions that allow expression of Na<sub>v</sub> 1.9 sodium channel protein  
CC to produce a sodium current into the transfected cell; (3) a method of  
CC screening for an agent that modulates sodium current in a cell by: (a)  
CC exposing the cell or cell line produced by the method to the agent; and  
CC (b) measuring sodium current following exposure to the agent, where an  
CC alteration in the level of sodium current is indicative of an agent  
CC capable of modulating sodium current in a cell; and (4) a recombinant  
CC cell comprising the expression vector. The expression vectors are useful  
CC for the stable cloning and expression of the Na<sub>v</sub> 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a human Na<sub>v</sub> 1.9 sodium channel protein, which  
CC is used in the exemplification of the present invention.  
XX  
XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
SQ  
Query Match 27.9%; Score 163.4; DB 9; Length 5860;  
Best Local Similarity 93.7%; Pred. No. 1.1e-34;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
XX  
XX 70 TACTTAACATGATGGCTTGAATGAGCTTAATATACACCAACCCCAAGCCATGGAAT 129

```
Db 4158 TATCCTAAACATGATAGCATGATGCGTGAATCATACACCA-CCAAAGCCATGAAT 4216
Qy 130 CCATCTTGACCATCTCCAACTGGGTCTTTGGTCACTTTAGCTTGAATGTCATC 189
Db 4217 CCATCTTGACCATCT-CAACTGGGTCTTTGGTCACTTTAGCTTGAATGTCATC 4275
Qy 190 AAAATCTTGCTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 249
Db 4276 AAAATCTTGCTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 4335
Qy 250 GTCGTCCTCTTCCATTTAGTA 274
Db 4336 GTCGTCCTCTTCCATTTAGTA 4360

RESULT 5
AAL42749
ID AAL42749 standard; cDNA; 6528 BP.
XX
AC AAL42749;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human sodium channel subunit SCN12A coding sequence.
XX
KW Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-g; SCN8A;
KW human nervous system; chromosome 3p23-21.3; excitatory cell;
KW drug development; familial hyperglycaemia; QT extending syndrome type 3;
KW motor endplate disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 200..5575
FT /tag= a
FT /product= "Human sodium channel subunit SCN12A"
XX
PN WO200190355-A1.
XX
PD 29-NOV-2001.
XX
PF 11-JUL-2000; 2000MO-JP004629.
XX
PR 23-MAY-2000; 2000JP-00152085.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI: 2002-393394/42.
DR P-FSDB; AAO14925.
XX
PT Sodium channel alpha subunits SCN12A and SCN8A of human nervous system
PT together with splicing variants, useful in studying physiological
PT mechanism relating to excitatory cells and in drug development.
XX
PS Claim 6; Page 29-46; 118pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequence of three
CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s
CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and
CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel
CC subunit proteins are useful in studying physiological mechanisms relating
CC to excitatory cells and in drug development. The sodium ion channel
CC subunit proteins are useful for treating diseases such as familial
CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.
CC The present cDNA sequence encodes the human SCN12A sodium channel subunit
XX
SQ Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;
Query Match 27.9%; Score 163.4; DB 6; Length 6528;
Best Local Similarity 93.7%; Pred. No. 1.2e-34;
```

```
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
Qy 70 TACCTAAACATGATAGCATGATGCGTGAATCATACACCA-CCAAAGCCATGAAT 129
Db 4327 TATCCTAAACATGATAGCATGATGCGTGAATCATACACCA-CCAAAGCCATGAAT 4385
Qy 130 CCATCTTGACCATCTCCAACTGGGTCTTTGGTCACTTTAGCTTGAATGTCATC 189
Db 4386 CCATCTTGACCATCT-CAACTGGGTCTTTGGTCACTTTAGCTTGAATGTCATC 4444
Qy 190 AAAATCTTGCTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 249
Db 4445 AAAATCTTGCTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 4504
Qy 250 GTCGTCCTCTTCCATTTAGTA 274
Db 4505 GTCGTCCTCTTCCATTTAGTA 4529

RESULT 6
AAK87602
ID AAK87602 standard; cDNA; 3638 BP.
XX
AC AAK87602;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human sodium channel NAN partial cDNA.
XX
KW Nan; sodium channel; ion transport; human; dorsal root ganglia; pain;
KW paraesthesia; hyperexcitability; therapy; SCN11a gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 200..5575
FT /tag= a
FT /product= "Human sodium channel subunit SCN12A"
XX
PN WO200190355-A1.
XX
PD 29-JAN-1999; 99MO-US002008.
XX
PF 29-JAN-1998; 98US-0072990P.
XX
PR 20-NOV-1998; 98US-0109402P.
XX
PA (UYVA ) UNIV YALE.
XX
PI Dib-Hajj S, Waxman S;
XX
DR WPI: 1999-479168/40.
DR P-FSDB; AAY06598.
XX
PT New isolated nucleic acids encoding sodium channels, used to develop
PT products for treating acute or chronic pain or hyperexcitability
PT phenomena.
XX
PS Claim 1; Fig 8A1-2; 91pp; English.
XX
CC This is the nucleotide sequence of a partial cDNA clone which codes for a
CC portion (see AAY06598) of human Nan, a previously unidentified voltage
CC gated sodium channel protein that is preferentially expressed in dorsal
CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R
CC sodium current. The Nan channel cDNA was obtained from human DRG tissue
CC cDNA by PCR amplification (see also AAK87620-22). Rat, mouse and human
CC Nan nucleic acids (see AAK87600-02) and polypeptides (see AAY06598-98)
CC are provided. The invention also includes expression vectors and
CC transformed host cells, methods for identifying tissues and cells that
CC express Nan, methods for identifying agents that modulate Nan channel
CC activity or Nan channel mRNA transcription or translation, and a method
CC for using such agents to treat acute or chronic pain, paraesthesia and
CC hyperexcitability phenomena. The preferential expression of Nan in
CC sensory DRG and trigeminal neurons provides a target for selectively
CC modifying the behaviour of these nerve cells while not affecting other
CC nerve cells in the brain and spinal cord. The gene is named SCN11a
```

SQ Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;  
 Query Match 22.5%; Score 131.4; DB 2; Length 3638;  
 Best Local Similarity 92.5%; Pred. No. 6.6e-26;  
 Matches 160; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
 QY 70 TACCTAAACCATGATGGCTTGATGGCTTAATATACACCAACCCCAAGCCATGGAAT 129  
 DB 3468 TATCTTAACATGATATGACATGATGCTGAATCATACACCA-CCCAAGCCATGGAAT 3526  
 QY 130 CCATCCTTGACCATCTCCCACTGGGCTTTGTGTCATCTTAGCTAGATGTCATC 189  
 DB 3527 CCATCCTTGACCATCT-CAACTGGGCTTTGTGTCATCTTAGCTAGATGTCATC 3585  
 QY 190 AAAATCTTGCTTTGAGGCAATACTACTTCCACCAATGGCTGGAATTATTGGA 242  
 DB 3586 AAAATCTTGCTTTGAGGCAATACTACTTCCACCAATGGCTGGAATTATTGGA 3638  
 RESULT 7  
 AAF30104  
 ID AAF30104 standard; cDNA; 3701 BP.  
 AC AAF30104;  
 XX 30-APR-2001 (first entry)  
 DT  
 XX Human sodium channel Nan partial cDNA.  
 DE  
 XX Sodium channel; Nan; human; tetrodotoxin resistant; pain; paraesthesia;  
 KW hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3639  
 FT /\*tag= a  
 FT /partial  
 FT  
 XX MO200105831-A1.  
 PN  
 PD 25-JAN-2001.  
 PF 14-JUL-2000; 2000MO-US019342.  
 XX  
 PR 16-JUL-1999; 99US-00354147.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI D1b-Hajj S, Waxman SG;  
 XX  
 XX WPI; 2001-103147/11.  
 DR P-PSDB; AAB20125.  
 XX  
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 FT channels, useful for preventing, diagnosing and treating pain,  
 PT paraesthesia and/or hyperexcitability phenomena.  
 XX  
 PS Example 4; Fig 8A; 162pp; English.  
 XX  
 CC The present sequence is that of a partial cDNA for a novel human  
 CC tetrodotoxin resistant sodium channel, termed Nan (see AAB20125). The  
 CC cDNA was isolated from a human dorsal root ganglia tissue library by  
 CC PCR amplification (see also AAF30122-23). A full-length sequence is given  
 CC in AAF30101. Human Nan belongs to the a-subunit voltage-gated sodium  
 CC channel protein family and produces a TTX-R sodium current. Such channels  
 CC underlie the generation and propagation of impulses in excitable cells  
 CC such as neurons and muscle fibres. Preferential expression of Nan on  
 CC sensory neurons innervating the body (dorsal root ganglia) and the face  
 CC (trigeminal ganglia), but not on other neurons, makes it a very useful  
 CC target for diagnostic and/or therapeutic uses in relation to acute and/or  
 CC chronic pain pathologies. A claimed method of treating pain, paraesthesia  
 CC and/or hyperexcitability phenomena in a human or animal subject involves

CC administering an agent that alters sodium current flow through Nan  
 CC channels, or which modulates transcription or translation of Nan mRNA, in  
 CC dorsal root ganglia or trigeminal neurons. Nan nucleic acids are used in  
 CC gene therapy to correct disorders associated with decreased sodium  
 CC channel expression or (antisense) to down-regulate Nan expression, in the  
 CC diagnosis of disease, and in the recombinant production of Nan  
 CC polypeptides  
 XX  
 SQ Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;  
 Query Match 22.5%; Score 131.4; DB 4; Length 3701;  
 Best Local Similarity 92.5%; Pred. No. 6.6e-26;  
 Matches 160; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
 QY 70 TACCTAAACCATGATGGCTTGATGGCTTAATATACACCAACCCCAAGCCATGGAAT 129  
 DB 3531 TATCTTAACATGATATGACATGATGCTGAATCATACACCA-CCCAAGCCATGGAAT 3589  
 QY 130 CCATCCTTGACCATCTCCCACTGGGCTTTGTGTCATCTTTAGCTAGATGTCATC 189  
 DB 3590 CCATCCTTGACCATCT-CAACTGGGCTTTGTGTCATCTTTAGCTAGATGTCATC 3648  
 QY 190 AAAATCTTGCTTTGAGGCAATACTACTTCCACCAATGGCTGGAATTATTGGA 242  
 DB 3649 AAAATCTTGCTTTGAGGCAATACTACTTCCACCAATGGCTGGAATTATTGGA 3701  
 RESULT 8  
 AAF30103  
 ID AAF30103 standard; cDNA; 5822 BP.  
 AC AAF30103;  
 XX 30-APR-2001 (first entry)  
 DT  
 XX Mouse sodium channel Nan cDNA.  
 DE  
 XX Sodium channel; Nan; Scn1a; mouse; tetrodotoxin resistant; pain;  
 KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;  
 diagnosis; ss.  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 19..5316  
 FT /\*tag= a  
 FT polyA\_signal 5789..5794  
 FT /\*tag= b  
 FT polyA\_site 5800..5822  
 FT /\*tag= c  
 FT  
 XX MO200105831-A1.  
 PN  
 PD 25-JAN-2001.  
 PF 14-JUL-2000; 2000MO-US019342.  
 XX  
 PR 16-JUL-1999; 99US-00354147.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI D1b-Hajj S, Waxman SG;  
 XX  
 XX WPI; 2001-103147/11.  
 DR P-PSDB; AAB20124.  
 XX  
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
 FT channels, useful for preventing, diagnosing and treating pain,  
 PT paraesthesia and/or hyperexcitability phenomena.  
 XX  
 PS Example 3; Fig 7A; 162pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding a novel mouse tetrodotoxin

CC resistant sodium channel, termed NaN (see AAB0124). The cDNA was  
CC isolated from trigeminal ganglia cDNA using primers (see AAF0120-21)  
CC based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN  
CC (see AAB0121). The gene encoding NaN, termed Scn1a, is located on mouse  
CC chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel  
CC protein family and produces a TTX-R sodium current. Such channels  
CC underlie the generation and propagation of impulses in excitable cells  
CC such as neurons and muscle fibres. Preferential expression of NaN on  
CC sensory neurons innervating the body (dorsal root ganglia) and the face  
CC (trigeminal ganglia), but not on other neurons, makes it a very useful  
CC target for diagnostic and/or therapeutic uses in relation to acute and/or  
CC chronic pain pathologies. A claimed method of treating pain, paraesthesia  
CC and/or hyperexcitability phenomena in a human or animal subject involves  
CC administering an agent that alters sodium current flow through NaN  
CC channels, or which modulates transcription or translation of NaN mRNA, in  
CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in  
CC gene therapy to correct disorders associated with decreased sodium  
CC channel expression or (antisense) to down-regulate NaN expression, in the  
CC diagnosis of disease, and in the recombinant production of NaN  
CC polypeptides  
CC  
SQ Sequence 5822 BP, 1499 A, 1425 C, 1362 G, 1535 T, 0 U, 1 Other;

Query Match 19.3%; Score 113; DB 4; Length 5822;  
Best Local Similarity 76.4%; Pred. No. 9.4e-21;  
Matches 152; Conservative 0; Mismatches 45; Indels 2; Gaps 1;

QY 76 AACCATGATGGCTGATGAGCTTAATATACACCAACCCCAAGCCATGATCATCC 135  
DB 4095 AACCATGATATCATGATGAGCTGAATCTGAAGCCAGCCC--AACGAAGTGAAGAAATC 4152  
QY 136 TTGACCATCTCCCACTGGGCTTTTGTCATCTTTAGCTGAATGCTCATCAAAATC 195  
DB 4153 TTGATATTTCTCAACATAGCTCTTGTGTCATCTTTACCTGATGATGCTCATCAAGTC 4212  
QY 196 TTGCTTTGAGGCAATACTACTTCAACCAATGCGTGAATTTATTTGACTGTGTCGTG 255  
DB 4213 TTGCTTTGAGGCAACACTACTTCAACCAATGCGTGAATTTATTTGATGTGTGTCGTG 4272  
QY 256 CTTCTTTCCATTTGATGA 274  
DB 4273 GTTCTTTCCATCATTAAGA 4291

RESULT 9  
ADD32195  
ID ADD32195 standard; cDNA; 5822 BP.

AC ADD32195;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:5.  
XX  
KW expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; mouse; gene; ss.  
XX  
OS Mus musculus.

XX Key Location/Qualifiers  
XX FH 19.5316  
XX FT CDS /\*tag= a  
XX FT /product= "Na v 1.9 sodium channel protein"  
XX  
XX WO2003080570-A2.  
XX  
XX PD 02-OCT-2003.  
XX  
XX PF 20-MAR-2003; 2003WO-US008611.  
XX  
XX PR 20-MAR-2002; 2002US-036550P.  
XX  
XX PA (TRAN-) TRANSMOLECULAR INC.

XX  
PI Gonda MA, Greenwood JD;  
XX WPI, 2003-876895/81.  
DR P-PSDB; ADD32196.  
XX

PT Expression vector useful for stable cloning and expression of Nav1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
PT fragment.

PS Disclosure; SEQ ID NO 5, 125pp; English.

XX  
XX The present invention describes an expression vector comprising a nucleic  
XX acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
XX its fragment, and producing a sodium current when transfected in a cell.  
XX Also described: (1) a recombinant cell comprising the plasmid selected  
XX from pNaN, pCMV-rNaN-GFP, pL338XN-rNaN and the plasmid described above;  
XX (2) a method of making a cell or cell line that produces a Na v 1.9  
XX sodium channel-dependent sodium current by: (a) providing a cell that has  
XX been transfected with the expression vector; and (b) culturing the cell  
XX under conditions that allow expression of Na v 1.9 sodium channel protein  
XX to produce a sodium current into the transfected cell; (3) a method of  
XX screening for an agent that modulates sodium current in a cell by: (a)  
XX exposing the cell or cell line produced by the method to the agent; and  
XX (b) measuring sodium current following exposure to the agent, where an  
XX alteration in the level of sodium current is indicative of an agent  
XX capable of modulating sodium current in a cell; and (4) a recombinant  
XX cell comprising the expression vector. The expression vectors are useful  
XX for the stable cloning and expression of the Na v 1.9 sodium channel at  
XX the mRNA and protein levels, and for producing sodium channel currents  
XX characteristic of native currents in dorsal root ganglion neurons. The  
XX present sequence encodes a mouse Na v 1.9 sodium channel protein, which  
XX is used in the exemplification of the present invention.

SQ Sequence 5822 BP, 1499 A, 1425 C, 1362 G, 1535 T, 0 U, 1 Other;  
Query Match 19.3%; Score 113; DB 9; Length 5822;  
Best Local Similarity 76.4%; Pred. No. 9.4e-21;  
Matches 152; Conservative 0; Mismatches 45; Indels 2; Gaps 1;

QY 76 AACCATGATGGCTGATGAGCTTAATATACACCAACCCCAAGCCATGATCATCC 135  
DB 4095 AACCATGATATCATGATGAGCTGAATCTGAAGCCAGCCC--AACGAAGTGAAGAAATC 4152  
QY 136 TTGACCATCTCCCACTGGGCTTTTGTCATCTTTAGCTGAATGCTCATCAAAATC 195  
DB 4153 TTGATATTTCTCAACATAGCTCTTGTGTCATCTTTACCTGATGATGCTCATCAAGTC 4212  
QY 196 TTGCTTTGAGGCAATACTACTTCAACCAATGCGTGAATTTATTTGACTGTGTCGTG 255  
DB 4213 TTGCTTTGAGGCAACACTACTTCAACCAATGCGTGAATTTATTTGATGTGTGTCGTG 4272  
QY 256 CTTCTTTCCATTTGATGA 274  
DB 4273 GTTCTTTCCATCATTAAGA 4291

RESULT 10  
ADD32209  
ID ADD32209 standard; cDNA; 5298 BP.

AC ADD32209;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Rat Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:19.  
XX  
KW expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; rat; gene; ss.  
XX  
XX Rattus norvegicus.

[illegible]

ID	AAx60244
AC	AAx60244 standard; cDNA; 5334 BP.
XX	
XX	AAx60244;
DT	11-AUG-1999 (first entry)
DE	Stabilised cDNA encoding type 5 sodium channel protein designated PNS.
XX	
XX	Type 5 sodium channel; PNS; nervous system; plexiform;
KW	dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
KW	diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
KW	neuropathic pain; migraine; headache; ss.
XX	
OS	Synthetic.
OS	Rattus sp.
XX	
PN	FR2771103-Al.
XX	
PD	21-MAY-1999.
XX	
PF	19-NOV-1998; 98FR-00014551.
XX	
PR	20-NOV-1997; 97US-0066225P.
XX	
PA	(HOFF ) HOFMANN LA ROCHE & CO AG F.
XX	
PI	Dietrich PS, Fish LM, Khare R, Robert DK, Sangameswaran L;
DR	WPI; 1999-315739/27.
XX	
PT	Isolated DNA encoding sodium channel of the nervous system.
XX	
PS	Example 7; Fig 5A-E; 90pp; French.
CC	
XX	The present sequence encodes a type 5 sodium channel protein designated
CC	PNS. The protein is a sodium ion channel of the nervous system, and is
CC	highly expressed in plexiform and dorsal root ganglia. The protein can be
CC	used to identify inhibitors of sodium channel proteins that are resistant
CC	to tetrodotoxin (TTX). The inhibitors are potentially useful for treating
CC	epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related
CC	neuropathy, and especially neuropathic pain, e.g. migraine and headache
XX	
SO	Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;
Query Match	19.3%; Score 112.8; DB 2; Length 5334;
Best Local Similarity	75.7%; Pred. No. 1e-20;
Matches 153; Conservative	0; Mismatches 47; Indels 2; Gaps 1;
OY	73 CTAAACCAGATTGGCTTGATGGCTTAATAATACCAACCAACCCGAAAGCATGAATCCA 132
DB	4094 CTTAATAATGATTTTCATGATGGCTGAATCGCGACGAGCCC--AAAAGATGTGAAGAA 4151
OY	133 TCCTTGCACATCTGCCACTGGGCTCTTTGGTCACTTTTAGTGAATGCTCATCAA 192
DB	4152 ACCTTTGATATCCCAACATAGCCCTTGCTGTCATCTTTACCATAGAGTGTCTATCAA 4211
OY	193 ATCTTGGCTTGAGGACAATACTACTTCACCAATGGCTGAATTTATTGACTGTGGTGC 252
DB	4212 GTCTTTGGCTTTGAGGACAACACTACTTCACTCACCAATGGCTGGAACCTTATTGATTGTGTC 4271
OY	253 GTGCTTCCTTTCCATGTGTAGA 274
DB	4272 GTGGTTCCTTTCTATCATTAGTA 4293
RESULT 12	
AAx87600	
ID	AAx87600 standard; cDNA; 5875 BP.
XX	
AC	AAx87600;
XX	
DT	26-OCT-1999 (first entry)

```

XX DE Rat sodium channel NaN cDNA.
XX
XX NaN, sodium channel, ion transport; rat, dorsal root ganglia; pain;
XX paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.
XX OS Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 41..5338
XX     /tag= a
XX     5551..5600
XX     /tag= b
XX /note= "these bases represent nucleotides missing from
XX the sequence given in Fig 1 of the specification. The
XX nucleotides are included to maintain the nucleotide
XX numbering given in the specification for this DNA
XX sequence"
XX
XX MO9938889-A2.
XX
XX 05-AUG-1999.
XX
XX 29-JAN-1999; 99WO-US002008.
XX
XX 29-JAN-1998; 98US-0072990P.
XX 20-NOV-1998; 98US-0109402P.
XX
XX (UYVA ) UNIV YALE.
XX
XX Dib-Hajj S, Waxman S;
XX
XX MPI. 1999-479168/40.
XX P-PSDB; AAY06596.
XX
XX New isolated nucleic acids encoding sodium channels, used to develop
XX products for treating acute or chronic pain or hyperexcitability
XX phenomena.
XX
XX Claim 1; Fig 1A-D; 91pp; English.
XX
XX This is the nucleotide sequence of an isolated nucleic acid which encodes
XX the rat NaN channel (see AAY06596), a previously unidentified voltage
XX gated sodium channel protein that is preferentially expressed in dorsal
XX root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R
XX sodium current. The NaN channel cDNA was obtained from Sprague-Dawley rat
XX DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse
XX and human NaN nucleic acids (see AAX87600-02) and polypeptides (see
XX AAY06596-98) are provided. The invention also includes expression vectors
XX and transformed host cells, methods for identifying tissues and cells
XX that express NaN, methods for identifying agents that modulate NaN
XX channel activity or NaN channel mRNA transcription or translation, and a
XX method for using such agents to treat acute or chronic pain, paraesthesia
XX and hyperexcitability phenomena. The preferential expression of NaN in
XX sensory DRG and trigeminal neurons provides a target for selectively
XX modifying the behaviour of these nerve cells while not affecting other
XX nerve cells in the brain and spinal cord. The NaN gene has been named
XX Scn1a
XX
XX Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;
XX
XX Query Match 19.3%; Score 112.8; DB 2; Length 5875;
XX Best Local Similarity 75.7%; Pred. No. 1.1e-20;
XX Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;
XX
XX 73 CTAAACCATGATGGCTGATGCGCTTAATATATACCAACCAACCAAGCCATGAAATCA 132
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 4111 CTTAATATGATATATATATATGCTGAATCTGCCACGACCC--AAATGTGAAGAA 4168
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 133 TCCATGACCATCTCCAACTGGGCTTTTGTGTCATCTTTAGCTTAGAATGTCATCAAA 192
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 4169 ACCTTGATATCTCTCAACATAGAGCTTCGTGTCATCTTACATAGAGTGTCTCATCAA 4228
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

OY 193 ATCTTGCTTGAGGACATACCTACCTCAACCATGGCTGGAATTTATTTGACTGTGGTC 252
DB 4229 GTCTTGCTTGAGGACCAACATCTACTTCACCATGGCTGGAATTTATTTGATGTGGTC 4288
OY 253 GTGCTTCTTTTCATGTTAGTA 274
DB 4289 GTGGTCTTTCTATCATATTAGTA 4310

RESULT 13
AAF30102
ID AAF30102 standard; cDNA; 5875 BP.
XX
XX AAF30102;
AC AAF30102;
DT 30-APR-2001 (first entry)
XX
XX Rat sodium channel NaN cDNA.
XX
XX Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia;
XX hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
XX
XX Rattus norvegicus.
XX
XX Key Location/Qualifiers
XX CDS 41..5338
XX     /tag= a
XX
XX MO200105831-A1.
XX
XX 25-JAN-2001.
XX
XX 14-JUL-2000; 2000WO-US019342.
XX
XX 16-JUL-1999; 99US-00354147.
XX
XX (UYVA ) UNIV YALE.
XX
XX Dib-Hajj S, Waxman SG;
XX
XX MPI. 2001-103147/11.
XX P-PSDB; AAB20122, AAB20123.
XX
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium
XX channels, useful for preventing, diagnosing and treating pain,
XX paraesthesia and/or hyperexcitability phenomena.
XX
XX Example 1; Fig 1, 162pp; English.
XX
XX The present sequence is that of cDNA encoding a novel rat tetrodotoxin
XX resistant sodium channel, termed NaN (see AAB20122). The cDNA was
XX isolated from a dorsal root ganglia tissue cDNA library by PCR
XX amplification using generic primers (from conserved regions of a-subunit
XX sodium channel proteins) and NaN-specific primers (see also AAF30105-19),
XX and RACE amplification. The open reading frame shows 73% similarity to
XX the human NaN sequence (see AAF30101). NaN belongs to the a-subunit
XX voltage-gated sodium channel protein family and produces a TTX-R sodium
XX current. Such channels underlie the generation and propagation of
XX impulses in excitable cells such as neurons and muscle fibres.
XX Preferential expression of NaN on sensory neurons innervating the body
XX (dorsal root ganglia) and the face (trigeminal ganglia), but not on other
XX neurons, makes it a very useful target for diagnostic and/or therapeutic
XX uses in relation to acute and/or chronic pain pathologies. A claimed
XX method of treating pain, paraesthesia and/or hyperexcitability phenomena
XX in a human or animal subject involves administering an agent that alters
XX sodium current flow through NaN channels, or which modulates
XX transcription or translation of NaN mRNA, in dorsal root ganglia or
XX trigeminal neurons. NaN nucleic acids are used in gene therapy to correct
XX disorders associated with decreased sodium channel expression or
XX (antisense) to down-regulate NaN expression, in the diagnosis of disease,
XX and in the recombinant production of NaN polypeptides
XX
XX Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;
XX

```



Query Match 19.3%; Score 112.8; DB 4; Length 5875;  
Best Local Similarity 75.7%; Pred. No. 1.1e-20;  
Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

QY 73 CTAACACGATGATGGCTTGATGGCTTAATATACACCAACCCCAAGCATGATCCA 132  
DB 4111 CTTAATATATGATATATCATGATGGCTGATCTGCCAGCACGCC--AAAGATGTGAAGAA 4168  
QY 133 TCCATGACCATCTCCCACTGGGCTTTGGTCATCTTTAGCTAGAAATGTCATCAA 192  
DB 4169 ACCTTGATATCTCCACATAGACCTTGTCATCTTTACATAGAGTGTCTATCAA 4228  
QY 193 ATCTTGCTTTGAGGCAATATCTTCCCAATGGCTGGAATTTATTTGACTGTGTGTC 252  
DB 4229 GTCTTGCTTTGAGGCAACACTACTTCCCAATGGCTGGAATTTATTTGATGTGTGTC 4288  
QY 253 GTGCTTCTTCCATTTGTTAGTA 274  
DB 4289 GTGGTCTTTCTATCATTTAGTA 4310

## RESULT 14

AAZ21480 ID AAZ21480 standard; CDNA, 5897 BP.

AAZ21480; AC

DT 03-DEC-1999 (first entry)

DE Rat sensory neurone specific 2a nucleotide sequence.

KW Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;  
voltage gated; hypersensitivity; ss.

OS Rattus sp.

FH Key Location/Qualifiers  
FT CDS 49..5346  
FT /tag= a  
FT /product= "sensory neurone specific 2a"

XX MO9947670-A1.

XX 23-SEP-1999.

XX PF 18-MAR-1999; 99WO-GB000838.

XX PR 18-MAR-1998; 98GB-00005793.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Grose DT, Hick CA, Tate SN;

XX DR WPI; 1999-562112/47.

XX DR P-PSDB; AA141668.

XX PT Mammalian sodium channel protein for treating pain and hypersensitivity.

XX PS Claim 4; Page 52-58; 73pp; English.

XX CC The present sequence encodes rat sensory neurone specific 2a (SNS-2a).

XX CC SNS-2a is a sodium channel protein. SNS-2a can be used in a method for

XX CC the identification of a modulator of a sodium channel, and for assaying

XX CC for compounds which modulate sodium flux. The sodium channel modulators

XX CC can be used in a medicament for the treatment of pain or hypersensitivity

XX SQ Sequence 5897 BP; 1474 A; 1471 C; 1435 G; 1517 T; 0 U; 0 Other;

XX Query Match 19.3%; Score 112.8; DB 2; Length 5897;  
Best Local Similarity 75.7%; Pred. No. 1.1e-20;  
Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

QY 73 CTAACACGATGATGGCTTGATGGCTTAATATACACCAACCCCAAGCATGATCCA 132  
DB 4119 CTTAATATATGATATATCATGATGGCTGATCTGCCAGCACGCC--AAAGATGTGAAGAA 4176  
QY 133 TCCATGACCATCTCCCACTGGGCTTTGGTCATCTTTAGCTAGAAATGTCATCAA 192  
DB 4177 ACCTTGATATCTCCACATAGACCTTGTCATCTTTACATAGAGTGTCTATCAA 4236  
QY 193 ATCTTGCTTTGAGGCAATATCTTCCCAATGGCTGGAATTTATTTGACTGTGTGTC 252  
DB 4237 GTCTTGCTTTGAGGCAACACTACTTCCCAATGGCTGGAATTTATTTGATGTGTGTC 4296  
QY 253 GTGCTTCTTCCATTTGTTAGTA 274  
DB 4297 GTGGTCTTTCTATCATTTAGTA 4318

## RESULT 15

ADB52929 ID ADB52929 standard; DNA, 5905 BP.

ADB52929; AC

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3471.

KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

KW toxicity marker; toxicity progression; drug screening;

KW primary rat hepatocyte toxicity modelling; gene; ds.

OS Rattus norvegicus.

PN MO2003065993-A2.

XX PD 14-AUG-2003.

XX PF 04-FEB-2003; 2003WO-US0003482.

XX PR 04-FEB-2002; 2002US-0353171P.

XX PR 13-MAR-2002; 2002US-0363534P.

XX PR 08-APR-2002; 2002US-0370248P.

XX PR 10-APR-2002; 2002US-0371134P.

XX PR 10-APR-2002; 2002US-0371135P.

XX PR 10-APR-2002; 2002US-0371150P.

XX PR 19-APR-2002; 2002US-0373601P.

XX PR 19-APR-2002; 2002US-0373602P.

XX PR 22-APR-2002; 2002US-0374139P.

XX PR 08-MAY-2002; 2002US-0378370P.

XX PR 09-MAY-2002; 2002US-0378652P.

XX PR 09-MAY-2002; 2002US-0378653P.

XX PR 09-MAY-2002; 2002US-0378665P.

XX PR 09-JUL-2002; 2002US-0394230P.

XX PR 09-JUL-2002; 2002US-0394253P.

XX PR 04-SEP-2002; 2002US-0407688P.

XX PR 28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elashoff M;

DR WPI; 2003-731472/69.

PT Determining if a compound induces a toxic effect on a tissue or cell, for

PT identifying hepatotoxic compounds, comprises comparing a gene expression

PT profile of a tissue or cell sample to a database of tox mean and non-tox

PT mean values.

PS Claim 44; SEQ ID NO 3471; 874pp; English.

XX The present invention describes a method for determining whether a

CC compound induces a toxic effect on a tissue or cell. The method comprises  
CC preparing a gene expression profile of a tissue or cell sample exposed to  
CC the compound, and comparing the gene expression profile to a database  
CC comprising data or information on the tox mean and non-tox mean value.  
CC The method is useful for predicting or identifying at least one toxic  
CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
CC genes listed in the specification are useful as diagnostic or toxicity  
CC markers for the prediction or identification of the physiological state  
CC of tissue or cell sample that has been exposed to a compound, or to  
CC identify or predict the toxic effects of a compound or an agent. These  
CC may also be used as markers for monitoring toxicity progression or for  
CC drug screening. The present sequence represents a primary rat hepatocyte  
CC toxicity modelling related gene sequence from the present invention.

XX  
SQ Sequence 5905 BP; 1476 A; 1471 C; 1439 G; 1519 T; 0 U; 0 Other;

Query Match 19.3%; Score 112.8; DB 9; Length 5905;

Best Local Similarity 75.7%; Pred. No. 1.1e-20;

Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

```
QY 73 CTAACCATGATGGCTTGAATGCGCTTAATATACAAACCAACCCCAAGCATGGAATCCA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4122 CTTAATATGATTATATCATGATGCTGAATCTGCCACGACGCC--AAAGATGGAAGAA 4179

QY 133 TCCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTTACGTTAGAAATGTCATCAA 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4180 ACCTTGATATCTCAACATAGCCCTTCGGTGCATCTTTACATAGAGTCTCATCAA 4239

QY 193 ATCTTTGCTTTGAGGCAATACTACTTCACCAATGGCTGGAATTATTGACTGTGTGTC 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4240 GTCTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAATTATTGATTTGTGTGTC 4299

QY 253 GTGCTTCTTTCCATGTTAGTA 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4300 GTGCTTCTTTCCATGTTAGTA 4321
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Job time : 425.441 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 19:33:04 ; Search time 358.296 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-16

Perfect score: 585  
Sequence: 1 ttccccagacatacaaggt.....tctgtgtgtagaataattc 585

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163.4	27.9	5860	US-10-388-470-41	Sequence 41, Appl
2	131.4	22.5	3701	US-10-388-470-6	Sequence 6, Appl
3	113	19.3	5822	US-10-388-470-4	Sequence 4, Appl
4	112.8	19.3	5875	US-10-388-470-1	Sequence 1, Appl
5	84.2	14.4	8530	US-10-220-120-104	Sequence 104, App
6	69.8	11.9	2573	US-10-202-824-3	Sequence 3, Appl
7	69.8	11.9	6344	US-10-209-776-1	Sequence 1, Appl
8	69.8	11.9	6524	US-10-202-824-1	Sequence 1, Appl
9	69.8	11.9	6527	US-10-202-824-7	Sequence 7, Appl
10	69.8	11.9	7052	US-10-202-824-5	Sequence 5, Appl
11	69.6	11.9	6048	US-09-840-125-3	Sequence 3, Appl
12	69.6	11.9	6048	US-09-896-994-1	Sequence 1, Appl
13	69.6	11.9	6091	US-10-077-054-1	Sequence 1, Appl
14	69.6	11.9	8490	US-10-101-510-617	Sequence 617, App
15	69.6	11.9	8491	US-10-333-191-1	Sequence 1, Appl

16	69.6	11.9	8491	US-10-333-191-3	Sequence 3, Appl
17	68.2	11.7	702	US-10-209-776-3	Sequence 3, Appl
18	67.4	11.5	264	US-09-864-761-27235	Sequence 27235, A
19	67.4	10.9	5889	US-09-930-871-3	Sequence 3, Appl
20	64	10.9	5922	US-09-930-871-13	Sequence 13, Appl
21	64	10.9	5997	US-09-930-871-1	Sequence 1, Appl
22	64	10.9	6027	US-10-297-022-40	Sequence 40, Appl
23	64	10.9	6030	US-09-930-871-11	Sequence 11, Appl
24	62.4	10.7	244	US-10-101-510-235	Sequence 235, App
25	61.2	10.5	6348	US-09-919-039-366	Sequence 366, App
26	61.2	10.5	6361	US-10-161-803-61	Sequence 61, Appl
27	61.2	10.5	6371	US-09-457-571-13	Sequence 13, Appl
28	61.2	10.5	6404	US-09-457-571-14	Sequence 14, Appl
29	60.4	10.3	6822	US-09-917-8008-1604	Sequence 1604, Ap
30	59.6	10.2	6328	US-10-161-803-60	Sequence 60, Appl
31	59.6	10.2	7028	US-10-101-510-630	Sequence 630, App
32	55.8	9.5	490	US-09-864-761-10615	Sequence 10615, A
33	55.8	9.5	6452	US-09-457-571-9	Sequence 9, Appl
34	52.6	9.0	3033	US-09-457-571-1	Sequence 1, Appl
35	52.2	8.9	6315	US-09-428-371-2	Sequence 2, Appl
36	52.2	8.9	6318	US-09-428-371-1	Sequence 1, Appl
37	49.6	8.5	5482	US-10-429-681-2	Sequence 2, Appl
38	41.2	7.0	6189	US-10-221-714A-321	Sequence 321, App
39	41.2	7.0	6189	US-10-240-485-145	Sequence 145, App
40	38.6	6.6	688	US-10-429-516A-5	Sequence 5, Appl
41	38.6	6.6	1749	US-10-429-516A-9	Sequence 9, Appl
42	38.6	6.6	1857	US-10-369-493-29360	Sequence 29360, A
43	38.6	6.6	3584	US-10-250-821-15	Sequence 15, Appl
44	38.6	6.6	3590	US-10-250-821-14	Sequence 14, Appl
45	38.6	6.6	3598	US-10-250-821-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-10-388-470-41  
Sequence 41, Application US/10388470  
Publication No. US20030228662A1  
GENERAL INFORMATION:  
APPLICANT: Ddb-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
PRIOR FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: full length cDNA sequence for human NAN  
US-10-388-470-41

Query Match 27.9%; Score 163.4; DB 15; Length 5860;  
Best Local Similarity 93.7%; Pred. No. 1.2e-34;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
Db 4158 TACTTAACCATGATGGCTGATGCTTAATATACCAACCAACCAAGCATGGAAT 129  
70 TACTTAACCATGATGGCTGATGCTTAATATACCAACCAACCAAGCATGGAAT 129  
4158 TACTTAACCATGATGGCTGATGCTTAATATACCAACCAACCAAGCATGGAAT 4216

QY 130 CCATCCTGACCAATCCAGCTGGCTTTGGTGCATCTTACGTAGATGCTCATC 189  
 DB 4217 CCATCCTGACCAATCT-CACCTGGCTTTGGTGCATCTTACGTAGATGCTCATC 4275  
 QY 190 AAAATCTTTGCTTGGAGCAATACTACTTCAACCAATGCTGGAATTTTGGACTGTG 249  
 DB 4216 AAAATCTTTGCTTGGAGCAATACTACTTCAACCAATGCTGGAATTTTGGACTGTG 4335  
 QY 250 GTCGCTCTTCTTCATTTAGTA 274  
 DB 4336 GTCGCTCTTCTTCATTTAGTA 4360

## RESULT 2

US-10-388-470-6  
 ; Sequence 6, Application US/10388470  
 ; Publication No. US20030228662A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dib-Hajj, Sulayman  
 ; APPLICANT: Waxman, Stephen G.  
 ; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
 ; FILE REFERENCE: 44574-5004-01-US  
 ; CURRENT APPLICATION NUMBER: US/10/388,470  
 ; PRIOR FILING DATE: 2003-03-17  
 ; PRIOR APPLICATION NUMBER: US/09/354,147C  
 ; PRIOR FILING DATE: 1999-07-16  
 ; PRIOR APPLICATION NUMBER: US 60/072,990  
 ; PRIOR FILING DATE: 1998-01-29  
 ; PRIOR APPLICATION NUMBER: US 60/109,402  
 ; PRIOR FILING DATE: 1998-11-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/02008  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 3701  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3699)  
 ; OTHER INFORMATION: partial human NaN cDNA sequence  
 ; NAME/KEY: unsure  
 ; LOCATION: (922)  
 ; OTHER INFORMATION: y = c or t. Xaa at amino acid position 308 is  
 ; OTHER INFORMATION: Leu.  
 ; US-10-388-470-6

Query Match 22.5%; Score 131.4; DB 15; Length 3701;  
 Best Local Similarity 92.5%; Pred. No. 8e-26;  
 Matches 160; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
 QY 70 TACCAACCAATGCTTGGTGGCCCAATATATACCAACCAACCAAGCCATGAGAT 129  
 DB 3531 TATCTTAACATGATTAGCATATGCTGAATCAATCAACCA-CCCAAGCCATGAGAT 3589  
 QY 130 CCATCCTTGGAGCAATCTCAACTGGCTTTGGTGCATCTTACGTAGATGCTCATC 189  
 DB 3590 CCATCCTTGGAGCAATCT-CACTGGGCTTTGGTGCATCTTACGTAGATGCTCATC 3648  
 QY 190 AAAATCTTTGCTTGGAGCAATCTTACCAATGCTGGAATTTATTTGA 242  
 DB 3649 AAAATCTTTGCTTGGAGCAATCTTACCAATGCTGGAATTTATTTGA 3701

RESULT 3  
 US-10-388-470-4  
 ; Sequence 4, Application US/10388470  
 ; Publication No. US20030228662A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Waxman, Stephen G.  
 ; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
 ; FILE REFERENCE: 44574-5004-01-US  
 ; CURRENT APPLICATION NUMBER: US/10/388,470  
 ; PRIOR FILING DATE: 2003-03-17  
 ; PRIOR APPLICATION NUMBER: US/09/354,147C  
 ; PRIOR FILING DATE: 1999-07-16  
 ; PRIOR APPLICATION NUMBER: US 60/072,990  
 ; PRIOR FILING DATE: 1998-01-29  
 ; PRIOR APPLICATION NUMBER: US 60/109,402  
 ; PRIOR FILING DATE: 1998-11-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/02008  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 5822  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (19)..(5313)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (5804)  
 ; OTHER INFORMATION: cDNA sequence of mouse NaN, n = a or c or g or t  
 ; US-10-388-470-4

Query Match 19.3%; Score 113; DB 15; Length 5822;  
 Best Local Similarity 76.4%; Pred. No. 1.4e-20;  
 Matches 152; Conservative 0; Mismatches 45; Indels 2; Gaps 1;  
 QY 76 AACATGATTTGGCTTGAATGCTTAATATACCAACCAACCAAGCCATGATCCATCC 135  
 DB 4095 AACATGATTTGAATGCTTGAATGCTTGAAGCCAGCC--AACGATGATGAATTC 4152  
 QY 136 TTGACATCTCCACTGGGCTTTGGTGCATCTTACGTAGATGCTCATCAAAATC 195  
 DB 4153 TTGATATCTCCACATAGTCTTGGTGCATCTTACCGTAGTGTCTATCAAAATC 4212  
 QY 196 TTTGCTTGGAGCAATACTACTTCAACCAATGCTGGAATTTATTTGACTGTGCTG 255  
 DB 4213 TTTGCTTGGAGCAACTACTTCAACCAATGCTGGAATTTATTTGATGTGTGCTG 4272  
 QY 256 CTTCTTCCATTTTATTA 274  
 DB 4273 GTTCTTCCATCATTTAGTA 4291

## RESULT 4

US-10-388-470-1  
 ; Sequence 1, Application US/10388470  
 ; Publication No. US20030228662A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dib-Hajj, Sulayman  
 ; APPLICANT: Waxman, Stephen G.  
 ; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
 ; FILE REFERENCE: 44574-5004-01-US  
 ; CURRENT APPLICATION NUMBER: US/10/388,470  
 ; PRIOR FILING DATE: 2003-03-17  
 ; PRIOR APPLICATION NUMBER: US/09/354,147C  
 ; PRIOR FILING DATE: 1999-07-16  
 ; PRIOR APPLICATION NUMBER: US 60/072,990  
 ; PRIOR FILING DATE: 1998-01-29  
 ; PRIOR APPLICATION NUMBER: US 60/109,402  
 ; PRIOR FILING DATE: 1998-11-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/02008  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 5875  
 ; TYPE: DNA

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: ORGANISM: Rattus norvegicus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (41)..(5335)
: OTHER INFORMATION: cDNA sequence for rat Nan
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1986)..(4042)
: OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
: OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1354 is Asn
: OTHER INFORMATION: or Lys.
US-10-388-470-1

Query Match      19.3%; Score 112.8; DB 15; Length 5875;
Best Local Similarity 75.7%; Pred. No. 1.6e-20;
Matches 153; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

QY          CTAAACCATGATGGCTTGAATGAGCGCTTAATAATVACAACCAACCACCAAGCCATGAAATCCA 132
Db          4111 CTTAATATATGATTATTCATCATGATGCGTGGAATCTGCCGACCA GCC--AAAGATGTAGAGAAA 4168

QY          TCCCTGACCATCTCCACTGGGATCTTGTGTGCATCTTTAGCTTAGAATGTCATCAA 192
Db          4169 ACCTTGTGATATCTCAACATCATGCGCTGTGGTGCATCTTTAACATAGAAGTCTCATCAA 42288

QY          ATCTTTGCTTTGAGGCAATATCTACTTCCACCAATGCGCTGGAATTTATTTGACTGTGTGATC 252
Db          4229 GTCTTTGCTTTGAGGCAACACTACTTCCACCAATGCGTGGAATTTATTTGATGTGTGTGCTC 42888

QY          GTGCTCTTTCCATTTGTTAGTA 274
Db          4289 GTGCTCTTTTCATCATTTAGTA 4310
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US-10-220-120-104  
Sequence 104, Application US/10202120  
Publication No. US2004004253A1  
GENERAL INFORMATION:  
INCYTE GENOMICS, INC.  
APPLICANT: PANZER, Scott R.  
APPLICANT: SPIRO, Peter A.  
APPLICANT: BANVILLE, Steven C.  
APPLICANT: SHAH, Puri  
APPLICANT: CHALUP, Michael S.  
APPLICANT: CHANG, Simon C.  
APPLICANT: CHEN, Alice  
APPLICANT: D'SA, Steven A.  
APPLICANT: AMSHEY, Stefan  
APPLICANT: DAHL, Christopher R.  
APPLICANT: DANIELS, Susan E.  
APPLICANT: DUFOUR, Gerard E.  
APPLICANT: FLORES, Vincent  
APPLICANT: FONG, Willy T.  
APPLICANT: GREENAWALT, Lila B.  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: JONES, Anissa L.  
APPLICANT: LIU, Tommy F.  
APPLICANT: ROSEBERRY, Ann M.  
APPLICANT: ROSEN, Bruce H.  
APPLICANT: RUSSO, Frank D.  
APPLICANT: STOCKBREHER, Theresa K.  
APPLICANT: DAPO, Abel  
APPLICANT: WRIGHT, Rachel J.  
APPLICANT: YAP, Pierre E.  
APPLICANT: YU, Jimmy Y.  
APPLICANT: BRADLEY, Diana L.  
APPLICANT: BRATCHER, Shawn R.  
APPLICANT: CHEN, Wenheng  
APPLICANT: COHEN, Howard J.  
APPLICANT: HODGSON, David M.  
APPLICANT: LINCOLN, Stephen E.

```

APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220.120
CURRENT FILING DATE: 2002-08-26
PRIORITY APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,698; 60/184,770; 60/184,774
60/184,693; 60/184,771; 60/184,813; 60/184,773; 60/184,776;
60/184,769; 60/184,768; 60/184,837; 60/184,697; 60/184,841;
60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/205,221;
60/204,815; 60/203,785; 60/204,821; 60/204,908; 60/204,226;
60/204,825; 60/205,285; 60/205,232; 60/205,323; 60/205,287;
60/205,324; 60/205,286
PRIORITY FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24;
2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-05-17;
2000-05-17; 2000-05-12; 2000-05-16; 2000-05-16; 2000-05-15;
2000-05-16; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;
2000-05-17; 2000-05-17
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PERL Program
SEQ ID NO 104
LENGTH: 8530
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:410188.1:2000MAY01
NAME/KEY: unsure
LOCATION: 6797, 7046, 7252, 7311, 7325-7326, 7502-7503, 7563
OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-104

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RESULT 202-824-3  
 US-10-10-26  
 ; Sequence 3, Application US/102002824  
 ; Publication No. US20030176648A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Wood, John N.  
 ;  
 ; TITLE OF INVENTION: Ion Channel  
 ;  
 ; NUMBER OF SEQUENCES: 31  
 ;  
 ; CORRESPONDENCE ADDRESS:  
 ;  
 ; ADDRESSEE: ZENCA Pharmaceuticals  
 ;  
 ; STREET: 1800 Concord Pike, P.O. Box 15437  
 ;  
 ; CITY: Wilmington  
 ;  
 ; STATE: Delaware  
 ;  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 19850  
 ;  
 ; COMPUTER READABLE FORM:  
 ;  
 ; MEDIUM TYPE: Floppy disk  
 ;

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2573 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 561..2126  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-202-824-3

Query Match 11.9%; Score 69.8; DB 14; Length 2573;  
Best Local Similarity 69.3%; Pred. No. 9.8e-09;  
Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 137 TGACCATCTCCACAGCGCTTTGGTCATCTTACGTGAATGCTCATCAAAATCT 196  
DB 781 TGGGAGATCAACAGCTTTGTCGCGCTTCACGGCGAGTGATGAAGATGT 840  
QY 197 TTGCTTTGAGCAATACTACTTACCAATGCTGGAATTTATTTGACTGTGTGCTGTC 256  
DB 841 TGGCCCTGCGACAGTACTTACCAACGCGTGAAGCTGTTCACTTCATAGTGGA 900  
QY 257 TTCTTTCCATTGTAGT 273  
DB 901 TCCTGTCCATTGGAGT 917

RESULT 7  
US-10-209-776-1  
Sequence 1, Application US/10209776  
Publication No. US20030096360A1  
GENERAL INFORMATION:  
APPLICANT: Herman, Ronald C  
Delgado, Stephen G  
Fish, Linda M  
Sangameswaran, Lakshmi  
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Syntex Corporation, Patent Department A2-200  
STREET: 3401 Hillview Avenue P.O. Box 10850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/209,776  
FILING DATE: 01-Aug-2002

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,828  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Perles, Roman  
REGISTRATION NUMBER: 35,752  
REFERENCE/DOCKET NUMBER: 28340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)-852-1698  
TELEFAX: (415)-496-3529  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6344 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: Dorsal root ganglia  
CELL TYPE: Peripheral nerve  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-209-776-1

Query Match 11.9%; Score 69.8; DB 14; Length 6344;  
Best Local Similarity 69.3%; Pred. No. 1.6e-08;  
Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 137 TGACCATCTCCACAGCGCTTTGGTCATCTTACGTGAATGCTCATCAAAATCT 196  
DB 458 TGGGAGATCAACAGCTTTGTCGCGCTTCACGGCGAGTGATGAAGATGT 4607  
QY 197 TTGCTTTGAGCAATACTACTTACCAATGCTGGAATTTATTTGACTGTGTGCTGTC 256  
DB 4608 TGGCCCTGCGACAGTACTTACCAACGCGTGAAGCTGTTCACTTCATAGTGGA 4667  
QY 257 TTCTTTCCATTGTAGT 273  
DB 4668 TCCTGTCCATTGGAGT 4684

RESULT 8  
US-10-202-824-1  
Sequence 1, Application US/10202824  
Publication No. US20030176648A1  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ZENBEA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6524 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-202-824-1

Query Match 11.9%; Score 69.8; DB 14; Length 6524;  
Best Local Similarity 69.3%; Pred. No. 1.6e-08;  
Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Db 137 TGACCATCTCCACTGGGCTCTTTGGTGCATCTTTAGCTAGAAATGCTCATCAAAATCT 196  
4732 TGGCGAATCAACCACTTCTTTGGCCCTTTCACGGCGAGTGTGATGAAGATGT 4791

QY 197 TTGCTTTAGGCAATACTACTTCCACCAATGGCTGGAATTTATTGACTGTGTGCTGTC 256  
4792 TCGCCCTGCAGACATCTACTTCAACCAAGCTGGAAGTGTGACTTCACTAGTGTGA 4851

QY 257 TTCTTTCATTGTAGT 273  
4852 TCTGTCCATTGGAGT 4868

Db 257 TTCTTTCATTGTAGT 273  
4852 TCTGTCCATTGGAGT 4868

RESULT 9  
US-10-202-824-7  
Sequence 7, Application US/10202824  
Publication No. US20030176648A1  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6527 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6077  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-202-824-7

Query Match 11.9%; Score 69.8; DB 14; Length 6527;  
Best Local Similarity 69.3%; Pred. No. 1.6e-08;  
Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 137 TGACCATCTCCACTGGGCTCTTTGGTGCATCTTTAGCTAGAAATGCTCATCAAAATCT 196  
Db 4732 TGGCGAATCAACCACTTCTTTGGCCCTTTCACGGCGAGTGTGATGAAGATGT 4791

QY 197 TTGCTTTAGGCAATACTACTTCCACCAATGGCTGGAATTTATTGACTGTGTGCTGTC 256  
Db 4792 TCGCCCTGCAGACATCTACTTCAACCAAGCTGGAAGTGTGACTTCACTAGTGTGA 4851

QY 257 TTCTTTCATTGTAGT 273  
Db 4852 TCTGTCCATTGGAGT 4868

RESULT 10  
US-10-202-824-5  
Sequence 5, Application US/10202824  
Publication No. US20030176648A1  
GENERAL INFORMATION:  
APPLICANT: Wood, John N.  
Akopian, Armen N.  
TITLE OF INVENTION: Ion Channel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ZENECA Pharmaceuticals  
STREET: 1800 Concord Pike, P.O. Box 15437  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/202,824  
FILING DATE: 26-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,656  
FILING DATE: 24-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PHM.70086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-7466  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7052 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..6602  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-202-824-5

Query Match 11.9%; Score 69.6; DB 14; Length 7052;  
Best Local Similarity 69.3%; Pred. No. 1.6e-08;  
Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 137 TGACCATCTCACTGGGCTTTTGGTGCATCTTTAGATGTCATCAAAATCT 196  
DB 5257 TGGGCAAGATCAACGATCTTTGGGCGCTTTCACGGGAGTGTGATGAAGATGT 5316  
QY 197 TTGCTTTAGGCAATACTACTTCAACCAATGGCTGGAATTTATTGACTGTGTCGTC 256  
DB 5317 TCGCCCTGCGACAGTACTTCTTCAACCAAGCTGGAAGCTTTCACCTTCAATGATGTA 5376  
QY 257 TTTCTTCCATTTGTAGT 273  
DB 5377 TCTGTCTCATTTGGGAGT 5393

## RESULT 11

US-09-840-125-3  
Sequence 3, Application US/09840125  
Patent No. US20020061524A1  
GENERAL INFORMATION:  
APPLICANT: Splawski, Igor  
APPLICANT: Keating, Mark T.  
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND  
FILE REFERENCE: 2323-155  
CURRENT APPLICATION NUMBER: US/09/840,125  
CURRENT FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: 09/634,920  
PRIOR FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: 60/147,488  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 6048  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(6048)  
US-09-840-125-3

Query Match 11.9%; Score 69.6; DB 9; Length 6048;

Best Local Similarity 68.6%; Pred. No. 1.7e-08;  
Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 135 CTTGACCATCTCACTGGGCTTTTGGTGCATCTTTAGATGTCATCAAAAT 194  
DB 4677 CTGGCCAAAGTCAACGCTTTTGGCCATCTTCACAGCGAGTATGTCAAGCT 4736  
QY 195 CTTGCTTTAGGCAATACTACTTCAACCAATGGCTGGAATTTATTGACTGTGTCGT 254  
DB 4737 GGGTCCCTGGGCGCACTACTTCAACCAAGCTGGAATTTCTTCAGCTTGTTGT 4796  
QY 255 GCTTCTTCCATTTGTAGT 274  
DB 4797 CATCTCTCATTCGTGGCA 4816

## RESULT 12

US-09-896-994-1  
Sequence 1, Application US/09896994  
Publication No. US20030074024A1  
GENERAL INFORMATION:  
APPLICANT: Ken Stokes  
APPLICANT: Jos e Morissette

TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATY  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1

STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/896,994

FILING DATE: 02-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/514,907

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6048 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-896-994-1

Query Match 11.9%; Score 69.6; DB 10; Length 6048;

Best Local Similarity 68.6%; Pred. No. 1.7e-08;  
Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 195 CTTGCTTTAGGCAATACTACTTCAACCAATGGCTGGAATTTATTGACTGTGTCGT 254  
DB 4737 GGGTCCCTGGGCGCACTACTTCAACCAAGCTGGAATTTCTTCAGCTTGTTGT 4796  
QY 255 GCTTCTTCCATTTGTAGT 274  
DB 4797 CATCTCTCATTCGTGGCA 4816

## RESULT 13

US-10-077-054-1

Sequence 1, Application US/10077054

Publication No. US20030157600A1

GENERAL INFORMATION:

APPLICANT: Makleleki, Jonathan C

APPLICANT: Ye, Bin

TITLE OF INVENTION: Sodium Channel Alpha Subunits

FILE REFERENCE: 960296.98032

CURRENT APPLICATION NUMBER: US/10/077,054

CURRENT FILING DATE: 2002-02-12

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 6091

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (10)..(6054)

US-10-077-054-1

Query Match 11.9%; Score 69.6; DB 14; Length 6091;



Best Local Similarity 68.6%; Pred. No. 1.7e-08;  
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Db 4887 GGCTGCCCTGGCGCACTACTTACCAACAGCTGGAATATCTTGCATCTTGGTGTGT 4946

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Db 4947 CATCTCTCCATCGTGGCA 4966

RESULT 14  
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; Publication No. US20030148295A1  
; GENERAL INFORMATION:  
; APPLICANT: WAN, JACKSON  
; APPLICANT: WANG, YIXIN  
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
; FILE REFERENCE: 15117.0012  
; CURRENT APPLICATION NUMBER: US/10/101,510  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/276,947  
; PRIOR FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 805  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 617  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
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; OTHER INFORMATION: a, t, c, g, other or unknown  
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US-10-101-510-617

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Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 255 GCTTCTTTCCATGTTAGTA 274  
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RESULT 15  
US-10-333-191-1  
; Sequence 1, Application US/10333191  
; Publication No. US20030235838A1  
; GENERAL INFORMATION:  
; APPLICANT: Splawski, Igor  
; APPLICANT: Keating, Mark T.  
; TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in Drug-Induced Cardiac  
; FILE REFERENCE: 2323-154-11  
; CURRENT APPLICATION NUMBER: US/10/333,191  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/US01/22639  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,738  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 8491  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (151)..  
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; NAME/KEY: misc\_feature  
; LOCATION: (1)..  
; OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 11.9%; Score 69.6; DB 15; Length 8491;  
Best Local Similarity 68.6%; Pred. No. 2.1e-08;  
Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 195 CTTGCTTTGAGGCAATACTACTTACCAATGGCTGGAATTATTTAGCTGTGTGCT 254  
Db 4887 GGCTGCCCTGGCGCACTACTTACCAACAGCTGGAATATCTTGCATCTTGGTGTGT 4946

QY 255 GCTTCTTTCCATGTTAGTA 274  
Db 4947 CATCTCTCCATCGTGGCA 4966

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Job time : 363.296 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 75154660

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Post-processing: Minimum Match 0%  
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SUMMARIES

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## ALIGNMENTS

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 APPLICANT: Glaxo Wellcome PLC  
 APPLICANT: Tate, Simon N  
 APPLICANT: Grose, David T  
 APPLICANT: Hicks, Carolin A  
 TITLE OF INVENTION: Ion Channels  
 FILE REFERENCE: PG3432  
 CURRENT APPLICATION NUMBER: US/09/646,224A  
 CURRENT FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: GB 9805793.8  
 PRIOR FILING DATE: 1998-03-18  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 16  
 LENGTH: 565  
 TYPE: DNA

Query Match	100.0%;	Score 585;	DB 27;	Length 585;
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Db	481	ACTACACAACGTAAATAGAGTTCAATTAATCATGACCTAATGTATTCATATGAAATAGAC	540	
OY	541	AAAAATTAATAGCTCAGAAAGTTTGTGTGTGTAGAAAAATTC	585	
Db	541	AAAAATTAATAGCTCAGAAAGTTTGTGTGTGTAGAAAAATTC	585	

```

RESULT 2
US-10-219-051B-910
; Sequence 910, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 910
; LENGTH: 5728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5728)

```

OTHER INFORMATION: n=a, c, g or t  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: EMBL / AF150882  
DATABASE ENTRY DATE: 2000-01-16  
US-10-219-051B-910

Query Match 72.8%; Score 425.8; DB 47; Length 5728;  
Best Local Similarity 93.2%; Pred. No. 6e-106;  
Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;

```
QY 70 TACCTAAACCATGATGGCTTGAATGCTTAATATACAAACCAACCCAAAGCCATGGAT 129
DB 4327 TATCTTAAACATGATTTGATGATGCTGATCATACAAACA-CCCAAAGCCATGAAAT 4385
QY 130 CCATCTTGACCATCTCCAACTGGGCTTTGTGTGTCATCTTTAGCTTGAATGTCATC 189
DB 4386 CCATCTTGACCATCT-CAACTGGGCTTTGTGTGTCATCTTTAGCTTGAATGTCATC 4444
QY 190 AAAATCTTGGCTTGAAGCAATACCTTCAACCAATGGCTGGAATTTATTTGACGTGTG 249
DB 4445 AAAATCTTGGCTTGAAGCAATACCTTCAACCAATGGCTGGAATTTATTTGACGTGTG 4504
QY 250 GTCTGCTCTTCTTCATTTAGTATGATTAATACAGCAGTCAAGGACCTTAAGAACCA 309
DB 4505 GTCTGCTCTTCTTCATTTAGTATGATTAATACAGCAGTCAAGGACCTTAAGAACCA 4564
QY 310 GAACTAAGTTGTAATCTTATCAATTTTGAAGTTGTTCAAACTATCCAAAGCAGA 369
DB 4665 GAACTAAGTTGTAATCTTATCAATTTTGAAGTTGTTCAAACTATCCAAAGCAGA 4624
QY 370 AAATGCGGCCAAGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTTACT 429
DB 4625 AAATGCGGCCAAGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTTACT 4684
QY 430 GGAAGTTGCTAGAGATAGAGGCGGTAATTTCTGGTCCCTTAACCTACATACAA 489
DB 4685 GGAAGTTGCTAGAGATAGAGGCGGTAATTTCTGGTCCCTTAACCTACATACAA 4738
QY 490 CTGAATAGATTCAATATCATGCACTAATGTAATTCATGAAATAGACAAATTTAA 549
DB 4739 CTGAATAGATTCAATATCATGCACTAATGTAATTCATGAAATAGACAAATTTAA 4798
QY 550 ATGACTCAGAAGTTTGTGTGTGTAGAAAAATTT 584
DB 4799 ATGACTCAGAAGTTTGTGTGTGTGTAGAACTGATTT 4833
```

## RESULT 3

US-10-296-130-3  
Sequence 3, Application US/10296130  
GENERAL INFORMATION:  
APPLICANT: KANAZAWA, Ichiro  
APPLICANT: GOTO, Jun  
TITLE OF INVENTION: Human Sodium Channel SCN12A and SCN8A  
FILE REFERENCE: 2002-1512A/WMC/00653  
CURRENT FILING DATE: 2003-07-30  
PRIOR APPLICATION NUMBER: PCT/JU00/04629  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: JP2000-152085  
PRIOR FILING DATE: 2000-05-23  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 5728  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (200)..(4534)  
FEATURE:  
NAME/KEY: modified base

LOCATION: 5632  
OTHER INFORMATION: n = a, g, c or t  
PUBLICATION INFORMATION:  
AUTHORS: Soen-Yong Jeong et al.  
TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel a Subunit  
TITLE: Gene, SCN12A  
JOURNAL: Biochem. Biophys. Res. Commun.  
VOLUME: 267  
ISSUE: 1  
PAGES: 262-270  
DATE: 2000-01-15  
DATABASE ACCESSION NUMBER: GenBank AF150882  
DATABASE ENTRY DATE: 2000-01-15  
US-10-296-130-3

Query Match 72.8%; Score 425.8; DB 48; Length 5728;  
Best Local Similarity 93.2%; Pred. No. 6e-106;  
Matches 480; Conservative 0; Mismatches 27; Indels 8; Gaps 3;

```
QY 70 TACCTAAACCATGATGGCTTGAATGCTTAATATACAAACCAACCCAAAGCCATGGAT 129
DB 4327 TATCTTAAACATGATTTGATGATGCTGATCATACAAACA-CCCAAAGCCATGAAAT 4385
QY 130 CCATCTTGACCATCTCCAACTGGGCTTTGTGTGTCATCTTTAGCTTGAATGTCATC 189
DB 4386 CCATCTTGACCATCT-CAACTGGGCTTTGTGTGTCATCTTTAGCTTGAATGTCATC 4444
QY 190 AAAATCTTGGCTTGAAGCAATACCTTCAACCAATGGCTGGAATTTATTTGACGTGTG 249
DB 4445 AAAATCTTGGCTTGAAGCAATACCTTCAACCAATGGCTGGAATTTATTTGACGTGTG 4504
QY 250 GTCTGCTCTTCTTCATTTAGTATGATTAATACAGCAGTCAAGGACCTTAAGAACCA 309
DB 4505 GTCTGCTCTTCTTCATTTAGTATGATTAATACAGCAGTCAAGGACCTTAAGAACCA 4564
QY 310 GAACTAAGTTGTAATCTTATCAATTTTGAAGTTGTTCAAACTATCCAAAGCAGA 369
DB 4665 GAACTAAGTTGTAATCTTATCAATTTTGAAGTTGTTCAAACTATCCAAAGCAGA 4624
QY 370 AAATGCGGCCAAGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTTACT 429
DB 4625 AAATGCGGCCAAGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTTACT 4684
QY 430 GGAAGTTGCTAGAGATAGAGGCGGTAATTTCTGGTCCCTTAACCTACATACAA 489
DB 4685 GGAAGTTGCTAGAGATAGAGGCGGTAATTTCTGGTCCCTTAACCTACATACAA 4738
QY 490 CTGAATAGATTCAATATCATGCACTAATGTAATTCATGAAATAGACAAATTTAA 549
DB 4739 CTGAATAGATTCAATATCATGCACTAATGTAATTCATGAAATAGACAAATTTAA 4798
QY 550 ATGACTCAGAAGTTTGTGTGTGTGTAGAAAAATTT 584
DB 4799 ATGACTCAGAAGTTTGTGTGTGTGTAGAACTGATTT 4833
```

## RESULT 4

US-60-466-412-84151  
Sequence 84151, Application US/60466412  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
APPLICANT: IAKUBOVA, Olga  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01466  
CURRENT APPLICATION NUMBER: US/60/466,412  
CURRENT FILING DATE: 2003-04-30  
NUMBER OF SEQ ID NOS: 429241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84151  
LENGTH: 115159  
TYPE: DNA  
ORGANISM: Homo sapiens

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(115159)
; OTHER INFORMATION: n = A,T,C or G
US-60-466-412-84151

```

Query Match	72.8%;	Score 425.8;	DB 103;	Length 115159;
Best Local Similarity	93.2%;	Pred. No. 2e-105;		
Matches 480;	Conservative	0;	Mismatches 27;	Indels 8;
				Gaps 32

QY	70	TACCCAAACCAATGATGGCTGATGGCCCTAAATATATGACACCAACCCCAAGCATGAAT	129
Db	105225	TATCTTAACAATGATTTAGCATATGGCTGAAATCATRACACCAA-CCCAAGCATGAAT	105293
QY	130	CCATCTTTGACCATCTCCAACTGGGCTCTTTGTGTGTCATCTTTACGTTAAGATGTCTCATC	189
Db	105294	CCATCTTTGACCATCTCT-CAACTGGGCTTTGTGTGTCATCTTTACGTTAAGATGTCTCATC	105352
QY	190	AAATCTTGCTTTAGGCAATACTCTCACCAATGGCTGGAAATTTATTTGACGTGTGG	249
Db	105353	AAATCTTTGCTTTAGGCAATACTCTCACCAATGGCTGGAAATTTATTTGACGTGTGG	105412
QY	250	GTCGTGCTTCTTTCATTTGTAAGTAAATACAGCACTCAGAGGACTTTAAGACCA	309
Db	105413	GTCGTGCTTCTTTCATTTGTAAGTAAATACAGCACTCAGAGGACTTTAAGACCA	105472
QY	310	GAAGTAATTTGTAATCTTATCATTTTTTGAAGTTGTTCAACTATCCAAACACACA	369
Db	105473	GAAGTAATTTGTAATCTTATCATTTTTTGAAGTTGTTCAACTATCCAAACACACA	105532
QY	370	AACTGGGCCAAGTACTTTCTGAAAGATATGACAGGGGTACTAAATGTCATTCTTACT	429
Db	105533	AACTGGGCCAAGTACTTTCTGAAAGATATGACAGGGGTACTAAATGTCATTCTTACT	105592
QY	430	GGGAAGTTGTAGAGGATAGAGGGGTAAATTTCTGTGTCCCTTAATCTACTAACA	489
Db	105593	GGGAAGTTGTAGAGGATAGAGGGGTAAATTTCTGTGTCCCTTAATCTACTAACA	105646
QY	490	CTGAATATGAGTTTCATATATCATGACAGCTAATGATTCATGGAATATGACAAATTTAA	549
Db	105647	CTGAATATGAGTTTCATATATCATGACAGCTAATGATTCATGGAATATGACAAATTTAA	105706
QY	550	ATGACTCAGAAAGTTTTTGTGGTGTGTAAGAAAATTT	584
Db	105707	ATGACTCAGAAAGTTTTTGTGGTGTGTAAGAAAATTT	105741

```

RESULT 5
US-60-162-357-124/c
: Sequence 124. Application US/60162357
: GENERAL INFORMATION:
: APPLICANT: Bonazzzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CLO00126
: CURRENT APPLICATION NUMBER: US/60162,357
: CURRENT FILING DATE: 1999-10-29
: NUMBER OF SEQ ID NOS: 1748
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 124
: LENGTH: 614
: TYPE: DNA
: ORGANISM: Human
US-60-162-357-124

```

	Query March	Similarity	Pred	No. 1.6e-93	DB 72	Length 614
Best Local	Similarity	94.8%	Pred	No. 1.6e-93		
Matches	416	Conservative	0	Mismatches	16	Indels 7; Gaps 2
Qy	147	CAACTGGATCTTTGTGTCATCTTTACGTTAGATGTCATCAAAATCTTTGGCTTTGAG	206			
Db	612	CAACTGGATCTTTGTGTCATCTTTACGTTAGATGTCATCAAAATCTTTGGCTTTGAG	553			

QY	20	GCATACCTACTCACCAGAAAGCGTGAATTTATTTGACTGCTGGTCCGCTCTTTCCAT	266
Db	552	GCAATCTACTTCACCAATAGCGCTGAAATTTATTTGACTGTGTGGTCTGCTCTTTCCAT	493
QY	267	TGTTAGTAAGTAAATCAACAGACTCAGAGGACCTTTAAGAACACAGAACTAAAGTTGTAAT	356
Db	492	TGTTAGTAAGTAAATCAGACTCAGAGGACCTTTAAGAACACAGAACTAAAGTTGTAAT	433
QY	327	CTTATCAATTTTGAAGTTTGTTCAACTATTCACAAAGCAGAAACTGGGCCAAGTGA	386
Db	432	CTTATCAATTTTGAAGTTTGTTCAACTATTCACAAAGCAGAAACTGGGCCAAGTGA	373
QY	387	CTTTTCGAAGAATAGACAGGGGTACTATGCGCATCTCTACTGGGAAGTTGCTAGAGAA	446
Db	372	CTTTTCGAAGAATAGACAGGGGTACTATGCGCATCTCTACTGGGAAGTTGCTAGAGAA	313
QY	447	TAGAGAGCGGTAAATTTCTGTTCCTCTTAACTCACTACACAACTGAATAGAGTTCAAT	506
Db	312	TA-----GAGAGTAAATTTCTGTTCCTCTTAACTCACTACACAACTGAATAGAGTTCAAT	259
QY	507	AATC-ATGCAGCTAATGTATTCAATGAAATAGACAAATTTAAATATGACTCAGAAAGTTT	565
Db	258	AATCAATAGCAGCTAATGTATTCAATGAAATAGACAAATTTAAATATGACTCAGAAAGTTT	199
QY	566	TGTGGTGTAGAAAAATTT 584	
Db	198	TGTGGTGTAGACTGATTT 180	

```

RESULT 6
US-60-163-080-93/c
; Sequence 93, Application US/60163080
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
; TITLE OF INVENTION: NOCTELIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000136
; CURRENT APPLICATION NUMBER: US/60/163,080
; CURRENT FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 760
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
US-60-163-080-93

```

Query Match	64.9%	Score 379.4	DB 72	Length 614
Best Local Similarity	94.8%	Pred 1.6e-93		
Matches 416	Conservative	0	Mismatches 16	Indels 7
			Gaps	2
QY	147	CAACTGGGCTCTTGTGTCATCTTTACGTTGAATGTCTCATCAAAAATCTTTGCTTTGAG	206	
Db	612	CAACTGGGCTCTTGTGTCATCTTTACGTTGAATGTCTCATCAAAAATCTTTGCTTTGAG	553	
QY	207	GCAATTACTACTACCAATATGCTGGAAATTTATTTAGCTGTGGTCGGCTCTTTCCAT	266	
Db	552	GCAATTACTACTACCAATATGCTGGAAATTTATTTAGCTGTGGTCGGCTCTTTCCAT	439	
QY	267	TGTTAGTAAGTAAATCAGACGCTCAGAGGACTTTAAGACCAAGATTAAGTTGTAAAT	326	
Db	492	TGTTAGTAAGTAAATCAGACGCTCAGAGGACTTTAAGACCAAGATTAAGTTGTAAAT	433	
QY	327	CTTATCAATTTTTGAAGTTTGTTCAAACATACCAAAAGCAGAAAATCTGGCCAAAGTGA	386	
Db	432	CTTATCAATTTTTGAAGTTTGTTCAAACATACCAAAAGCAGAAAATCTGGCCAAAGTGA	373	
QY	387	CTTTCTGAAAGATATGACAGGGGTACTAATGCCATCTCTACTGGGAATTTGCTTAGAGA	446	
Db	372	CTTTCTGAAAGATATGACAGGGGTACTAATGCCATCTCTACTGGGAATTTGCTTAGAGA	313	

```
OY 447 TAGAGGCGGTAATTTCTGGTCCCTTAACCTACACAGCACTGAATGAGTTCAAT 506
|||
DB 312 TA-----GAGAGTAATTTCTGTTCCCTTAACCTACACAGCACTGAATGAGTTCAAT 259
|||
OY 507 AATC-ATGACCTAATGATTTCAATGAGAAATAGACAAATTAATTAATGACTGAGAGTTT 565
|||
DB 258 AATCAATGACCTAATGATTTCAATGAGAAATAGACAAATTAATTAATGACTGAGAGTTT 199
|||
OY 566 TGTGCTGTAGAAAATTT 584
|||
DB 198 TGTGCTGTAGAAAATTT 180
|||
```

RESULT 7  
US-09-364-791-49

```
; Sequence 49, Application US/09364791
; GENERAL INFORMATION:
; APPLICANT: Robison, Kieth E.
; TITLE OF INVENTION: Novel Ion Channel Homologs
; FILE REFERENCE: 5800-42
; CURRENT APPLICATION NUMBER: US/09/364,791
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CALCIUM AND SODIUM CHANNELS
US-09-364-791-49
```

Query Match 54.2%; Score 316.8; DB 19; Length 435;  
Best Local Similarity 96.1%; Pred. No. 2.5e-76;  
Matches 346; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

```
OY 70 TACCTAAACATGATGGCTTGATGCGCTTAATATACACCAACCCCAAGCCATGAAAT 129
|||
DB 78 TATCCTAAACATGATGATGATGCGCTGAATCATACCAACCA-CCCAAGCCATGAAAT 136
|||
OY 130 CCATCTTGACCATCTCCAACTGGGCTTTGTGTCATCTTTAGTTGATGATCTCATC 189
|||
DB 137 CCATCTTGACCATCT-CAACTGGGCTTTGTGTCATCTTTAGTTGATGATCTCATC 195
|||
OY 190 AAAATCTTGCTTGGGCAATGACTTCACTTCCCAATGCTGGAATTTATTTGACTGTGTG 249
|||
DB 196 AAAATCTTGCTTGGGCAATGACTTCACTTCCCAATGCTGGAATTTATTTGACTGTGTG 255
|||
OY 250 GTGCTGCTTTCTTCCATTTAGTAAGTAATACAGAGTCAGAGGACTTTAAGAACCA 309
|||
DB 256 GTGCTGCTTTCTTCCATTTAGTAAGTAATACAGAGTCAGAGGACTTTAAGAACCA 315
|||
OY 310 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTCAACTATCCACAAAGCAGA 369
|||
DB 316 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTCAACTATCCACAAAGCAGA 375
|||
OY 370 AAACGTGGGCAAGGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTCTACT 429
|||
DB 376 AAACGTGGGCAAGGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTCTACT 435
|||
```

RESULT 8  
US-09-364-791A-49

```
; Sequence 49, Application US/09364791A
; GENERAL INFORMATION:
; APPLICANT: Robison, Kieth E.
; TITLE OF INVENTION: Novel Ion Channel Homologs
; FILE REFERENCE: 5800-42
; CURRENT APPLICATION NUMBER: US/09/364,791A
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 76
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CALCIUM AND SODIUM CHANNELS
US-09-364-791A-49
```

Query Match 54.2%; Score 316.8; DB 19; Length 435;  
Best Local Similarity 96.1%; Pred. No. 2.5e-76;  
Matches 346; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

```
OY 70 TACCTAAACATGATGGCTTGATGCGCTTAATATACACCAACCCCAAGCCATGAAAT 129
|||
DB 78 TATCCTAAACATGATGATGATGCGCTGAATCATACCAACCA-CCCAAGCCATGAAAT 136
|||
OY 130 CCATCTTGACCATCTCCAACTGGGCTTTGTGTCATCTTTAGTTGATGATCTCATC 189
|||
DB 137 CCATCTTGACCATCT-CAACTGGGCTTTGTGTCATCTTTAGTTGATGATCTCATC 195
|||
OY 190 AAAATCTTGCTTGGGCAATGACTTCACTTCCCAATGCTGGAATTTATTTGACTGTGTG 249
|||
DB 196 AAAATCTTGCTTGGGCAATGACTTCACTTCCCAATGCTGGAATTTATTTGACTGTGTG 255
|||
OY 250 GTGCTGCTTTCTTCCATTTAGTAAGTAATACAGAGTCAGAGGACTTTAAGAACCA 309
|||
DB 256 GTGCTGCTTTCTTCCATTTAGTAAGTAATACAGAGTCAGAGGACTTTAAGAACCA 315
|||
OY 310 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTCAACTATCCACAAAGCAGA 369
|||
DB 316 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTCAACTATCCACAAAGCAGA 375
|||
OY 370 AAACGTGGGCAAGGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTCTACT 429
|||
DB 376 AAACGTGGGCAAGGTACTTCTGAAAGATAGACAGGGGTACTAATGCCATTTCTCTACT 435
|||
```

RESULT 9  
US-10-001-187-49

```
; Sequence 49, Application US/10001187
; GENERAL INFORMATION:
; APPLICANT: Robison, Kieth E.
; TITLE OF INVENTION: Novel Ion Channel Homologs
; FILE REFERENCE: 5800-42
; CURRENT APPLICATION NUMBER: US/10/001,187
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US/09/364,791
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CALCIUM AND SODIUM CHANNELS
US-10-001-187-49
```

Query Match 54.2%; Score 316.8; DB 43; Length 435;  
Best Local Similarity 96.1%; Pred. No. 2.5e-76;  
Matches 346; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

```
OY 70 TACCTAAACATGATGGCTTGATGCGCTTAATATACACCAACCCCAAGCCATGAAAT 129
|||
DB 78 TATCCTAAACATGATGATGATGCGCTGAATCATACCAACCA-CCCAAGCCATGAAAT 136
|||
OY 130 CCATCTTGACCATCTCCAACTGGGCTTTGTGTCATCTTTAGTTGATGATCTCATC 189
|||
```

Db 137 CCATCCTTGACCATCT -CAACTGGGCTTTGGTGCATCTTACGTTAGATGTCATC 195  
Qy 130 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 249  
Db 196 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 255  
Qy 250 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 309  
Db 256 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 315  
Qy 310 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTTCAACTATTCACAAAGCAGA 369  
Db 316 GAAGTAAGTTGTAAATCTTATCATTTTGAAGTTGTTCAACTATTCACAAAGCAGA 375  
Qy 370 AAACGGGCAAGTACTTCTGAAAGATGACAGGGGTCTATATGCAATCTCTACT 429  
Db 376 AAACGGGCAAGTACTTCTGAAAGATGACAGGGGTCTATATGCAATCTCTACT 435

## RESULT 10

US-10-170-235-13985  
; Sequence 13985, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 13985  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-13985

Query Match 27.9%; Score 163.4; DB 46; Length 5080;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 70 TACTTAACCATGATTGGCTTGATGGCTTAATATACCAACCAAGCCCAAGCCATGAAT 129  
Db 4039 TATCTTAACCATGATTAGATGATGCTGAATCATCAACCA-CCCAAGCCATGAAT 4097  
Qy 130 CCATCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 189  
Db 4098 CCATCTTGACCATCT -CAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 4156  
Qy 190 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 249  
Db 4157 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 4216  
Qy 250 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 274  
Db 4217 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 4241

## RESULT 11

US-60-453-050-2171  
; Sequence 2171, Application US/60453050  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: LUKE, May  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001457  
; CURRENT APPLICATION NUMBER: US/60/453,050  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-60-453-050-2171

Query Match 27.9%; Score 163.4; DB 102; Length 5080;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 70 TACTTAACCATGATTGGCTTGATGGCTTAATATACCAACCAAGCCCAAGCCATGAAT 129  
Db 4039 TATCTTAACCATGATTAGATGATGCTGAATCATCAACCA-CCCAAGCCATGAAT 4097  
Qy 130 CCATCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 189  
Db 4098 CCATCTTGACCATCT -CAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 4156  
Qy 190 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 249  
Db 4157 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 4216  
Qy 250 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 274  
Db 4217 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 4241

## RESULT 12

US-60-453-135-2171  
; Sequence 2171, Application US/60453135  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001456  
; CURRENT APPLICATION NUMBER: US/60/453,135  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-2171

Query Match 27.9%; Score 163.4; DB 102; Length 5080;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 70 TACTTAACCATGATTGGCTTGATGGCTTAATATACCAACCAAGCCCAAGCCATGAAT 129  
Db 4039 TATCTTAACCATGATTAGATGATGCTGAATCATCAACCA-CCCAAGCCATGAAT 4097  
Qy 130 CCATCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 189  
Db 4098 CCATCTTGACCATCT -CAACTGGGCTTTGGTGCATCTTACGTTAGAAATGTCATC 4156  
Qy 190 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 249  
Db 4157 AAAATCTTGGCTTTGAGGAATATACCTTACCAATGGCTGGAATTTATTTAGACTGTG 4216  
Qy 250 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 274  
Db 4217 GTCGTGCTTCTTCCATTTGTAGTAAATACGACATCAGAGGACTTTAGAACCA 4241

## RESULT 13

US-60-466-412-2171  
; Sequence 2171, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2171  
; LENGTH: 5080  
; TYPE: DNA



CURRENT APPLICATION NUMBER: US/60/466,412  
CURRENT FILING DATE: 2003-04-30  
NUMBER OF SEQ ID NOS: 429241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2171  
LENGTH: 5080  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-466-412-2171

Query Match 27.9%; Score 163.4; DB 103; Length 5080;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 70 TACCTAAACCATGATGGCTTGATGGCTTAATATACCAACCAACCCAAAGCCATGAAAT 129  
DB 4039 TATCCTAAACCATGATGATGATGCTGAATCATACCAACCA-CCCAAAAGCCATGAAAT 4097  
QY 130 CCATCCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 189  
DB 4098 CCATCCTTGACCATCT-CAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 4156  
QY 190 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 249  
DB 4157 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 4216  
QY 250 GTCGTGCTTTCTTCCATTTAGTA 274  
DB 4217 GTCGTGCTTTCTTCCATTTAGTA 4241

RESULT 14  
PCT-US00-19342-41

Sequence 41, Application PC/TUS0019342  
GENERAL INFORMATION:  
APPLICANT: Yale University  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-02-WO  
CURRENT APPLICATION NUMBER: PCT/US00/19342  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/354,147  
PRIOR FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: full length cDNA sequence for human Nan  
PCT-US00-19342-41

Query Match 27.9%; Score 163.4; DB 1; Length 5860;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 70 TACCTAAACCATGATGGCTTGATGGCTTAATATACCAACCAACCCAAAGCCATGAAAT 129  
DB 4158 TATCCTAAACCATGATGATGCTGAATCATACCAACCA-CCCAAAAGCCATGAAAT 4216  
QY 130 CCATCCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 189  
DB 4217 CCATCCTTGACCATCT-CAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 4275  
QY 190 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 249  
DB 4276 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 4335  
QY 250 GTCGTGCTTTCTTCCATTTAGTA 274

DB 4336 GTCGTGCTTTCTTCCATTTAGTA 4360

RESULT 15  
PCT-US03-08611-3

Sequence 3, Application PC/TUS0308611  
GENERAL INFORMATION:  
APPLICANT: Transmolecular, Inc.  
APPLICANT: GONDA, Matthew A  
APPLICANT: GREENWOOD, John D  
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Channel  
FILE REFERENCE: 51530-5007-WO  
CURRENT APPLICATION NUMBER: PCT/US03/08611  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: US 60/365,550  
PRIOR FILING DATE: 2002-03-20  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION:  
PCT-US03-08611-3

Query Match 27.9%; Score 163.4; DB 1; Length 5860;  
Best Local Similarity 93.7%; Pred. No. 1.4e-33;  
Matches 192; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 70 TACCTAAACCATGATGGCTTGATGGCTTAATATACCAACCAACCCAAAGCCATGAAAT 129  
DB 4158 TATCCTAAACCATGATGATGCTGAATCATACCAACCA-CCCAAAAGCCATGAAAT 4216  
QY 130 CCATCCTTGACCATCTCCAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 189  
DB 4217 CCATCCTTGACCATCT-CAACTGGGCTTTGGTGCATCTTTAGCTTGAATGCTCATC 4275  
QY 190 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 249  
DB 4276 AAAATCTTGCTTTGAGGCAATACTACTTCAACCAATGGCTGGAATTTATTTGACTGTG 4335  
QY 250 GTCGTGCTTTCTTCCATTTAGTA 274  
DB 4336 GTCGTGCTTTCTTCCATTTAGTA 4360

Search completed: March 23, 2004, 04:00:39  
Job time: 441.36 secs

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OM nucleic - nucleic search, using SW model

Run on: March 22, 2004, 16:13:34 ; Search time 741.347 Seconds  
(without alignments)  
414.412 Million cell updates/sec

Title: US-09-646-224A-16

Perfect score: 585  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1155024 seqs, 262583689 residues

Total number of hits satisfying chosen parameters: 2310048

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB\_seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB\_seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB\_seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB\_seq.\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB\_seq.\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB\_seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.6	13.9	5874	6 US-10-487-337-5	Sequence 5, Appli
2	75	12.8	100374	7 US-60-548-091-5675	Sequence 5675, Ap
3	69.8	11.9	6524	6 US-10-487-337-1	Sequence 1, Appli
4	69.6	11.9	4852	7 US-60-548-091-267	Sequence 267, App
5	69.6	11.9	4855	7 US-60-548-091-266	Sequence 266, App
6	69.6	11.9	4855	7 US-60-548-091-268	Sequence 268, App
7	43.4	7.4	201	7 US-60-548-091-5582	Sequence 5582, Ap
8	39.8	6.8	201	7 US-60-548-091-5566	Sequence 5566, Ap
9	38.2	6.5	201	6 US-10-796-280-6719	Sequence 6719, Ap
10	38.2	6.5	201	6 US-10-796-280-6751	Sequence 6751, Ap
11	38.2	6.5	201	6 US-10-796-280-6783	Sequence 6783, Ap
12	38.2	6.5	201	6 US-10-796-280-6815	Sequence 6815, Ap
13	38.2	6.5	201	6 US-10-796-280-6845	Sequence 6845, Ap
14	38.2	6.5	201	6 US-10-796-280-6873	Sequence 6873, Ap
15	38.2	6.5	201	6 US-10-796-280-6903	Sequence 6903, Ap
16	38.2	6.5	5742	6 US-10-796-280-381	Sequence 381, App
17	38.2	6.5	5842	6 US-10-796-280-383	Sequence 383, App
18	38.2	6.5	5938	6 US-10-796-280-384	Sequence 384, App
19	38.2	6.5	6029	6 US-10-796-280-385	Sequence 385, App
20	38.2	6.5	6056	6 US-10-796-280-386	Sequence 386, App
21	38.2	6.5	6062	6 US-10-796-280-379	Sequence 379, App
22	38.2	6.5	6075	6 US-10-796-280-382	Sequence 382, App
23	36.8	6.3	6572	6 US-10-467-491-1	Sequence 1, Appli
24	36.8	6.3	8374	6 US-10-784-004-592	Sequence 592, App
25	36.8	6.3	8374	6 US-10-784-004-1021	Sequence 1021, Ap
26	36.2	6.2	32285	1 PCT-US03-51591-3	Sequence 3, Appli

27	35.4	6.1	22047	6 US-10-417-375A-12	Sequence 12, Appli
28	35.2	6.0	483	5 US-09-969-034-1306	Sequence 1306, Ap
C 29	35	6.0	81609	7 US-60-550-051-2987	Sequence 2987, Ap
C 30	34.6	5.9	1077	6 US-10-667-762-23	Sequence 23, Appl
31	34.4	5.9	913	5 US-09-554-151C-39	Sequence 39, Appl
32	34.2	5.8	533	6 US-10-793-479-13604	Sequence 13604, A
33	34	5.8	3993	6 US-10-646-301A-10	Sequence 10, Appl
34	34	5.8	3993	6 US-10-663-208A-10	Sequence 10, Appl
35	33.6	5.7	492	5 US-09-796-692B-8469	Sequence 8469, Ap
36	33.4	5.7	201	6 US-10-796-280-6707	Sequence 6707, Ap
37	33.4	5.7	201	6 US-10-796-280-6739	Sequence 6739, Ap
38	33.4	5.7	201	6 US-10-796-280-6771	Sequence 6771, Ap
39	33.4	5.7	201	6 US-10-796-280-6803	Sequence 6803, Ap
40	33.4	5.7	201	6 US-10-796-280-6835	Sequence 6835, Ap
41	33.4	5.7	201	6 US-10-796-280-6863	Sequence 6863, Ap
42	33.4	5.7	201	6 US-10-796-280-6891	Sequence 6891, Ap
43	33.4	5.7	201	6 US-60-548-091-5581	Sequence 5581, Ap
44	33.4	5.7	93722	6 US-10-796-280-12377	Sequence 12377, A
C 45	33.2	5.7	18259	6 US-10-021-698A-898	Sequence 898, App

## ALIGNMENTS

RESULT 1  
US-10-487-337-5  
Sequence 5, Application US/10487337  
GENERAL INFORMATION:  
APPLICANT: Kenji OKUSE  
APPLICANT: Mark BAKER  
APPLICANT: Louis POON  
APPLICANT: John Nicholas WOOD  
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS  
FILE REFERENCE: 117-492 / N.86242A GCW  
CURRENT APPLICATION NUMBER: US/10/487,337  
PCT FILING DATE: 2004-02-20  
PCT APPLICATION NUMBER: PCT/GB02/03852  
PCT FILING DATE: 2002-08-20  
PCT APPLICATION NUMBER: GB 0120238.1  
PCT FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: Patencin version 3.1  
SEQ ID NO 5  
LENGTH: 5874  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(5874)  
OTHER INFORMATION:  
US-10-487-337-5  
Query Match 13.9%; Score 81.6; DB 6; Length 5874;  
Best Local Similarity 75.0%; Pred. No. 1.3e+14;  
Matches 102; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
DB 137 TGACCATTCACAGCGGCTTTGGTCATCTTACCTTAGAATGCTCAAAATCT 196  
DB 4523 TGGGAAATCAACAGCTTTTGGCGCTTACACAGGGAATGTCAGAAATCT 4582  
DB 197 TTGCTTGGAGCAATACCTTACCAATAGCTGAATTTATTGACTGTGTGCTGC 256  
DB 4583 TCGCTTGGAGCAATACCTTACCAATAGCTGAATGTTGTTGACTTATTTGCTG 4642  
DB 257 TTCTTTCATTTGTTG 272  
DB 4643 TTCTCTCATTCGCGAG 4658  
RESULT 2  
US-60-548-091-5675  
Sequence 5675, Application US/60548091

GENERAL INFORMATION: Michele et al.  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001506  
 CURRENT APPLICATION NUMBER: US/60/548,091  
 CURRENT FILING DATE: 2004-02-27  
 NUMBER OF SEQ ID NOS: 24433  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 5675  
 LENGTH: 100374  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)...(100374)  
 OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
 US-60-548-091-5675

Query Match 12.8%; Score 75; DB 7; Length 100374;  
 Best Local Similarity 66.3%; Pred. No. 4,6e-12;  
 Matches 108; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 135 CTGACCATCTCCAGCTGGGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 194  
 DB 88075 CTGGCCAGATCACTGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 88134  
 QY 195 CTTTGCTTTGAGCAATCTACTTCAACCAATGGCTGGAATTTATTGACTGTGTGCTGT 254  
 DB 88135 GGCTGCCCTGGCCGCACTACTTCAACCAAGCTGGAATTTATTGACTGTGTGCTGT 88194  
 QY 255 GCTCTCTTCATTTAGTAAATCAAGCAGTCAAGGGA 297  
 DB 88195 CATCTCTTCATTTAGTAAATCAAGCAGTCAAGGGA 88237

RESULT 3  
 US-10-487-337-1  
 Sequence 1, Application US/10487337  
 GENERAL INFORMATION:  
 APPLICANT: Kenji OKUSE  
 APPLICANT: Mark BAKER  
 APPLICANT: Louis POON  
 APPLICANT: John Nicholas WOOD  
 APPLICANT: Mubashir Malik-Hall  
 TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS  
 FILE REFERENCE: 117-492 / N.86242A GCM  
 CURRENT APPLICATION NUMBER: US/10/487,337  
 CURRENT FILING DATE: 2004-02-20  
 PRIOR APPLICATION NUMBER: PCT/GB02/03852  
 PRIOR FILING DATE: 2002-08-20  
 PRIOR APPLICATION NUMBER: GB 0120238.1  
 PRIOR FILING DATE: 2001-08-20  
 NUMBER OF SEQ ID NOS: 55  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 1  
 LENGTH: 6524  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (204)...(6074)  
 OTHER INFORMATION:  
 US-10-487-337-1

Query Match 11.9%; Score 69.8; DB 6; Length 6524;  
 Best Local Similarity 69.3%; Pred. No. 5.3e-11;  
 Matches 95; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 137 TGACCATCTCCAGCTGGGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAATCT 196  
 DB 4732 TGAGCAGATCACTGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAATCT 4791

QY 197 TTGCTTTGAGCAATCTACTTCAACCAATGGCTGGAATTTATTGATGTCATCAAAAT 256  
 DB 4792 TGCCCTCGACAGATCACTTCAACCAAGCTGGAATTTATTGATGTCATCAAAAT 4851  
 QY 257 TTCTTTCCATTTAGT 273  
 DB 4852 TCCTGTCCATTTAGT 4868

RESULT 4  
 US-60-548-091-267  
 Sequence 267, Application US/60548091  
 GENERAL INFORMATION:  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001506  
 CURRENT APPLICATION NUMBER: US/60/548,091  
 CURRENT FILING DATE: 2004-02-27  
 NUMBER OF SEQ ID NOS: 24433  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 267  
 LENGTH: 4852  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-60-548-091-267

Query Match 11.9%; Score 69.6; DB 7; Length 4852;  
 Best Local Similarity 68.6%; Pred. No. 5.3e-11;  
 Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 135 CTGACCATCTCCAGCTGGGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 194  
 DB 3569 CTGGCCAGATCACTGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 3628  
 QY 195 CTTTGCTTTGAGCAATCTACTTCAACCAATGGCTGGAATTTATTGACTGTGTGCTGT 254  
 DB 3629 GGCTGCCCTGGCCGCACTACTTCAACCAAGCTGGAATTTATTGACTGTGTGCTGT 3688  
 QY 255 GCTCTCTTCATTTAGTAAATCAAGCAGTCAAGGGA 297  
 DB 3689 CATCTCTTCATTTAGTAAATCAAGCAGTCAAGGGA 3708

RESULT 5  
 US-60-548-091-266  
 Sequence 266, Application US/60548091  
 GENERAL INFORMATION:  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001506  
 CURRENT APPLICATION NUMBER: US/60/548,091  
 CURRENT FILING DATE: 2004-02-27  
 NUMBER OF SEQ ID NOS: 24433  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 266  
 LENGTH: 4855  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-60-548-091-266

Query Match 11.9%; Score 69.6; DB 7; Length 4855;  
 Best Local Similarity 68.6%; Pred. No. 5.3e-11;  
 Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 135 CTGACCATCTCCAGCTGGGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 194  
 DB 3572 CTGGCCAGATCACTGCTCTTTGTGTCATCTTTAGATTGATGTCATCAAAAT 3631  
 QY 195 CTTTGCTTTGAGCAATCTACTTCAACCAATGGCTGGAATTTATTGACTGTGTGCTGT 254  
 DB 3632 GGCTGCCCTGGCCGCACTACTTCAACCAAGCTGGAATTTATTGACTGTGTGCTGT 3691

OY 255 GCTTCTTCCATTGTTAGTA 274  
DB 3692 CATCCTCCATCGTGGGCA 3711

## RESULT 6

US-60-548-091-268  
; Sequence 268, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001506  
; CURRENT APPLICATION NUMBER: US/60/548,091  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 268  
; LENGTH: 4855  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-268

Query Match 11.9%; Score 69.6; DB 7; Length 4855;  
Best Local Similarity 68.6%; Pred. No. 5.3e-11;  
Matches 96; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 135 CTTCGACATCTCAATGGGCTTTGGTCACTTTACGTTAGATGTCATCAAAAT 194  
DB 3572 CTTCGACCAAGATCAACGCTCTTTGTGGCCATCTTCACAGGCAAGTATTTGCAACT 3631  
OY 195 CTTCGCTTGAAGCAATCTACTTACCAATGGCTGAATTTATTTGACTGTGTGCT 254  
DB 3632 GGCTGGCCCTGGGCACTACTACTTACCAAGCTGAATATCTTCGACTTGTGTGT 3691  
OY 255 GCTTCTTCCATTGTTAGTA 274  
DB 3692 CATCCTCCATCGTGGGCA 3711

## RESULT 7

US-60-548-091-5582  
; Sequence 5582, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001506  
; CURRENT APPLICATION NUMBER: US/60/548,091  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5582  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-5582

Query Match 7.4%; Score 43.4; DB 7; Length 201;  
Best Local Similarity 72.7%; Pred. No. 0.0012;  
Matches 56; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 198 TGCTTTGAGCAATCTACTTACCAATGGCTGAATTTATTTGACTGTGTGCT 257  
DB 3 TGCCCTGGCCACTACTTACCAACAGCTGGAATATCTTCGACTTGTGTGTGCT 62

OY 258 TCTTTCATTGTTAGTA 274  
DB 63 CCTTCATCGTGGGCA 79

## RESULT 8

US-60-548-091-5566  
; Sequence 5566, Application US/60548091  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001506  
; CURRENT APPLICATION NUMBER: US/60/548,091  
; CURRENT FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 24433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5566  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-548-091-5566

Query Match 6.8%; Score 39.8; DB 7; Length 201;  
Best Local Similarity 74.6%; Pred. No. 0.014;  
Matches 50; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 208 CAATCTACTTCAACCAATGGCTGAATTTATTTGACTGTGTGCTTCTTCATT 267  
DB 2 CACTACTACTTCAACCAAGCTGAATATCTTCGACTTGTGTGCTTCTTCATT 61

OY 268 GTTGTGA 274  
DB 62 GTGGGCA 68

## RESULT 9

US-10-796-280-6719  
; Sequence 6719, Application US/10796280  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001510  
; CURRENT APPLICATION NUMBER: US/10/796,280  
; CURRENT FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 68533  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6719  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-796-280-6719

Query Match 6.5%; Score 38.2; DB 6; Length 201;  
Best Local Similarity 56.7%; Pred. No. 0.044;  
Matches 89; Conservative 1; Mismatches 64; Indels 3; Gaps 1;

OY 121 CCATGAATCATCTTACCATCTTCAATGGGCTTTGTGTCATCTTACGTTAGAA 180  
DB 43 CCTTCATCTATGCAATGACATCTTCAATGCTTTCACCTTTCATCTATTTG 102

OY 181 TGCTCATCAAAATCTTGTGTTAGGC--AATACTACTTACCAATGGCTGAATTA 237  
DB 103 ATGGTGTCAAAATCATGCTTCAAGCCAAAGATTACTTACATGATGCTGAAACAG 162

OY 238 TTTGACTGTGTGCTGCTTCTTTCATTTTGTAGTA 274  
DB 163 TTTGACGCTTATTTGTGTGGGACATAGTGTAGTA 199

## RESULT 10

US-10-796-280-6751  
; Sequence 6751, Application US/10796280  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001510

; CURRENT APPLICATION NUMBER: US/10/796,280  
 ; CURRENT FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 68533  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 6751  
 ; LENGTH: 201  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-796-280-6751

Query Match  
 Best Local Similarity 56.7%; Pred. No. 0.044;  
 Matches 89; Conservative 1; Mismatches 64; Indels 3; Gaps 1;

QY 121 CCATGAATCCATCCTTGACCATCCACATGGGCTTTGGTGCATCTTTACGTTAGA 180  
 DB 43 CCCTTCAACTATGCCATGACATCCTCAACATGGCTTACATGGCCTCTTCACTATTG 102  
 QY 181 TGTCTCATCAAAATCTTTGCTTTGAGGC--ATACTACTTCACCAATGGCTGAATT 237  
 DB 103 ATGGTCTCAAAATATATCGCTTCAAGCCCAAGCATTAATCTCATGATGCTGGAACAG 162  
 QY 238 TTTGACTGTGTGCTGCTCTTTCCATTGTAGTA 274  
 DB 163 TTTGACGCTCTTATTGTGTGGGAGCAGATAGTGATA 199

RESULT 11  
 US-10-796-280-6783  
 ; Sequence 6783, Application US/10796280  
 ; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CL001510  
 ; CURRENT APPLICATION NUMBER: US/10/796,280  
 ; CURRENT FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 68533  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 6783  
 ; LENGTH: 201  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-796-280-6783

Query Match  
 Best Local Similarity 56.7%; Pred. No. 0.044;  
 Matches 89; Conservative 1; Mismatches 64; Indels 3; Gaps 1;

QY 121 CCATGAATCCATCCTTGACCATCCACATGGGCTTTGGTGCATCTTTACGTTAGA 180  
 DB 43 CCCTTCAACTATGCCATGACATCCTCAACATGGCTTACATGGCCTCTTCACTATTG 102  
 QY 181 TGTCTCATCAAAATCTTTGCTTTGAGGC--ATACTACTTCACCAATGGCTGAATT 237  
 DB 103 ATGGTCTCAAAATATATCGCTTCAAGCCCAAGCATTAATCTCATGATGCTGGAACAG 162  
 QY 238 TTTGACTGTGTGCTGCTCTTTCCATTGTAGTA 274  
 DB 163 TTTGACGCTCTTATTGTGTGGGAGCAGATAGTGATA 199

RESULT 12  
 US-10-796-280-6815  
 ; Sequence 6815, Application US/10796280  
 ; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CL001510  
 ; CURRENT APPLICATION NUMBER: US/10/796,280  
 ; CURRENT FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 68533

; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 6815  
 ; LENGTH: 201  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-796-280-6815

Query Match  
 Best Local Similarity 56.7%; Pred. No. 0.044;  
 Matches 89; Conservative 1; Mismatches 64; Indels 3; Gaps 1;

QY 121 CCATGAATCCATCCTTGACCATCCACATGGGCTTTGGTGCATCTTTACGTTAGA 180  
 DB 43 CCCTTCAACTATGCCATGACATCCTCAACATGGCTTACATGGCCTCTTCACTATTG 102  
 QY 181 TGTCTCATCAAAATCTTTGCTTTGAGGC--ATACTACTTCACCAATGGCTGAATT 237  
 DB 103 ATGGTCTCAAAATATATCGCTTCAAGCCCAAGCATTAATCTCATGATGCTGGAACAG 162  
 QY 238 TTTGACTGTGTGCTGCTCTTTCCATTGTAGTA 274  
 DB 163 TTTGACGCTCTTATTGTGTGGGAGCAGATAGTGATA 199

RESULT 13  
 US-10-796-280-6845  
 ; Sequence 6845, Application US/10796280  
 ; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CL001510  
 ; CURRENT APPLICATION NUMBER: US/10/796,280  
 ; CURRENT FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 68533  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 6845  
 ; LENGTH: 201  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-796-280-6845

Query Match  
 Best Local Similarity 56.7%; Pred. No. 0.044;  
 Matches 89; Conservative 1; Mismatches 64; Indels 3; Gaps 1;

QY 121 CCATGAATCCATCCTTGACCATCCACATGGGCTTTGGTGCATCTTTACGTTAGA 180  
 DB 43 CCCTTCAACTATGCCATGACATCCTCAACATGGCTTACATGGCCTCTTCACTATTG 102  
 QY 181 TGTCTCATCAAAATCTTTGCTTTGAGGC--ATACTACTTCACCAATGGCTGAATT 237  
 DB 103 ATGGTCTCAAAATATATCGCTTCAAGCCCAAGCATTAATCTCATGATGCTGGAACAG 162  
 QY 238 TTTGACTGTGTGCTGCTCTTTCCATTGTAGTA 274  
 DB 163 TTTGACGCTCTTATTGTGTGGGAGCAGATAGTGATA 199

RESULT 14  
 US-10-796-280-6873  
 ; Sequence 6873, Application US/10796280  
 ; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CL001510  
 ; CURRENT APPLICATION NUMBER: US/10/796,280  
 ; CURRENT FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 68533  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 6873  
 ; LENGTH: 201



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 343.35 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-16  
Perfect score: 585  
Sequence: 1 ttccccgacacatacaaggt.....tgctgtgtgtgagaaatttc 585

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_estbm:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_dln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	360.8	61.7	523	13	BX112455 BX112455
2	316.8	54.2	435	5	AA885211 am34c11.8
3	213.4	36.5	330	9	AA913881 om21h12.8
4	160.4	27.4	4614	29	AY404475 Homo sapi

5	143.6	24.5	3772	29	AY404476	AY404476 Pan trogl
6	110	18.8	4556	29	AY404477	AY404477 Mus muscu
C 7	88.2	15.1	555	14	CB613444	CB613444 AMGNINC:C
8	77.2	13.2	402	13	BY267638	BY267638 B1267638
9	77.2	13.2	473	14	CF535148	CF535148 UI-M-G10-
10	77.2	13.2	908	13	BQ946179	BQ946179 AGENCOURT
11	77.2	13.2	4675	11	AK083220	AK083220 Mus muscu
12	77.2	13.2	5666	29	AY416501	AY416501 Mus muscu
13	77.2	13.2	5943	29	AY416499	AY416499 Homo sapi
14	72.4	12.4	518	12	BG578677	BG578677 dac36c11.
15	71.8	12.3	610	9	AL588672	AL588672 AL588672
16	71.8	12.3	632	9	AJ396135	AJ396135 AJ396135
17	71	12.1	529	9	AA183990	AA183990 mes3e02.r
18	69.8	11.9	553	14	CB613903	CB613903 AMGNINC:N
19	69.2	11.8	944	13	BQ731018	BQ731018 AGENCOURT
20	69.2	11.8	1043	29	CNS02Y6B	AL215260 Tetradon
21	67	11.5	446	13	BX499931	BX499931 DKFZP779F
22	67	11.5	778	9	AU035605	AU035605 AU035605
C 23	65.6	11.2	663	28	AZ091181	AZ091181 RPCT-23-4
24	65.4	11.2	5710	29	AY416500	AY416500 Pan trogl
25	64.8	11.1	544	10	BF323267	BF323267 ma38e08.
C 26	64.8	11.1	604	29	FR0002761	286544 F.rubripes
27	63.4	10.8	768	14	CB520657	CB520657 UI-M-BH3-
28	60.4	10.3	402	12	BM484672	BM484672 538604 MA
29	60.2	10.3	768	29	CC586299	CC586299 CH240.383
30	59	10.1	718	14	CD804204	CD804204 UI-M-GV0-
31	57.8	9.9	602	9	AL706368	AL706368 DKFZP686H
32	57.2	9.8	674	12	BG342331	BG342331 602374246
33	56.8	9.7	911	14	CD327202	CD327202 AGENCOURT
34	55.8	9.5	547	10	BF470392	BF470392 UI-M-BH3-
35	55.8	9.5	561	10	BF076296	BF076296 225823 MA
C 36	55.4	9.5	840	29	CNS02ZFO	AL221253 Tetradon
37	55	9.4	287	28	AZ081279	AZ081279 SCNA4.Fel
38	51.8	8.9	592	13	BW228334	BW228334 BW228334
39	50.2	8.6	724	13	BW223297	BW223297 BW223297
40	50	8.5	502	12	BM633126	BM633126 170006875
41	48.6	8.3	658	13	BX501378	BX501378 DKFZP779J
42	46	7.9	1126	13	BX446391	BX446391 BX446391
43	45.4	7.8	619	29	FR0002759	286542 F.rubripes
44	43.6	7.5	873	28	AZ534875	AZ534875 ENTCAB3TF
45	42.4	7.2	774	28	AQ743380	AQ743380 HS_5387_B

#### ALIGNMENTS

RESULT 1  
LOCUS BX112455/c 523 bp mRNA linear EST 07-FEB-2003  
DEFINITION BX112455 Soares\_NFL.T.GBC.SI Homo sapiens cDNA clone  
IMAGP998B213715 ; IMAGE:1468724, mRNA sequence.  
ACCESSION BX112455  
VERSION BX112455.1 GI:27878914  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Patsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
HUMAN UNIGENES - RZPD3  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP998B213715.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-  
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTACACAGGAAACAGCTATGAC.

# FEATURES

source

1..523  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE98B213715 ; IMAGE:1468724"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 61.7%; Score 360.8; DB 13; Length 523;  
Best Local Similarity 93.2%; Pred. No. 1.4e-83;  
Matches 412; Conservative 0; Mismatches 22; Indels 8; Gaps 3;

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QY 70 TACCTAAACGATGATGGCTTGAATGCTTAATATATCAACCAACCCCAAGCATGGAT 129
   |||
Db 434 TATCTTAAACATGATTTAGCATGATGCTGATCATCAACCA-CCCAAGCCATGAAT 376
   |||
QY 130 CCATCCTTACCATCCCACTGCGCTTGTGTCATCTTTAGTAAATGTCATC 189
   |||
Db 375 CCATCCTTACCATCT-CACTGCGCTTGTGTCATCTTTAGTAAATGTCATC 317
   |||
QY 190 AAAATCTTTGCTTGAAGCAATCTACTTACCAATGCTGAATTTATTTGACTGTG 249
   |||
Db 316 AAAATCTTTGCTTGAAGCAATCTACTTACCAATGCTGAATTTATTTGACTGTG 257
   |||
QY 250 GTGTCCTTCTTCCATTTGTAGTAATTAATACAGCATCAGAGGACTTTAAGAACCA 309
   |||
Db 256 GTGTCCTTCTTCCATTTGTAGTAATTAATTAATTAATTAATTAATTAATTAATTA 197
   |||
QY 310 GAAGTAAGTTTGAATCTTATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 369
   |||
Db 196 GAAGTAAGTTTGAATCTTATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 137
   |||
QY 370 AAATGCGGCAAGTACTTCTGAAAGATAGACAGGGGTACTTAATGCAATCTCTACT 429
   |||
Db 136 AAATGCGGCAAGTACTTCTGAAAGATAGACAGGGGTACTTAATGCAATCTCTACT 77
   |||
QY 430 GGAAGTGTCTAGAGATAGAGAGCGGTAAATTTCTGTTCCCTTAATCTACTACACAA 489
   |||
Db 76 GGAAGTGTCTAGAGATA-----GAGAGTAATTTCTGTTCCCTTAATCTACTACACAA 23
   |||
QY 490 CTGAATAGGTTCAATATCA 511
   |||
Db 22 CTGAATAGGTTCAATATCA 1
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RESULT 2  
LOCUS AA885211 435 bp mRNA linear EST 04-JAN-1999  
DEFINITION am34c11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1468724 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE  
X, ALPHA POLYPEPTIDE ;, mRNA sequence.  
ACCESSION AA885211  
VERSION AA885211.1 GI:2994288

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

EST.  
Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 435)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

Possible reversed clone; similarity on wrong strand

Insert Length: 561 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 390.

Location/Qualifiers

1..435

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1468724"

/lab\_host="DH10B"

/clone\_lib="Soares\_NFL\_T\_GBC\_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI CGAP GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 54.2%; Score 316.8; DB 9; Length 435;  
Best Local Similarity 96.1%; Pred. No. 4.5e-72;  
Matches 346; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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QY 70 TACCTAAACGATGATGGCTTGAATGCTTAATATATCAACCAACCCCAAGCATGGAT 129
   |||
Db 78 TATCTTAAACATGATTTAGCATGATGCTGATCATCAACCA-CCCAAGCCATGAAT 136
   |||
QY 130 CCATCCTTACCATCCCACTGCGCTTGTGTCATCTTTAGTAAATGTCATC 189
   |||
Db 137 CCATCCTTACCATCT-CACTGCGCTTGTGTCATCTTTAGTAAATGTCATC 195
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QY 190 AAAATCTTTGCTTGAAGCAATCTACTTACCAATGCTGAATTTATTTGACTGTG 249
   |||
Db 196 AAAATCTTTGCTTGAAGCAATCTACTTACCAATGCTGAATTTATTTGACTGTG 255
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QY 250 GTGTCCTTCTTCCATTTGTAGTAATTAATACAGCATCAGAGGACTTTAAGAACCA 309
   |||
Db 256 GTGTCCTTCTTCCATTTGTAGTAATTAATTAATTAATTAATTAATTAATTAATTA 315
   |||
QY 310 GAAGTAAGTTTGAATCTTATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 369
   |||
Db 316 GAAGTAAGTTTGAATCTTATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 375
   |||
QY 370 AAATGCGGCAAGTACTTCTGAAAGATAGACAGGGGTACTTAATGCCATTTCTACT 429
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Db 376 AAATGCGGCAAGTACTTCTGAAAGATAGACAGGGGTACTTAATGCCATTTCTACT 435
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```

RESULT 3  
LOCUS AA913881 330 bp mRNA linear EST 10-JUN-1998  
DEFINITION cm21h12.s2 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
IMAGE:1541735.3'				
X, ALPHA POLYPEPTIDE ; , mRNA sequence.				
AA913881				
AA913881.1	GI:3053273			
EST.				
Homo sapiens	(human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
Tumor Gene Index				
Unpublished (1997)				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-remail.nih.gov				
This clone is available royally-free through LNL; contact the				
IMAGE Consortium ( <a href="http://infoimage.lnl.gov/">infoimage.lnl.gov/</a> ) for further information.				
Insert Length: 562 Scd Error: 0.00				
Seq primer: -40m13 fwd. ET from Amer sham				
High quality sequence stop: 322.				
Location/Qualifiers				
1..330				
/organism="Homo sapiens"				
/mol_type="mRNA"				
/db_xref="taxon:9606"				
/clone="IMAGE:1541735"				
/lab_host="DH10B"				
/clone_lib="Soares NFL T GBC S1"				
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with				
a modified polylinker; Site_1: Not I; Site_2: Eco RI;				
Equal amounts of plasmid DNA from three normalized				
libraries (fetal lung NDHL19w, testis NHT, and B-cell				
NCI CGAP GCBI) were mixed, and ss circles were made in				
vitro. Following HAP purification, this DNA was used as				
tracer in a subtractive hybridization reaction. The diver				
was PCR-amplified cDNAs from pools of 5,000 clones made				
from the same 3 libraries. The pools consisted of				
I.M.A.G.E. clones 297480-302087, 682632-687239,				
726408-728711, and 729096-731399. Subtraction by Bento				
Soares and M. Fatima Bonaldo."				
ORIGIN				
Query Match	36.5%; Score 213.4; DB 9; Length 330;			
Best Local Similarity	94.9%; Pred. No. 4.7e-45;			
Matches	242; Conservative 0; Mismatches 11; Indels 2; Gaps 2;			
OY	70 TACTAAACCATGATGGCTTGATGGCTTAATAATACAACCAGCCATGTGAAT	129		
Db	78 TATCCTAACAATGATTAGCATGATGGCTGAATCAACAACCA-CCCAAGCATGAAAT	136		
OY	130 CCATCCTTGACCATTCACAACTGGCTTTGGGCATCTTAGCTTAGAATGTCATC	189		
Db	137 CCATCCTTGACCATTC-CAACTGGCTTTGGGCATCTTAGCTTAGAATGTCATC	195		
OY	190 AAAATCTTGGCTTGAAGGCAATACTACTTCCAATGGCTGGAAATTTATGACTGTGTG	249		
Db	196 AAAATCTTGGCTTGAAGGCAATACTACTTCCAATGGCTGGAAATTTATGACTGTGTG	255		
OY	250 GTCGTGTCTTTCCATGTTAGTAAATACGACGTCAGAGGGGACTTTAAGAACA	309		
Db	256 GTCGGCTCTTCCATGTTAGTAAATACGACGTCAGAGGGGACTTTAAGAACA	315		
OY	310 GAAGTAAGTTGTAA 324			
Db	316 GAAGTAAGTTGTAA 330			
RESULT 4				
LOCUS	AY040475	4614 bp	DNA	linear
DEFINITION	Homo sapiens SCN11A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
		GSS 16-DEC-2003		

ACCSSION	AY404475
VERSION	AY404475.1
KEYWORDS	GI:39760452
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 4614) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 4614)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..4614 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>4614 /gene="SCN11A" /locus_tag="HCM1903"
ORIGIN	
Query Match	27.4%; Score 160.4; DB 29; Length 4614;
Best Local Similarity	93.6%; Pred. No. 4e-31;
Matches 189; Conservative	0; Mismatches 11; Indels 2; Gaps 2;
QY	70 TACCTAACCATGATGGCTTGATGGCTTAATGATTAACACCAACCCCAAGCCATGAT 129 
DB	3573 TATCTTAACATGATTAAGCATGATGAGCTGATCATACCAACCCCAAGCCATGAT 3631 
QY	130 CCATCTTGGACCATCTCCACCTGGGCTTTGGTGCATCTTTACGTAGATGTCATC 189 
DB	3632 CCATCTTGGACCATCT-CACTGGGCTTTGGTGCATCTTTAGTAGATGTCATC 3690 
QY	190 AAAATCTTTGCTTGAAGGCATTAATCTTCAACCATGGCTGGAATTTATTTACTGTGTG 249 
DB	3691 AAAATCTTTGCTTGAAGGCATTAATCTTCAACCATGGCTGGAATTTATTTACTGTGTG 3750 
QY	250 GTCTGCTCTTCTTCCATGTTTA 271 
DB	3751 GTCTGCTCTTCTTCCATGTTTA 3772 
RESULT 5	
LOCUS	AY404476 3772 bp DNA linear GSS 16-DEC-2003
DEFINITION	Pan troglodytes SCN11A gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION	AY404476
VERSION	AY404476.1
KEYWORDS	GI:39760453
SOURCE	GSS.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
AUTHORS	1 (bases 1 to 3772) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J.,

TITLE Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3772)  
 AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment  
 FEATURES  
 source Location/Qualifiers  
 1..3772  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>3772  
 /gene="SCN11A"  
 /locus\_tag="HCM1903"  
 ORIGIN  
 Query Match 24.5%; Score 143.6; DB 29; Length 3772;  
 Best Local Similarity 96.9%; Pred. No. 9,7e-27;  
 Matches 157; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 110 CAACCCCAAGCCATGATCCATCCTTACCATCTCCACATGAGTCTTGGTGCATCT 169  
 DB 3612 CCAACCCCAAGCCATGATCCATCCTTACCATCT-CACTGGGCTTTGGTGCATCT 3670  
 QY 170 TTACGTTAGATGCTCATCAAAATCTTTGCTTTGAGGCAATACATTCACCAATGGCT 229  
 DB 3671 TTACATTTAGATGCTCATCAAAATCTTTGCTTTGAGGCAATACATTCACCAATGGCT 3730  
 QY 230 GGAATTTATTTGACGTGTCGTGTCGTCTCTTCCATTTGTA 271  
 DB 3731 GGAATTTATTTGACGTGTCGTGTCGTCTCTTCCATTTGTA 3772  
 RESULT 6  
 AY404477 4556 bp DNA linear GSS 16-DEC-2003  
 LOCUS Mus musculus SCN11A gene, VIRUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY404477  
 VERSION AY404477.1 GI:39760454  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 4556)  
 REFERENCE 1 (bases 1 to 4556)  
 AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 COMMENT

FEATURES  
 source Location/Qualifiers  
 1..4556  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
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 /gene="SCN11A"  
 /locus\_tag="HCM1903"  
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 Query Match 18.8%; Score 110; DB 29; Length 4556;  
 Best Local Similarity 76.0%; Pred. No. 6e-18;  
 Matches 149; Conservative 0; Mismatches 45; Indels 2; Gaps 1;  
 QY 76 AACCATGATGCTGATGAGCCCTTAATATACAAACCAACCCCAAGCATGATCCATCC 135  
 DB 3539 AACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3596  
 QY 136 TTGACCATCTCCACATGAGTCTTTGGTGCATCTTTAGATGATCTCATCAAAATC 195  
 DB 3597 TTGATATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3656  
 QY 196 TTGCTTTGAGGCAATACATCTTCAACCAATGGCTGGAATTTATTGACTGTGTGCTG 255  
 DB 3657 TTGCTTTGAGGCAACATCACTTCAACCAATGGCTGGAATTTATTGATGATGATGATG 3716  
 QY 256 CTTCCTTCATTTGTA 271  
 DB 3717 GTTCTTTCATCATTTA 3732  
 RESULT 7  
 CB613444/c 555 bp mRNA linear EST 07-APR-2003  
 LOCUS AMGNNUC:CDRG2-00013-C5-A cdrg2 (10902) Rattus norvegicus cDNA clone  
 DEFINITION cdrg2-00013-c5 5', mRNA sequence.  
 ACCESSION CB613444  
 VERSION CB613444.1 GI:29573332  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 555)  
 REFERENCE 1 (bases 1 to 555)  
 AUTHORS Amgen EST Program  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00013 row: C column: 5.  
 FEATURES  
 source Location/Qualifiers  
 1..555  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="cdrg2-00013-c5"  
 /cissue\_type="peptide and housekee"  
 /clone\_1b="cdrg2 (10902)"  
 /note="Vector: multiple; peptides and housekeeping"  
 ORIGIN  
 Query Match 15.1%; Score 88.2; DB 14; Length 555;  
 Best Local Similarity 74.5%; Pred. No. 2.6e-12;  
 Matches 111; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
 QY 126 GAATCATCTTGTACATCTCAACATGAGTCTTTGGTGCATCTTTAGCTTAAGTCT 185  
 DB 548 GAAGAAACCTTGTATCTTCAACATGATGATGATGATGATGATGATGATGATGATGATG 489  
 QY 186 CATCAAAATCTTGTGTTGAGGCAATACATTCACCAATGAGCTGGAATTTATTGACTG 245

Db	Oy	Dd	RESULT 8 BY267638 LOCUS DEFINITION ACCESSION VERSION SOURCE ORGANISM
468	246	428	<p>CATGAGACTCTTGTCTGTAAAGCACTGTGGCTTCACCATGCTCGAATTATTTGATTG 429</p> <p>TGTGGTGCTGCTCTCTTTCCATTGTTAGTA 274</p> <p>TGTGGTGCTGCTCTTTCCATTGTTAGTA 400</p> <p>BY267638 402 bp mRNA linear EST 11-DEC-2002</p> <p>BY267638 RIKEN full-length enriched, visual cortex Mus musculus</p> <p>cDNA clone KJ30018G10 5', mRNA sequence.</p> <p>BY267638.1 GI:26457845</p> <p>Mus musculus (house mouse)</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 402)</p> <p>Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamana,K.I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gotohori,T., Baldarelli,R., Hill,D.P., Bulc,C., Hune,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.B., Bradt,D., Brusic,V., Chociba,C., Corbani,L.E., Cousins,S., Della,E., Dreganti,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Glasi,C., Godzik,A., Gough,J., Grimmond,S., Guertincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurtochkin,I.V., Lee,Y., Lehar,B., Lyons,P.A., Maglott,D.R., Mallat,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pereira,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S., Ravasi,T., Reed,J.C., Reed,D.T., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shindada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavoian,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Komio,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,U., Aizawa,K., Akazawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,K., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterson,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.</p> <p>Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)</p> <p>Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suheiho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Aizawa,K., Akimura,T., Arakawa,T., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Komio,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numasaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watanuki,A., Watanatsu,M. and Hayashizaki,Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10) 1617-1630 (2000)</p>

FEATURES	SOURCE
ORIGIN	<p>RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)</p> <p>Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research at Riken contributed to prepare mouse tissues.</p> <p>Tissues were provided by Michela Fagioli and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirooawa, Wako-shi, Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (<a href="http://genome.98c.riken.go.jp">http://genome.98c.riken.go.jp</a>) for further details.</p> <p>Location/Qualifiers</p> <p>1..402</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="K430018G10"</p> <p>/tissue_type="visual cortex"</p> <p>/clone_1ib="RIKEN full-length enriched, visual cortex"</p>
Query Match	13.2%; Score 77.2; DB 13; Length 402;
Best Local Similarity	74.6%; Prod. No. 1.9e-09;
Matches	Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY	148 AACTGGCTCTTTGGTGCATCTTTACGTTGAATGTCTATCAAAATCTTGGCTTAGG 207
DB	254 AATCTGCTCTTCGCATCTTCTTCACCTGCGAGTGTGTCTCAAAAAGTTTGCCTTGAGA 313
QY	208 CAATACACTTCCACCATGCTGGAAATTATTTGACGTGTGCGTCTTTTCATT 267
DB	314 CACTACTATTTCACCATGCTGGAAACATCTTTGACTTTGTGTGTCATCTTCATTT 373
QY	268 GTTAGTAGT 277
DB	374 GTGGAGATGT 383
RESULT 9	
CF535148	473 bp mRNA linear EST 12-SEP-2003
LOCUS	UF-M-GIO-chg-f-20-0-UF.r1 NIH_BMAP_GIO Mus musculus cDNA clone
DEFINITION	IMAGE:30536371 5', mRNA sequence.
ACCESSION	CF535148
VERSION	CF535148.1 GI:34587116
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Embryonic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 473)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strauberg, Ph.D. Email: <a href="mailto:cgabds-remail.nih.gov">cgabds-remail.nih.gov</a> Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at <a href="http://genome.uiowa.edu/distribution/mousefl.html">http://genome.uiowa.edu/distribution/mousefl.html</a> This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
FEATURES	Seq primer: PYX-5.
SOURCE	Location/Qualifiers 1..473

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30536971"  
/tissue\_type="whole brain"  
/tissue="embryo 13.5,14.5,16.5,17.5dp"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP G10"  
/note="Organ: Brain; Vector: pYX-Anc; Site\_1: Ecor I; Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Anc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemu Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 13.2%; Score 77.2; DB 14; Length 473;  
Best Local Similarity 74.6%; Pred. No. 1.9e-09;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACTGGGCTTTGGTCATCTTACGTTAGATGTCATCAAACTTTGCTTAGG 207  
DB 254 AATCTGCTCTGTCATCTTTCACCTGGAGTGTGCTCAAAAGTTGCTTGAAG 313  
QY 208 CACTACTCTTCAACCAATGGCTGAATTTATTTGACTGTGCTGCTCTTCCATT 267  
DB 314 CACTACTATTTCAACCAATGGCTGAACATCTTGTGCTGTCATCTTCCATT 373  
QY 268 GTTAGTAGT 277  
DB 374 GTGGGAATGT 383

RESULT 10  
B0946179 908 bp mRNA linear EST 21-ANG-2002  
LOCUS AGENCOURT\_8926526 NIH\_MGC\_94 Mus musculus cDNA IMAGE:6469275  
DEFINITION 5', mRNA sequence.  
ACCESSION B0946179  
VERSION B0946179.1 GI:22361657  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 908)  
TITLES NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM13998 Row: C Column: 04  
High quality sequence stop: 596.  
Location/Qualifiers  
1. 908  
/organism="Mus musculus"

## FEATURES

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1. 908  
/organism="Mus musculus"

/mol\_type="mRNA"  
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/clone="IMAGE:6469275"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_94"  
/note="Organ: eye; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 13.2%; Score 77.2; DB 13; Length 908;  
Best Local Similarity 74.6%; Pred. No. 2e-09;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACTGGGCTTTGGTCATCTTACGTTAGATGTCATCAAACTTTGCTTAGG 207  
DB 558 AATCTGCTCTGTCATCTTTCACCTGGAGTGTGCTCAAAAGTTGCTTGAAG 617  
QY 208 CACTACTCTTCAACCAATGGCTGAATTTATTTGACTGTGCTGCTCTTCCATT 267  
DB 618 CACTACTATTTCAACCAATGGCTGAACATCTTGTGCTGTCATCTTCCATT 677  
QY 268 GTTAGTAGT 277  
DB 678 GTGGGAATGT 687

RESULT 11  
AK083220 4675 bp mRNA linear HTC 20-SEP-2003  
LOCUS Mus musculus adult male hippocampus cDNA, RIKEN full-length  
DEFINITION enriched library, clone: C630028C19 product: sodium channel,  
voltage-gated, type VIII, alpha polypeptide, full insert sequence.  
ACCESSION AK083220  
VERSION AK083220.1 GI:26101130  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1  
TITLES Carninci, P. and Hayashizaki, Y.  
JOURNAL High-efficiency full-length cDNA cloning  
MEDLINE Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 99279253  
10349636

REFERENCE 2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159

3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 4675)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Iehi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.  
Location/Qualifiers

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source  
1. .4675  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="MGI:2417601"  
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/clone="C630029C19"  
/sex="male"  
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/clone\_id="RIKEN full-length enriched mouse cDNA library"  
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Best Local Similarity 74.6%; Pred. No. 2.2e-09;  
Matches 97; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 148 AACTGGGCTTTGGTCATCTTTACGTTAGATGCTCATCAAAATCTTGGCTTGAAG 207  
DB 2318 AATCGGCTTCGTCATCTTTACCTGCAGTGCTGCTCAAAATGTTGCCCTTGAGA 2377  
QY 208 CAATACCTCTACCAATGGCTGGAATATTATTTGACTGTGTGCTGCTTCTTCATT 267  
DB 2378 CACTACTATTTACCACTGGCTGGAACATCTTTGACTTTGTGTGCTCATTTCTTCATT 2437  
QY 268 GTTAGTAAGT 277  
DB 2438 GTGGGAATGT 2447

RESULT 12  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

AY16501  
Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY16501  
AY16501.1 GI:39772461  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 5666)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
Location/Qualifiers

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1. .5666  
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DB 4395 AATCGGCTTCGTCATCTTTACCTGCAGTGCTGCTCAAAATGTTGCCCTTGAGA 4454  
QY 208 CAATACCTCTACCAATGGCTGGAATATTATTTGACTGTGTGCTGCTTCTTCATT 267  
DB 4455 CACTACTATTTACCACTGGCTGGAACATCTTTGACTTTGTGTGCTCATTTCTTCATT 4514  
QY 268 GTTAGTAAGT 277  
DB 4515 GTGGGAATGT 4524

RESULT 13  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AY16499  
Homo sapiens SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY16499  
AY16499.1 GI:39772459  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 5943)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,



Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

# JOURNAL PUBMED REFERENCE AUTHORS

2 (bases 1 to 5943)  
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

# TITLE JOURNAL

COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

# FEATURES source

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QY 148 AACTGGGCTTTGGTGCATCTTACGTAGATGTCATCAAACTTTGGTGGAG 207  
DB 4672 AACCTGGTCTTGTATCTTCTTCACTGTGAGTGTCTCAAAATGTTGGTGGAG 4731  
QY 208 CAATACCTTCCACCAATGCTGGAATTTATTTGACTGTGCTGCTCTTCCATT 267  
DB 4732 CACTACTTCTTCCACCTGCTGGAACATCTTCACTGTGAGTGTCTCAAAATGTTGGTGGAG 4791  
QY 268 GTTATGTAAT 277  
DB 4792 GTGGGAATGT 4801

# RESULT 14

LOCUS BG578677 518 bp mRNA linear EST 11-APR-2001  
DEFINITION dacc36c11.y1 NICHD XGC Hel Xenopus laevis cDNA clone IMAGE:4409085  
5' similar to TR:062242 Q62242 SODIUM CHANNEL 1; mRNA sequence.  
ACCESSION BG578677  
VERSION BG578677.1 GI:13593741  
KEYWORDS EST.

# SOURCE ORGANISM

Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus.

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 518)  
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,  
Page, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,  
Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,  
Waterson, R. and Wilson, R.  
Washu Xenopus EST project, 1999  
Unpublished (1999)  
Contact: Sandy Clifton, Ph.D.  
Washu Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estowatson.wustl.edu  
Library constructed by Life Technologies. DNA Sequencing by:  
Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/BLMT at: info@image.llnl.gov  
Seq primer: -40RP from Gibco  
High quality sequence atop: 392.

# FEATURES source

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/clone\_lib="NICHD\_XGC\_Hel"  
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Average insert size 1.6 kb. Constructed by Life  
Technologies."

# ORIGIN

Query Match 12.4%; Score 72.4; DB 12; Length 518;  
Best Local Similarity 70.3%; Pred. No. 3.5e-08;  
Matches 97; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 137 TGACCATCTCCACCTGCGCTTTGGTGCATCTTACGTTAGAAATGTCACCAATCT 196  
DB 46 TGTACAAATCAACCTGTGCTGTATCTTCCGGGAATGCTTCAAGATCC 105  
QY 197 TTGCTTTGAGGCAACTACTTACCAATGCTGGAATTTATTTGACTGTGTGCTGTC 256  
DB 106 TTGCCTCAGGACACTTCTTCACTTCACTGCTGGAATGCTTCACTTGTGTGTTGA 165  
QY 257 TTCTTTCAATGTTAGTA 274  
DB 166 TACTTTCATGTTGAA 183

# RESULT 15

LOCUS AL588672 610 bp mRNA linear EST 02-MAR-2001  
DEFINITION AL588672 BP Chicken Brain Library Gallus gallus cDNA clone  
ROS075604, mRNA sequence.  
ACCESSION AL588672  
VERSION AL588672.1 GI:13193706  
KEYWORDS EST.

# SOURCE ORGANISM

Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 610)  
Murray, F.  
BP Chicken Brain Library  
Unpublished (2001)  
Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 0400  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk  
GCCGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech  
(\*6854-  
Seq primer: 77.  
Location/Qualifiers  
1..610  
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/lab\_host="DH10B"  
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/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; Cloned



unidirectionally. Primer: Oligo dT, 5' adaptor sequence: 5' TCGACTTCGAG 3', 3' adaptor sequence: 5' GCGGCGCGCTTTTCTTTTCTT 3' Poly A RNA purchased from Clontech (\*6854-1) "

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:11 ; Search time 1186.12 Seconds

(without alignments)  
8148.824 Million cell updates/sec

Title: US-09-646-224A-17

Perfect score: 223

Sequence: 1 tgaccaggtgaccacaaat.....ggagagtgatccacaaat 223

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*
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6: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	223	100.0	223	6	AX017233	AX017233 Sequence
2	223	100.0	223	6	BD138455	BD138455 Mammalian
3	200.6	90.0	5860	6	AR340678	AR340678 Sequence
4	200.6	90.0	6237	9	AF188679	AF188679 Homo sapi
5	200.6	90.0	167476	9	AC116038	AC116038 Homo sapi
6	199	89.2	6528	6	BD012082	BD012082 Human sod
7	199	89.2	6528	6	BD082951	BD082951 Human sod
8	199	89.2	6528	6	AF109737	AF109737 Homo sapi
9	136.6	61.3	5419	9	HSA417790	AJ237852 Homo sapi
10	100.6	45.1	5849	10	RNO237852	AR340646 Sequence
11	100.6	45.1	5875	6	AR340646	BD17791 Regulatio
12	100.6	45.1	5875	6	BD17791	BD17791 Regulatio
13	100.6	45.1	5897	6	AX017217	AX017217 Sequence
14	100.6	45.1	5897	6	BD138440	BD138440 Mammalian
15	100.6	45.1	5905	10	AF059030	AF059030 Rattus no
16	100.6	45.1	5908	6	E36122	E36122 Nucleic aci
17	100.6	45.1	203255	2	AC117294	AC117294 Rattus no
18	100.6	45.1	210800	2	AC127824	AC127824 Rattus no
19	100.6	45.1	243048	2	AC127215	AC127215 Rattus no
20	86.4	38.7	5822	6	AR340647	AR340647 Sequence
21	86.4	38.7	5822	6	BD217792	BD217792 Regulatio
22	86.4	38.7	5858	10	AF118044	AF118044 Mus muscu
23	86.4	38.7	5921	10	AB031389	AB031389 Mus muscu
24	86.4	38.7	241289	2	AC124662	AC124662 Mus muscu
25	65	29.1	5334	6	E36125	E36125 Nucleic aci
26	36	16.1	262545	2	AC126287	AC126287 Rattus no
27	35.8	16.1	102812	2	AL158215	AL158215 Homo sapi
28	35.8	16.1	147047	9	AL353778	AL353778 Human DNA
29	35	15.7	112961	9	HS322112	AL033518 Human DNA
30	34.8	15.6	110000	2	LMF1CHR31_09	Continuation (10 o
31	34.8	15.6	181401	2	AL954127	AL954127 Mus muscu
32	34.8	15.6	182885	2	LMF1CHR31	LMF1CHR31 Mus muscu
33	34.8	15.6	188624	10	AL772282	AL772282 Mouse DNA
34	34.8	15.6	227066	2	AC114674	AC114674 Mus muscu
35	34.6	15.5	217682	2	AC108913	AC108913 Mus muscu
36	34.6	15.5	217680	10	AC123714	AC123714 Mus muscu
37	34.4	15.4	224710	2	AC129758	AC129758 Rattus no
38	34.4	15.4	249668	2	AC094436	AC094436 Rattus no
39	34.4	15.4	293939	2	AC113622	AC113622 Rattus no
40	34	15.2	41680	10	AF049091	AF049091 Mus muscu
41	34	15.2	101491	10	AP003183	AP003183 Mus muscu
42	34	15.2	222560	2	AC013548	AC013548 Mus muscu
43	34	15.2	236172	2	AC094494	AC094494 Rattus no
44	34	15.2	248466	2	AC105146	AC105146 Rattus no
45	33.8	15.2	5685	9	HSM807476	BX647332 Homo sapi

# ALIGNMENTS

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RESULT 1
LOCUS AX017233
DEFINITION Sequence 17 from Patent WO9947670.
ACCESSION AX017233
VERSION AX017233.1 GI:10042153
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Tate,S.N., Grose,D.T. and Hick,C.A.
Mammalian sodium channel proteins
Patent: WO 9947670-A 17 23-SEP-1999;
JOURNAL
```

TATE SIMON NICHOLAS (GB) ; GLAXO GROUP LTD (GB) ; GROSE DAVID THOMAS  
(GB) ; HICK CAROLINE ANNE (GB)  
Location/Qualifiers  
1..223

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## ORIGIN

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QY 1 TGACCAAGGTGACCAAAATGACTTGGGAAAACGGGCGCTCATTCACCACTCCAGACTCTT 60  
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QY 61 TGCAATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACGCC 120  
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QY 121 CTCACCTCCAGCGCTTCACTCATAGCTTTCACAGCTTTGCTTCAAGCTCTGAGCTCCAGGG 180  
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QY 181 GTCACAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 181 GTCACAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223

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LOCUS BD138455  
DEFINITION Mammalian sodium channel protein.  
ACCESSION BD138455  
VERSION BD138455.1 GI:23233400  
KEYWORDS JP 2002508941-A/16.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 223)  
AUTHORS Grose,D.T., Hick,C.A. and Tate,S.N.  
TITLE Mammalian sodium channel protein  
JOURNAL Patent: JP 2002508941-A 16 26-MAR-2002;  
GLAXO GROUP LTD

COMMENT OS Homo sapiens (human)  
PN JP 2002508941-A/16  
PD 26-MAR-2002  
PF 18-MAR-1999 JP 2000536853  
PR 18-MAR-1998 GB 9805793.8  
PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC  
C12N15/09,A61K45/00,A61P17/04,A61P25/02,C07K14/705,C07K16/28, PC  
C12N1/15, PC  
C12N1/19,C12N1/21,C12N5/10,C12Q1/02,G01N33/15,G01N33/50,G01N33/ PC  
68, PC  
C12N15/00,C12N5/00  
CC Mammalian sodium channel protein  
FH Key 1..223  
FT source Location/Qualifiers  
FT 1..223 /organism="Homo sapiens (human)"

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QY 121 CTCACCTCCAGCGCTTCACTCATAGCTTTCACAGCTTTGCTTCAAGCTCTGAGCTCCAGGG 180  
DB 121 CTCACCTCCAGCGCTTCACTCATAGCTTTCACAGCTTTGCTTCAAGCTCTGAGCTCCAGGG 180  
QY 181 GTCACAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 181 GTCACAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223

RESULT 3  
AR340678 5860 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340678  
DEFINITION Sequence 41 from patent US 6573067.  
ACCESSION AR340678  
VERSION AR340678.1 GI:33732410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5860)  
AUTHORS Dib-Hajj,S. and Waxman,S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 41 03-JUN-2003;  
LOCATION/Qualifiers  
1..5860  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

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Best Local Similarity 97.7%; Pred. No. 1.7e-49;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCGCTCATTCACCACTCCAGACTCTTGGCA 64  
DB 5295 CCAAGGTGACCAAAATGACTTGGGAAAACGGGCGCTCATTCACCACTCCAGACTCTTGGCA 5353  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 124  
DB 5354 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 5413  
QY 125 CCTCAACGCTTCACTCATAGCTTTCACAGCTTTGCTTCAAGCTCTGAGCTCCAGGGGTCA 184  
DB 5414 CCTCAACGCTTCACTCATAGCTTTCACAGCTTTGCTTCAAGCTCTGAGCTCCAGGGGTCA 5473  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512

RESULT 4  
AF188679 6237 bp mRNA linear PRI 14-DEC-1999  
LOCUS AF188679  
DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit  
(SCN11A) mRNA, complete cds.  
ACCESSION AF188679  
VERSION AF188679.1 GI:6572949  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 6237)  
AUTHORS Dib-Hajj,S.D., Tyrell,L., Cummins,T.R., Black,J.A., Wood,P.M. and Waxman,S.G.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 6237)

TITLE Two tetrodotoxin-resistant sodium channels in human dorsal root ganglion neurons  
JOURNAL FEBS Lett. 462 (1-2), 117-120 (1999)  
MEDLINE 10580103  
PUBMED 2 (bases 1 to 6237)  
REFERENCE Db-Hajj S.D., Tyrrell L., Cummins T.R., Black J.A. and Waxman S.G.  
AUTHORS Direct Submission  
JOURNAL Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A, Bldg 34, 950 Campbell Ave., West Haven, CT 06516, USA

FEATURES  
source 1. 6237  
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Best Local Similarity 97.7%; Pred. No. 1.7e-49;  
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Qy 125 CCTCAGACCTTACCTTACGCTTACAGACCTTGCCTTACGCTTGCAGCTCCAGGGGTCA 184  
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LOCUS Homo sapiens chromosome 3 clone RP11-134U21, complete sequence.  
DEFINITION AC116038  
ACCESSION AC116038 GI:37537604  
VERSION AC116038.3  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.  
Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.  
Direct Submission  
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
REFERENCE 3 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.  
Direct Submission  
JOURNAL Submitted (28-JUN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
REFERENCE 4 (bases 1 to 167476)  
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.  
Direct Submission  
JOURNAL Submitted (07-OCT-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
On Oct 7, 2003 this sequence version replaced gi:21622736.  
COMMENT  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgchgs@u.washington.edu  
----- Project Information  
Center project name: chr-3  
Center clone name: RP11-134U21 (bc0780)  
----- Summary Statistics  
Sequencing vector: plasmid; 100% of reads  
Chemistry: Dye-terminator B7; 4% of reads  
Chemistry: Dye-terminator Big Dye; 5% of reads  
Assembly program: Phred; version 0.990319  
Consensus quality: 167467 bases at least Q40  
Consensus quality: 167476 bases at least Q30  
Consensus quality: 167476 bases at least Q20

Insert size: 167476; sum-of-contigs  
Quality coverage: 18.9x in Q20 bases; sum-of-contigs

# Overlapping Sequences:

5': RP11-11443 AC137625, 2001-bp overlap  
3': RP11-182A24 (UWGC:bc0782) AC123903, 41341-bp overlap

# Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

# Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted sequence consists of both insert and vector. In order to accurately represent the entire circular BAC, small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcORI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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9345	449	800	2317	2259	
2016	2707	2741	2813	2744	
4889	4809	4878	2537	2550	
3455	184	800	1923	2008	
245	5818	5899	2486	2550	
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762	1891	1888	6949	6960	

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182	5444	5397	3022	3007	
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ACCESSION	BD012082					
VERSION	BD012082.1 GI:22092271					
KEYWORDS	WO 0190355-A/1.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	Kanazawa, I., Goto, J., and Jeong, S. Y.					
TITLE	Human sodium channel SCN12A and SCN8A					
JOURNAL	Patent: WO 0190355-A 1 29-NOV-2001;					
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PD	29-NOV-2001					
PF	11-JUL-2000 WO 2000JP004629					
PR	23-MAY-2000 JP 00P 152085					
PI	ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG					
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DEFINITION	Human sodium channel SCN12A.		
ACCESSION	BD082951		
VERSION	BD082951.1	GI:22628561	
KEYWORDS	JP 2001327294-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Kanazawa, I., Goto, J., and Tei, Y.		
TITLE	Human sodium channel SCN12A		
JOURNAL	Patent: JP 2001327294-A 1 27-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP		
COMMENT	OS Homo sapiens (human)		
	PN	JP 2001327294-A/1	
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	PI	ICHIRO KANAZAWA, JUN GOTO, YOSHIOHRO TEI	
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Qy	185	GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT	223
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ACCESSION	AF109737		
VERSION	AF109737.1	GI:6693696	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 6528)		

AUTHORS Jeong,S.Y., Goto,J., Hashida,H., Suzuki,T., Ogata,K., Maesuda,N., Hirai,M., Ishihara,K., Uchiyama,Y. and Kanazawa,I.  
 TITLE Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A  
 JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)  
 MEDLINE 10623608  
 PUBMED 10623608  
 REFERENCE 2 (bases 1 to 6528)  
 AUTHORS Jeong,S.Y., Suzuki,T., Hashida,H., Maesuda,N., Goto,J. and Kanazawa,I.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-NOV-1998) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan  
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 QY 5 CAAGTGACCAAAAGACTTGGGAAAAGGGGCTATTTCACCACTCCAGACTCTTGA 64  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Blum,R., Kafitz,K.W. and Konnerth,A.  
 TITLE Na(V)1.9  
 JOURNAL Nature 419 (6908), 687-693 (2002)  
 MEDLINE 22272672  
 PUBMED 12384689  
 REFERENCE 2 (bases 1 to 5419)  
 AUTHORS Blum,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-OCT-2001) Blum R., Ineritnt fuer Physiologie, Ludwig-Maximilians-Universitaet, Biedersteiner Strasse 29, Geb. 608, 80802 Muenchen, GERMANY  
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## ORIGIN

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Query Match 61.3%; Score 136.6; DB 9; Length 5419;  
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Matches 150; Conservative 0;

QY 5 CAAGGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64  
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QY 65 ATGAGACTTGTCTAGCTTTGGGTGGCCAAAGGGAGGTCCTGACTGAGAGCCCTCA 124  
DB 5324 ATGAGACTTGTCTAGCTTTGGGTGGCCAAAGGGAGGTCCTGACTGAGAGCCCTCA 5383  
QY 125 CCTCAGCCCTTACCTCATAGCTTTCACAGCTTTGCC 159  
DB 5384 CCTCAGCCCTTACCTCATAGCTTTCACAGCTTTGCC 5418

RESULT 10 5849 bp mRNA linear ROD 03-MAY-1999  
LOCUS R237852  
DEFINITION Rattus norvegicus mRNA for voltage-gated sodium channel alpha subunit.  
ACCESSION AJ237852  
VERSION 1  
KEYWORDS alpha subunit; sm2 gene; voltage-gated sodium channel.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1  
AUTHORS Tate, S., Benn, S., Hick, C., Trezise, D., John, V., Mannion, R.J., Coetign, M., Plunton, C., Grose, D., Gladwell, Z., Kendall, G., Dale, K., Bountrea, C. and Woolf, C.J.  
TITLE Two sodium channels contribute to the TRX-R sodium current in primary sensory neurons  
JOURNAL Nat. Neurosci. 1 (8), 653-655 (1998)  
MEDLINE 99212311  
PUBMED 10196578  
REFERENCE 2 (bases 1 to 5849)  
AUTHORS Tate, S.N.  
TITLE Direct Submission  
JOURNAL Submitted (28-APR-1999) Tate S.N., Molecular Pharmacology, GlaxoWellcome Research and Development, Medicines Research Centre, Gunnels Wood Road, Stevenage, Hertfordshire, SG1 2NY, UNITED KINGDOM

FEATURES  
SOURCE  
1. 5849  
Location/Qualifiers

1. /organism="Rattus norvegicus"  
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1. 5849  
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## ORIGIN

Query Match 45.1%; Score 100.6; DB 10; Length 5849;  
Best Local Similarity 74.3%; Pred. No. 2e-19; Mismatches 44; Indels 0; Gaps 0;  
Matches 127; Conservative 0;

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DB 5196 CAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTGCAATGAGACTT 5255  
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DB 5256 GTCTAGCTTTGGGTGGCCAAAGGGAGGTCCTGACTGAGAGCCCTCAGCCCAAGCC 5315  
QY 135 TACCTCATAGCTTACAGGCTTGCCTTACGCTTGAAGCTCCAGGGGTGAG 185  
DB 5316 TACCTCATAGCTTACAGGCTTGCCTTGAAGCTCCAGGGGTGAG 5366

RESULT 11  
LOCUS AR340646  
DEFINITION Sequence 1 from patent US 6573067.  
ACCESSION AR340646  
VERSION AR340646.1  
KEYWORDS GI:3732378  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5875)  
AUTHORS Ddb-Hajj, S. and Waxman, S.G.  
TITLE Nucleic acid encoding sodium channels in dorsal root ganglia  
JOURNAL Patent: US 6573067-A 1 03-JUN-2003;  
FEATURES  
Location/Qualifiers

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/organism="unknown"  
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ORIGIN

Query Match 45.1%; Score 100.6; DB 6; Length 5875;  
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Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 75 GTCTAGCTTGGGGGCGCAAGGAGGTCACCTGACCTGAGCCCTCCAGCCG 134  
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DB 5296 GTCCAGCTTGGAGTGTGCGCAAGGTCACCTGACCTGAGCCCTCCAGCCG 5355  
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QY 135 TACCTCATGCTTCCAGGCTTGCCTTCCAGCTTGCAGCTCCAGGGGTCAG 185  
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RESULT 12  
LOCUS BD217791 5875 bp DNA linear PAT 17-JUL-2003  
DEFINITION Regulation of sodium channel in posterior root ganglion.  
ACCESSION BD217791  
VERSION BD217791.1 GI:33027561  
KEYWORDS UP 2002509860-A/1.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 5875)  
Hajj,S.D. and Waxman,S.  
Regulation of sodium channel in posterior root ganglion  
Patent: JP 2002509860-A 1 02-APR-2002;  
YALE UNIVERSITY  
COMMENT OS Rattus norvegicus (rat)  
PN UP 2002509860-A/1  
PD 02-APR-2002  
PF 29-JAN-1999 JP 2000529355  
PR 29-JAN-1998 US 60/072990, 20-NOV-1998 US 60/109402 PI  
SULAYMAN DIB HAJJ STEPHEN WAXMAN  
PC C07K14/435,A61K38/00,A61K39/395,A61I45/00,A61I25/04,A61I43/00,  
PC C07K16/18,  
PC C12N5/10,C12N15/09,C12P21/02,G01N33/566,G01N33/84,A61K37/02,  
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FT CDS (41). (5335)  
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Query Match 45.1%; Score 100.6; DB 6; Length 5875;  
Best Local Similarity 74.3%; Pred. No. 2e-19;  
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QY 75 GTCTAGCTTGGGGGCGCAAGGAGGTCACCTGACCTGAGCCCTCCAGCCG 134  
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QY 135 TACCTCATGCTTCCAGGCTTGCCTTCCAGCTTGCAGCTCCAGGGGTCAG 185  
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DB 5356 TACCTCATGCTTCCAGGCTTGCCTTCCAGCTTGCAGGAGGCGGAG 5406  
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DB 5296 GTCCAGCTTGGAGTGTGCGCAAGGTCACCTGACCTGAGCCCTCCAGCCG 5355

QY 135 TACCTCATGCTTCCAGGCTTGCCTTCCAGCTTGCAGCTCCAGGGGTCAG 185  
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RESULT 13  
LOCUS AX017217 5897 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from Patent WO9947670.  
ACCESSION AX017217  
VERSION AX017217.1 GI:10042137  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1  
Tate,S.N., Grose,D.T. and Hick,C.A.  
Mammalian sodium channel proteins  
Patent: WO 9947670-A 1 23-SEP-1999;  
TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS  
(GB); HICK CAROLINE ANNE (GB)  
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ORIGIN

Query Match 45.1%; Score 100.6; DB 6; Length 5897;  
Best Local Similarity 74.3%; Pred. No. 2e-19;  
Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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DEFINITION			Mammalian sodium channel protein.	
VERSION			BD138440.1 GI:23233385	
KEYWORDS			JP 2002508941-A/1.	(Norway rat)
SOURCE			Rattus norvegicus	
ORGANISM			Rattus norvegicus	
			Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
			Rattus.	
REFERENCE			1 (bases 1 to 5897)	
AUTHORS			Grose,D.T., Hick,C.A. and Tate,S.N.	
TITLE			Mammalian sodium channel protein	
JOURNAL			Patent: JP 2002508941-A 1 26-MAR-2002;	
COMMENT			GLAXO GROUP LTD	
			OS Rattus norvegicus (rat)	
			PN JP 2002508941-A/1	
			PD 26-MAR-2002	
			PF 18-MAR-1999 JP 2000536853	
			PI 18-MAR-1998 GB 9805793.8	
			PI DAVID THOMAS GROSE,CAROLINE ANNE HICK,SIMON NICHOLAS TATE PC	
			C12N15/09,A61K45/00,A61P17/04,A61P25/02,C07K14/705,C07K16/28, PC	
			C12N1/15,	
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			PC C12N15/00,C12N5/00	
			CC Mammalian sodium channel protein	
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Matches			127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	
Oy		15	CAAAATGACTTTGGGAAAAGCGGCCCTCATTCACACACTCCAGACTCTTTTGCAATGAGACTT	74
Dd		5244	CAAATGAGGCTGAAGAAGCAGGTCAAGTTTACATCGCACAGAGGTGTTTGCAATGAGACTT	5303
Oy		75	GTTAGACTTTGGGGTGCGCCAAGGCGAAGTCCACTGTGACTGAGGCCCTCAACCTCCAGCCC	134
Dd		5304	GTCACAGCTTGGATGTGGCCCAAGGTCAAGATTTCACAATGACTGAACCTTCATCTCCACC	5363
Oy		135	TACCTCATAGCTTTCACAGACTTTCCTTTAGCCTCTGAGCTCCAGGGGCTCAG	185
Dd		5364	TACCTCACTGCCTCACAGCTTAGCCTTCAGCCTCTGCGGAGAGCGGCGAG	5414
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LOCUS				
DEFINITION			mRNA 5905 bp linear ROD 16-JUL-2001	
			Rattus norvegicus voltage-gated Na channel alpha subunit NaN mRNA,	

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Best Local Similarity 74.3%; Pred. No. 2e-19; Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 5247 CAACTGAGGCTGAAAGACAGGTCAGTTCATCGCACAGGTGTTTGCATGGAGACTT 5306
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OY 75 GTCTAGCTTTGGGGGTGGCCAAAGGTCACACTGTGACTGAGCCCTCACCTCCAGGCC 134
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Db 5307 GTCCAGCTTGAGATGTGGCCAAAGTTCAGATGACTGAACTTCACTCCACCCC 5366
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OY 135 TACCTCATAGCTTCACAGGCTTGCTTCAGCTCTGAGCTCCAGGGGTGAG 185
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Db 5367 TACCTCAGCTTCACAGGCTTGAGCTTCAGCTCTGAGCTCCAGGGGTGAG 5417
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:33:04 ; Search time 161.414 Seconds  
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
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7: geneseq2003as:\*  
8: geneseq2003bs:\*  
9: geneseq2003cs:\*  
10: geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	199	89.2	6528	AAI42749	Aai42749 Human sod
5	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
6	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
7	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
8	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
9	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
10	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
11	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
12	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
13	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
14	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
15	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
16	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
17	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
18	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
19	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
20	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
21	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
22	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu
23	100.6	45.1	5875	AAK87600	Aak87600 Rat sodiu

C 24	31.4	14.1	284	5	ABV14474	Abv14474 Human pro
C 25	31.4	14.1	393	5	ABV05305	Abv05305 Human pro
C 26	31.4	14.1	413	5	ABV44363	Abv44363 Human pro
C 27	31.4	14.1	413	5	ABV35555	Abv35555 Human pro
C 28	30.6	13.7	14536	6	ABK49423	Abk49423 DNA encod
C 29	30.6	13.7	14536	6	ABK49423	Abk49423 Human cad
C 30	30.6	13.7	14536	6	AAI54470	Aai54470 Human cad
C 31	30.6	13.7	14536	6	AAI54471	Aai54471 Human cad
C 32	30.6	13.7	14536	6	ACA63043	ACA63043 Human cad
C 33	30.4	13.6	505	9	ACB63042	ACB63042 Human cad
C 34	30.4	13.6	505	9	ADB50969	ADB50969 Primary r
C 35	30.4	13.6	75236	7	Aah14551	Aah14551 Human CDN
C 36	30.4	13.6	174424	6	ABV75557	Abv75557 Saccharop
C 37	30.2	13.5	942	2	ABL68122	ABl68122 Ovary can
C 38	30	13.5	1208	2	AAK86269	Aak86269 DNA encod
C 39	30	13.5	1208	2	AAV32838	Aav32838 Human low
C 40	30	13.5	1336	3	AAH26494	Aah26494 Human low
C 41	30	13.5	1336	3	AAE21860	Aae21860 Human bre
C 42	30	13.5	1395	7	AAQ48135	Aaq48135 Human VIP
C 43	29.8	13.4	735	9	AAH26495	Aah26495 Human low
C 44	29.8	13.4	845	7	ADG76297	Adg76297 Human BSK
C 45	29.8	13.4	1998	4	ACF66511	ACf66511 Phototrab
					ABL22855	ABl22855 Drosophila

#### ALIGNMENTS

RESULT 1	AAZ21495	standard; cDNA; 223 BP.
ID	AAZ21495	
XX	AAZ21495;	
AC		
XX		
DT	03-DEC-1999	(first entry)
DB	Human sensory neurone specific 2a nucleotide sequence fragment #15.	
KW	Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;	
KW	voltage gated; hypersensitivity; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9947670-A1.	
XX		
PD	23-SEP-1999.	
XX		
PF	18-MAR-1999; 99WC-GB000838.	
XX		
PR	18-MAR-1998; 98GB-00005793.	
XX		
PA	(GLAX) GLAXO GROUP LTD.	
XX		
PI	Groze DT, Hick CA, Tate SN,	
XX		
DR	WPI; 1999-562112/47.	
XX		
PT	Mammalian sodium channel protein for treating pain and hypersensitivity.	
XX		
PS	Claim 6; Page 68; 73pp; English.	
CC	AAZ21495 to AAZ21495 represent fragments of the human sensory neurone	
CC	specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel	
CC	protein. SNS-2a can be used in a method for the identification of a	
CC	modulator of a sodium channel, and for assaying for compounds which	
CC	modulate sodium flux. The sodium channel modulators can be used in a	
CC	medicament for the treatment of pain or hypersensitivity	
XX		
SQ	Sequence 223 BP; 53 A; 64 C; 55 G; 51 T; 0 U; 0 Other;	
Query Match	100.0%; Score 223; DB 2; Length 223;	
Best Local Similarity	100.0%; Pred. No. 2.6e-63;	
Matches 223; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

QY 1 TGACCAAGTGTGACCAAAATGACTTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTT 60  
Db 1 TGACCAAGTGTGACCAAAATGACTTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTT 60  
QY 61 TGCATGAGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGGTTCACCTGTGATGAGCC 120  
Db 61 TGCATGAGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGGTTCACCTGTGATGAGCC 120  
QY 121 CTCACCTCCAGCCCTACCTCATCTAGCTTCACAGCCCTTGCTTCAGCTTCGACGCCAGGG 180  
Db 121 CTCACCTCCAGCCCTACCTCATCTAGCTTCACAGCCCTTGCTTCAGCTTCGACGCCAGGG 180  
QY 181 GTCAGCAGCTTAGTGATCAACAGGAGTGATTCACCAAAATT 223  
Db 181 GTCAGCAGCTTAGTGATCAACAGGAGTGATTCACCAAAATT 223  
RESULT 2  
AAF30101 ID AAF30101 standard; cDNA; 5860 BP.  
XX AAF30101;  
XX 30-APR-2001 (first entry).  
XX Human sodium channel NaN cDNA.  
XX  
XX Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia;  
XX hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 31..5402  
XX /\*tag= a  
XX  
XX MO200105831-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 14-JUL-2000; 2000WO-US019342.  
XX  
XX 16-JUL-1999; 99US-00354147.  
XX  
XX (UYVA ) UNIV YALE.  
XX  
XX Ddb-Hajj S, Waxman SG;  
XX  
XX WPI; 2001-103147/11.  
XX P-PSDB; AAB20121.  
XX  
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium  
XX channels, useful for preventing, diagnosing and treating pain,  
XX paraesthesia and/or hyperexcitability phenomena.  
XX  
XX Claim 1; Fig 11A; 162pp; English.  
XX  
XX The present sequence is that of cDNA encoding a novel human tetrodotoxin  
XX resistant sodium channel, termed NaN (see AAB20121). The cDNA was  
XX isolated from a human dorsal root ganglia tissue cDNA library by PCR  
XX amplification (see also AAF30122-23). NaN belongs to the a-subunit  
XX voltage-gated sodium channel protein family and produces a TTX-R sodium  
XX current. Such channels underlie the generation and propagation of  
XX impulses in excitable cells such as neurons and muscle fibres.  
XX Preferential expression of NaN on sensory neurons innervating the body  
XX (dorsal root ganglia) and the face (trigeminal ganglia), but not on other  
XX neurons, makes it a very useful target for diagnostic and/or therapeutic  
XX uses in relation to acute and/or chronic pain pathologies. A claimed  
XX method of treating pain, paraesthesia and/or hyperexcitability phenomena  
XX in a human or animal subject involves administering an agent that alters  
XX sodium current flow through NaN channels, or which modulates  
XX transcription or translation of NaN mRNA, in dorsal root ganglia or  
XX trigeminal neurons. NaN nucleic acids are used in gene therapy to correct

CC disorders associated with decreased sodium channel expression or  
CC (antisense) to down-regulate NaN expression, in the diagnosis of disease,  
CC and in the recombinant production of NaN polypeptides  
XX  
XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;  
SQ  
Query Match 90.0%; Score 200.6; DB 4; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 2e-55;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 5 CAAAGTGTGACCAAAATGACTTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTGGCA 64  
Db 5295 CCAAGTGTGACCAAAATGACTTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTGGCA 5353  
QY 65 ATGAGAGCTTGTCTAGCTTTGGGGTGCCCAAGGCAAGGTTCACCTGTGATGAGCCCTCA 124  
Db 5354 ATGAGAGCTTGTCTAGCTTTGGGGTGCCCAAGGCAAGGTTCACCTGTGATGAGCCCTCA 5413  
QY 125 CCTCCAGCCCTACCTCATCTAGCTTCACAGCCCTTGCTTCAGCTTCGAGCTCCAGGGGTCA 184  
Db 5414 CCTCCAGCCCTACCTCATCTAGCTTCACAGCCCTTGCTTCAGCTTCGAGCTCCAGGGGTCA 5473  
QY 185 GCAGCTTAGTGATCAACAGGAGTGATTCACCAAAATT 223  
Db 5474 GCAGCTTAGTGATCAACAGGAGTGATTCACCAAAATT 5512  
RESULT 3  
ADD32193 ID ADD32193 standard; cDNA; 5860 BP.  
XX ADD32193;  
XX  
XX ADD32193;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
XX Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.  
XX  
XX expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; human; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 31..5406  
XX /\*tag= a  
XX /product= "Na v 1.9 sodium channel protein"  
XX  
XX MO2003080570-A2.  
XX  
XX 02-OCT-2003.  
XX  
XX 20-MAR-2003; 2003MO-US008611.  
XX  
XX 20-MAR-2002; 2002US-0365550P.  
XX  
XX (TRAN-) TRANSMOLECULAR INC.  
XX  
XX Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
XX P-PSDB; ADD32194.  
XX  
XX Expression vector useful for stable cloning and expression of Nav1.9  
XX sodium channel at the mRNA and protein levels comprises a nucleic acid  
XX sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
XX fragment.  
XX  
XX Disclosure; SEQ ID NO 3; 125pp; English.  
XX  
XX The present invention describes an expression vector comprising a nucleic  
XX acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
XX its fragment, and producing a sodium current when transfected in a cell.  
XX Also described: (1) a recombinant cell comprising the plasmid selected

CC from pNAN, pCMV-rNAN-GFP, pLg338XW-rNAN and the plasmid described above;  
 CC (2) a method of making a cell or cell line that produces a Na v 1.9  
 CC sodium channel-dependent sodium current by: (a) providing a cell that has  
 CC been transfected with the expression vector; and (b) culturing the cell  
 CC under conditions that allow expression of Na v 1.9 sodium channel protein  
 CC to produce a sodium current into the transfected cell; (3) a method of  
 CC screening for an agent that modulates sodium current in a cell by: (a)  
 CC exposing the cell or cell line produced by the method to the agent; and  
 CC (b) measuring sodium current following exposure to the agent, where an  
 CC alteration in the level of sodium current is indicative of an agent  
 CC capable of modulating sodium current in a cell; and (4) a recombinant  
 CC cell comprising the expression vector. The expression vectors are useful  
 CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
 CC the mRNA and protein levels, and for producing sodium channel currents  
 CC characteristic of native currents in dorsal root ganglion neurons. The  
 CC present sequence encodes a human Na v 1.9 sodium channel protein, which  
 CC is used in the exemplification of the present invention.

SQ Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;

Query Match 90.0%; Score 200.6; DB 9; Length 5860;

Best Local Similarity 97.7%; Pred. No. 2e-55;  
 Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCA 64

DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTGCA 5353

QY 65 ATGGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGACTGAGCCCTCA 124

DB 5354 ATGGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGACTGAGCCCTCA 5413

QY 125 CCTCCAGCCTTACTCTTACCTTACAGAGCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 184

DB 5414 CCTCCAGCCTTACTCTTACCTTACAGAGCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 5473

QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 223

DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 5512

RESULT 4

AAI42749 ID AAI42749 standard; cDNA; 6528 BP.

AC AAI42749;

DT 19-JUL-2002 (first entry)

DE Human sodium channel subunit SCN12A coding sequence.

XX Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A;

KW human nervous system; chromosome 3p23-21.3; excitatory cell;

KW drug development; familial hyperglycaemia; QT extending syndrome type 3;

KW motor endplate disease.

XX Homo sapiens.

OS Homo sapiens.

XX Key CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

PI Kanazawa I, Goto J, Jeong S;

XX WPI; 2002-393394/42.

DR P-PSDB; AA014925.

XX Sodium channel alpha subunits SCN12A and SCN8A of human nervous system

PT together with splicing variants, useful in studying physiological

PT mechanism relating to excitatory cells and in drug development.

XX Claim 6; Page 29-46; 118pp; Japanese.

XX The invention comprises the amino acid and coding sequence of three

CC sodium channel subunits from the human nervous system (SCN12A, SCN12A-s

CC and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and

CC the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel

CC subunit proteins are useful in studying physiological mechanisms relating

CC to excitatory cells and in drug development. The sodium ion channel

CC subunit proteins are useful for treating diseases such as familial

CC hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases.

CC The present cDNA sequence encodes the human SCN12A sodium channel subunit

XX SQ Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;

Query Match 89.2%; Score 199; DB 6; Length 6528;

Best Local Similarity 97.3%; Pred. No. 7e-55;

Matches 213; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCA 64

DB 5464 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTGCA 5522

QY 65 ATGGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGACTGAGCCCTCA 124

DB 5523 ATGGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGACTGAGCCCTCA 5582

QY 125 CCTCCAGCCTTACTCTTACCTTACAGAGCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 184

DB 5583 CCTCCAGCCTTACTCTTACCTTACAGAGCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 5642

QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 223

DB 5643 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 5681

RESULT 5

AAI87600 ID AAI87600 standard; cDNA; 5875 BP.

AC AAI87600;

DT 26-OCT-1999 (first entry)

DE Rat sodium channel NaV cDNA.

XX NAN; sodium channel; ion transport; rat; dorsal root ganglia; pain;

KW paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

XX Rattus sp.

XX Key CDS

FT CDS

Location/Qualifiers

/tag= a

/tag= b

/note= "these bases represent nucleotides missing from

the sequence given in Fig 1 of the specification. The

nucleotides are included to maintain the nucleotide

numbering given in the specification for this DNA

sequence"

WT0938889-A2.

XX WT0938889-A2.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

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XX 05-AUG-1999.

XX 05-AUG-1999.

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XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

XX 05-AUG-1999.

PF	29-JAN-1999;	99WO-US002008.
XX		
XX	29-JAN-1998;	98US-0072990P.
PR	20-NOV-1998;	98US-0109402P.
XX		
PA	(UYVA ) UNIV YALE.	
XX		
PI	Dib-Hajj S, Waxman S;	
XX		
DR	WPI, 1999-479168/40.	
DR	P-PSDB; AAY06596.	
PT	New isolated nucleic acids encoding sodium channels, used to develop	
PT	products for treating acute or chronic pain or hyperexcitability	
PT	phenomena.	
XX		
PS	Claim 1; Fig 1A-D; 91pp; English.	
XX		
CC	This is the nucleotide sequence of an isolated nucleic acid which encodes	
CC	the rat NaN channel (see AAY06596), a previously unidentified voltage	
CC	gated sodium channel protein that is preferentially expressed in dorsal	
CC	root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R	
CC	sodium current. The NaN channel cDNA was obtained from Sprague-Dawley rat	
CC	DRG cDNA by PCR and RAGC amplification (see also AAX87603-17). Rat, mouse	
CC	and human NaN nucleic acids (see AAX87600-02) and polypeptides (see	
CC	AAY06596-98) are provided. The invention also includes expression vectors	
CC	and transformed host cells, methods for identifying tissues and cells	
CC	that express NaN, methods for identifying agents that modulate NaN	
CC	channel activity or NaN channel mRNA transcription or translation, and a	
CC	method for using such agents to treat acute or chronic pain, paraesthesia	
CC	and hyperexcitability phenomena. The preferential expression of NaN in	
CC	sensory DRG and trigeminal neurons provides a target for selectively	
CC	modifying the behaviour of these nerve cells while not affecting other	
CC	nerve cells in the brain and spinal cord. The NaN gene has been named	
CC	Scn1a	
XX		
SO	Sequence 5875 BP, 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;	
	Query Match	45.1%; Score 100.6; DB 2; Length 5875;
	Best Local Similarity	74.3%; Pred. No. 1,8e-22;
	Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	
OY	15 CAAATGACTTGGGAAAAGGAGGCTCATTCACACTCCAGACTCTTGGCATGAGACTT	74
DB	5236 CAACTGAGGCTGAAGGACAGGTCAAGTTCAATCGACAGGCTTTTGCATGAGACTT	5295
OY	75 GTCTAGCTTTGGGGGCGCAAGGGGAAAGTCCATCTGATGAGGCCCTCACTCCAGCC	134
DB	5296 GTCCAGCTTGATGTGGCCCAAGGTCAAGGTTCACATGACATGAACTTCATCTCCAGCC	5355
OY	135 TACCTCATAGCTTCCACAGCTTGTGCTTGAAGCTTCAGAGCTCCAGGGGTGAG	185
DB	5356 TACCTCACTGCTCAACAGCTTACCTCCAGCTCTGGGAGAGAGGCGGAG	5406
RESULT 6		
AAAF30102		
ID	AAAF30102 standard; CDNA; 5875 BP.	
AC	AAAF30102;	
XX		
DT	30-APR-2001 (first entry)	
XX		
DE	Rat sodium channel NaN cDNA.	
XX		
XX	Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia;	
KW	hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.	
XX		
OS	Rattus norvegicus.	
XX		
Key	Location/Qualifiers	
TH	CDS	41..5338
FT		

```

XX          /*tag= a
XX
XX          WO200105831-A1.
XX
XX          25-JAN-2001.
XX
XX          14-JUL-2000; 2000MO-US019342.
XX
XX          16-JUL-1999; 99US-00354147.
XX
XX          (UYVA ) UNIV YALE.
XX
XX          DiB-Hajj S, Maxman SG;
XX
XX          WPI; 2001-103147/11.
XX
XX          P-PSDB; AAB20122, AAB20123.
XX
XX          Nucleic acid molecules encoding human tetrodotoxin resistant sodium
XX          channels, useful for preventing, diagnosing and treating pain,
XX          paraesthesia and/or hyperexcitability phenomena.
XX
XX          Example 1; Fig 1; 162pp; English.
XX
XX          The present sequence is that of cDNA encoding a novel rat tetrodotoxin
XX          resistant sodium channel, termed Nan (see AAB20122). The cDNA was
XX          isolated from a dorsal root ganglia tissue cDNA library by PCR
XX          amplification using generic primers (from conserved regions of a-subunit
XX          sodium channel proteins) and Nan-specific primers (see also AAF30105-15),
XX          and RACE amplification. The open reading frame shows 734 similarity to
XX          the human Nan sequence (see AAF30101). Nan belongs to the a-subunit
XX          voltage-gated sodium channel protein family and produces a TRX-R sodium
XX          current. Such channels underlie the generation and propagation of
XX          impulses in excitable cells such as neurons and muscle fibres.
XX          Preferential expression of Nan on sensory neurons innervating the body
XX          (dorsal root ganglia) and the face (trigeminal ganglia), but not on other
XX          neurons, makes it a very useful target for diagnostic and/or therapeutic
XX          uses in relation to acute and/or chronic pain pathologies. A claimed
XX          method of treating pain, paraesthesia and/or hyperexcitability phenomena
XX          in a human or animal subject involves administering an agent that alters
XX          sodium current flow through Nan channels, or which modulates
XX          transcription or translation of Nan mRNA, in dorsal root ganglia or
XX          trigeminal neurons. Nan nucleic acids are used in gene therapy to correct
XX          disorders associated with decreased sodium channel expression or
XX          (antisense) to down-regulate Nan expression, in the diagnosis of disease,
XX          and in the recombinant production of Nan polypeptides
XX
XX          Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;
XX
XX          Query Match 45.1%; Score 100.6; DB 4; Length 5875;
XX          Best Local Similarity 74.3%; Pred. No. 1.8e-22;
XX          Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
XX
XX          15 CAAATGACTTGGGAAAACGGGCGCTCATTCACCACTCCAGACTCTTTGCATGTGAGACTT 74
XX          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX          Db CAAACTGAGGCTGAAGACACAGTAAAGTTCAATCGCACCAAGGTGTTTGCATGTGAGACTT 5295
XX
XX          75 GTTAGAGCTTTGGGCTGGCCAAAGGCAAGTCCACTGTGACTGAGCCCTCACTCCACGCC 134
XX          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX          Db GTCAACGCTGGATGTGGCCAAAGTCAAGTTCACAATGACGTGAACCTCATCTCCACACCC 5355
XX
XX          135 TACCTCATAGCTTCACAGCCTTGCTTCAGCCTCTGAGCTTCAGGGGTCAAG 185
XX          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX          Db TACCTCACTGCTTCACAGCTTAGGCTTCAGCCTTGCGCGAGCAGGCGGCGAG 5406
XX
XX          RESULT 7
XX          AA221480
XX          AA221480 standard; cDNA; 5897 BP.
XX
XX          AA221480;
XX
XX          03-DEC-1999 (first entry)
XX

```



DE Rat sensory neuron specific 2a nucleotide sequence.  
 XX Sensory neuron specific 2a; SNS-2a; sodium channel protein; pain;  
 KM voltage gated; hypersensitivity; ss.  
 XX Rattus sp.  
 OS  
 XX  
 FT Key Location/Qualifiers  
 FT CDS /\*tag= a  
 49..5346  
 /product= "sensory neuron specific 2a"  
 PN MO947670-A1.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 18-MAR-1999; 99MO-GB000838.  
 XX  
 PR 18-MAR-1998; 98GB-00005793.  
 XX  
 PA (GLAXO ) GLAXO GROUP LTD.  
 XX  
 PI Grose DT, Hick CA, Tate SN;  
 XX  
 DR WPI; 1999-562112/47.  
 DR P-PSDB; AAY41668.  
 XX  
 PT Mammalian sodium channel protein for treating pain and hypersensitivity.  
 XX  
 PS Claim 4; Page 52-58; 73pp; English.  
 XX  
 CC The present sequence encodes rat sensory neuron specific 2a (SNS-2a).  
 CC SNS-2a is a sodium channel protein. SNS-2a can be used in a method for  
 CC the identification of a modulator of a sodium channel, and for assaying  
 CC for compounds which modulate sodium flux. The sodium channel modulators  
 CC can be used in a medicament for the treatment of pain or hypersensitivity  
 XX  
 SO Sequence 5897 BP; 1474 A; 1471 C; 1435 G; 1517 T; 0 U; 0 Other;  
 Query Match 45.1%; Score 100.6; DB 2; Length 5897;  
 Best Local Similarity 74.3%; Pred. No. 1.8e-22;  
 Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
 QY 15 CAAATGACTTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCAATGAGACTT 74  
 DB 5244 CAAACTGAGCTGAGGACAGGATCAAGTTGATCGCACAGGTGTTTGCAATGAGACTT 5303  
 QY 75 GTCTAGCTTTGGGGTGGCCAAAGGCGAAGTCCACTGTCAGTCCAGCCCTCCACCGCC 134  
 DB 5304 GTCCAGCTTGAGTGTGGCCAAAGGTTCACAAATGACTGAACCTTCATCTCCACCCC 5363  
 QY 135 TACCTCATAGCTTCACAGCCTTGCTTCAGCTCTGAGTCCAGGGGCTAG 185  
 DB 5364 TACCTCATGCTGCTTCACAGCTTACGCTCCAGCCTTGCGGAGCGGCGAG 5414

XX  
 PD 14-AUG-2003.  
 XX  
 PF 04-FEB-2003; 2003MO-US003482.  
 XX  
 PR 04-FEB-2002; 2002US-0353171P.  
 PR 13-MAR-2002; 2002US-0363534P.  
 PR 08-APR-2002; 2002US-0370248P.  
 PR 10-APR-2002; 2002US-0371134P.  
 PR 10-APR-2002; 2002US-0371150P.  
 PR 10-APR-2002; 2002US-0371413P.  
 PR 11-APR-2002; 2002US-0371413P.  
 PR 19-APR-2002; 2002US-0373601P.  
 PR 19-APR-2002; 2002US-0373602P.  
 PR 22-APR-2002; 2002US-0374139P.  
 PR 08-MAY-2002; 2002US-0378370P.  
 PR 09-MAY-2002; 2002US-0378652P.  
 PR 09-MAY-2002; 2002US-0378653P.  
 PR 09-MAY-2002; 2002US-0378655P.  
 PR 09-JUL-2002; 2002US-0394230P.  
 PR 09-JUL-2002; 2002US-0394253P.  
 PR 04-SEP-2002; 2002US-0407688P.  
 PR 28-JAN-2003; 2003US-0442900P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;  
 PI Elashoff M;  
 XX  
 DR WPI; 2003-731472/69.  
 XX  
 PT Determining if a compound induces a toxic effect on a tissue or cell, for  
 PT identifying hepatotoxic compounds, comprises comparing a gene expression  
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
 PT mean values.  
 XX  
 PS Claim 44; SEQ ID NO 3471; 874pp; English.  
 XX  
 CC The present invention describes a method for determining whether a  
 CC compound induces a toxic effect on a tissue or cell. The method comprises  
 CC preparing a gene expression profile of a tissue or cell sample exposed to  
 CC the compound, and comparing the gene expression profile to a database  
 CC comprising data or information on the Tox mean and non-Tox mean value.  
 CC The method is useful for predicting or identifying at least one toxic  
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
 CC genes listed in the specification are useful as diagnostic or toxicity  
 CC markers for the prediction or identification of the physiological state  
 CC of tissue or cell sample that has been exposed to a compound, or to  
 CC identify or predict the toxic effects of a compound or an agent. These  
 CC may also be used as markers for monitoring toxicity progression or for  
 CC drug screening. The present sequence represents a primary rat hepatocyte  
 CC toxicity modelling related gene sequence from the present invention.  
 XX  
 SO Sequence 5905 BP; 1476 A; 1471 C; 1439 G; 1519 T; 0 U; 0 Other;  
 Query Match 45.1%; Score 100.6; DB 9; Length 5905;  
 Best Local Similarity 74.3%; Pred. No. 1.8e-22;  
 Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
 QY 15 CAAATGACTTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCAATGAGACTT 74  
 DB 5247 CAAACTGAGCTGAGGACAGGATCAAGTTGATGACAGGTGTTTGCAATGAGACTT 5306  
 QY 75 GTCTAGCTTTGGGGTGGCCAAAGGCGAAGTCCACTGTCAGTCCAGCCCTCCACCGCC 134  
 DB 5307 GTCCAGCTTGAGTGTGGCCAAAGGTTCACAAATGACTGAACCTTCATCTCCACCCC 5366  
 QY 135 TACCTCATAGCTTCACAGCCTTGCTTCAGCTCTGAGTCCAGGGGCTAG 185  
 DB 5367 TACCTCATGCTGCTTCACAGCTTACGCTCCAGCCTTGCGGAGCGGCGAG 5417

RESULT 9

ADD32191  
ID ADD32191 standard; cDNA; 5905 BP.  
XX  
AC ADD32191;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Rat Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:1.  
XX  
KM expression vector; Na v 1.9 sodium channel protein;  
KM sodium channel protein; dorsal root ganglion neuron; rat; gene; ss.  
XX  
OS Rattus norvegicus.  
XX  
FH Key location/Qualifiers  
FT CDS 52..5349  
FT /\*tag= a  
FT /product= "Na v 1.9 sodium channel protein"  
XX  
FN MO2003080570-A2.  
XX  
PD 02-OCT-2003.  
XX  
PE 20-MAR-2003; 2003WO-US008611.  
XX  
PR 20-MAR-2002; 2002US-0365550P.  
XX  
PA (TRAN-) TRANSMOLECULAR INC.  
XX  
PI Gonda MA, Greenwood JD;  
XX  
XX WPI; 2003-876895/81.  
DR P-PSDB; ADD32192.  
XX  
PT Expression vector useful for stable cloning and expression of Nav1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
PT fragment.  
XX  
PS Disclosure; SEQ ID NO 1; 125bp; English.  
XX  
CC The present invention describes an expression vector comprising a nucleic  
CC acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
CC its fragment, and producing a sodium current when transfected in a cell.  
CC Also described: (1) a recombinant cell comprising the plasmid selected  
CC from pNAN, pCMV-rNAN-GFP, pEG338M-rNAN and the plasmid described above;  
CC (2) a method of making a cell or cell line that produces a Na v 1.9  
CC sodium channel-dependent sodium current by: (a) providing a cell that has  
CC been transfected with the expression vector; and (b) culturing the cell  
CC under conditions that allow expression of Na v 1.9 sodium channel protein  
CC to produce a sodium current into the transfected cell; (3) a method of  
CC screening for an agent that modulates sodium current in a cell by: (a)  
CC exposing the cell or cell line produced by the method to the agent; and  
CC (b) measuring sodium current following exposure to the agent, where an  
CC alteration in the level of sodium current is indicative of an agent  
CC capable of modulating sodium current in a cell; and (4) a recombinant  
CC cell comprising the expression vector. The expression vectors are useful  
CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a rat Na v 1.9 sodium channel protein, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 5905 BP; 1476 A; 1471 C; 1439 G; 1519 T; 0 U; 0 Other;  
XX  
Query Match 45.1%; Score 100.6; DB 9; Length 5905;  
Best Local Similarity 74.3%; Pred. No. 1.8e-22;  
Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
OY 15 CAAGATGACTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCAATGAGACTT 74  
DB 5247 CAAGCTGAGCTGAAGGACAGGTCAAGTTCATCGACCAAGGTGTTTCAATGAGACTT 5306

OY 75 GTCTAGCTTTGGGGTGGCCAAAGGCGAAGGTTCACCTGTGACTGAGCCCTTCACGCC 134  
DB 5307 GTCCAGCTTGAGATGTGGCCAAAGGTTCACCAATGACTGAACCTCATCTCCACCCC 5366  
OY 135 TACCTCATAGCTTCACAGCCTTGCTTGCCTCTGTGAGCTCCAGGGGTCCAG 185  
DB 5367 TACCTCATGCTCCTCACAAGCTTTCACAGCTTCACAGCTTCGCGAGCGGCGAG 5417  
RESULT 10  
AAX60241  
ID AAX60241 standard; cDNA; 5908 BP.  
XX  
AC AAX60241;  
XX  
DT 11-AUG-1999 (first entry)  
XX  
DE cDNA encoding type 5 sodium channel protein designated PNS.  
XX  
KM Type 5 sodium channel; PNS; nervous system; plexiform;  
KM dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;  
KM diabetic neuropathy; traumatic injury; AIDS-related neuropathy;  
KM neuropathic pain; migraine; headache; ss.  
XX  
OS Rattus sp.  
XX  
FN FR2771103-A1.  
XX  
PD 21-MAY-1999.  
XX  
PE 19-NOV-1998; 98FR-00014551.  
XX  
PR 20-NOV-1997; 97US-0066225P.  
XX  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
XX  
PI Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;  
XX  
XX WPI; 1999-315739/27.  
DR P-PSDB; MAY16572.  
XX  
PT Isolated DNA encoding sodium channel of the nervous system.  
XX  
PS Claim 1; Fig 1A-E; 90bp; French.  
XX  
CC The present sequence encodes a type 5 sodium channel protein designated  
CC PNS. The protein is a sodium ion channel of the nervous system, and is  
CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
CC used to identify inhibitors of sodium channel proteins that are resistant  
CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
XX  
SQ Sequence 5908 BP; 1458 A; 1474 C; 1451 G; 1525 T; 0 U; 0 Other;  
XX  
Query Match 45.1%; Score 100.6; DB 2; Length 5908;  
Best Local Similarity 74.3%; Pred. No. 1.8e-22;  
Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
OY 15 CAAGATGACTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCAATGAGACTT 74  
DB 5274 CAAGCTGAGCTGAAGGACAGGTCAAGTTCATCGACCAAGGTGTTTGAATGAGACTT 5333  
OY 75 GTCTAGCTTTGGGGTGGCCAAAGGCGAAGGTTCACCTGTGACTGAGCCCTTCACGCC 134  
DB 5334 GTCCAGCTTGAGATGTGGCCAAAGGTTCACCAATGACTGAACCTCATCTCCACCCC 5393  
OY 135 TACCTCATAGCTTCACAGCCTTGCTTGCCTCTGTGAGCTCCAGGGGTCCAG 185  
DB 5394 TACCTCATGCTCCTCACAAGCTTTCACAGCTTCACAGCTTCGCGAGCGGCGAG 5444  
RESULT 11

ID	AAx87601
ID	AAx87601 standard; cDNA, 5822 BP.
AC	AAx87601;
DT	26-OCT-1999 (first entry)
XX	
DE	Mouse sodium channel Nan cDNA.
KW	Nan; sodium channel; ion transport; mouse; dorsal root ganglia; pain; paraesthesia; hyperexcitability; therapy; Scnlla gene; ss.
OS	Mus musculus.
FH	Key
FT	CDS
FT	mlec_feature
FT	/tag= b /note= "these bases represent nucleotides missing from the sequence given in Fig 7 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
FT	polyA_signal
FN	polyA_signal 5789..5794 /*tag= C
PN	MOJ938889-A2.
PD	05-AUG-1999.
PX	
PF	29-JAN-1999; 99WO-US002008.  29-JAN-1998; 98US-0072990P. PR 20-NOV-1998; 98US-0109402P. PX (UYVA ) UNIV YALE.
PI	Dib-Hajj S, Waxman S; DR WPI; 1999-479168/40. PT P-PSDB; AAY06597.
PT	New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability phenomena.
PS	Claim 1; Fig 7A1-3; 91pp; English.
XX	This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse Nan channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a tTX-R sodium current. The Nan channel cDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat Nan-based primers (see AAX87618-19). Rat, mouse and human Nan nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express Nan, methods for identifying agents that modulate Nan channel activity or Nan channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferred expression of Nan in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The gene encoding Nan has been named Scnlla
SQ	Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 0 U; 61 Other;
Query Match	38.7%; Score 86.4; DB 2; Length 5822;
Best Local Similarity	71.1% ; Pred No. 8.4e-18;
Matches 128; Conservative	0; Mismatches 51; Indels 1; Gaps 1

Oy	7	AGGTGGACCAAAATGACTTGGGAAAAAGGGGCTTATTCACACACCTCCAGACTCTTGGCAAT	66
Db	5206	AAGATGATCAGAGCTGAAGAGCTGAAGAGGACAGTCAAGTTCATCGCTCCAGGTGTTTGGCAAT	5265
Oy	67	GGAGACTTGTCTAGACTTTGGGGGTGGCCAGGAGGCAAGTTCACATGTGA CTG -AGCCCTCAC	125
Db	5266	GGAGACTTGTCTAGACTTTGGATGTGCCCCAAGATCAAGGTTTATTTGACTGAAAACCCCCAC	5325
Oy	126	CTCCAGGCGCTAAGCTCATAGACTTTCACAGCCTTTCCTTACAGCCTCTGAGCTCCAGGGGTTACG	185
Db	5326	CTGCAGCCCTTAAGCTTCACAGCCTTCACAGCTCAGCCCCAGCCTCTTGCGCAACAGCGCGG	5385
RESULT 12			
AAAF30103			
ID	AAAF30103	standard; cDNA; 5822 BP.	
XX	AAAF30103;		
XX	30-APR-2001	(first entry)	
XX	Mouse sodium channel NAN cDNA.		
XX	Sodium channel; NaN; Scylla; mouse; tetrodotoxin resistant; pain;		
KM	paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;		
KW	diagnosis; ss.		
XX	Mus musculus.		
XX	Key	Location/Qualifiers	
XX	CDS	19..5316	
FT	/*tag= a		
FT	polyA_signal	5789..5794	
FT	/*tag= b		
FT	polyA_site	5800..5822	
FT	/*tag= c		
XX	WO200105831-A1.		
XX	25-JAN-2001.		
XX	14-JUL-2000; 2000WO-US019342.		
XX	16-JUL-1999; 99US-00354147.		
XX	(UYVA ) UNIV YALE.		
XX	Dib-Hajj S, Waxman SG;		
XX	WPI; 2001-103147/11.		
XX	P-PSDB; AAB20124.		
XX	Nucleic acid molecules encoding human tetrodotoxin resistant sodium		
XX	channels, useful for preventing, diagnosing and treating pain,		
XX	paraesthesia and/or hyperexcitability phenomena.		
XX	Example 3; Fig 7A; 162pp; English.		
XX	The present sequence is that of cDNA encoding a novel mouse tetrodotoxin		
XX	resistant sodium channel, termed NaN (see AAB20124). The cDNA was		
XX	isolated from trigeminal ganglia cDNA using primers (see AAF30120-21)		
XX	based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN		
XX	(see AAB20121). The gene encoding NaN, termed Scylla, is located on mouse		
XX	chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel		
XX	protein family and produces a TTX-R sodium current. Such channels		
XX	underlie the generation and propagation of impulses in excitable cells		
XX	such as neurons and muscle fibres. Preferential expression of NaN on		
XX	sensory neurons innervating the body (dorsal root ganglia) and the face		
XX	(trigeminal ganglia), but not on other neurons, makes it a very useful		
XX	target for diagnostic and/or therapeutic uses in relation to acute and/or		
XX	chronic pain pathologies. A claimed method of treating pain, paraesthesia		
XX	and/or hyperexcitability phenomena in a human or animal subject involves		
XX	administering an agent that alters sodium current flow through NaN		

CC channels, or which modulates transcription or translation of NaN mRNA, in  
CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in  
CC gene therapy to correct disorders associated with decreased sodium  
CC channel expression or (antisense) to down-regulate NaN expression, in the  
CC diagnosis of disease, and in the recombinant production of NaN  
CC polypeptides  
XX

Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;

Query Match 38.7%; Score 86.4; DB 4; Length 5822;  
Best Local Similarity 71.1%; Pred. No. 8.4e-18;  
Matches 128; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

7 AGGTGACCAAAATGACTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTGCAT 66  
Db AAGATGATCAAGCTGACCTGAAGGCAAGCTCAAGTTCATGCTCCAGGTGTTGCAAT 5265  
67 GGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTCACTGTGACTG-AGCCCTCAC 125  
Db GGAGACTTGTCTAGCTTGAATGTGCCCCAAGATCAAGTTGATGATGAAACCCCCAC 5325  
5266 GGAGACTTGTCTAGCTTGAATGTGCCCCAAGATCAAGTTGATGATGAAACCCCCAC 5325  
Qy 126 CTCACGCTTACCTCATATGCTTCAAGCTTGCCTTCAGCTTCAGGCTCCAGGGTCCAG 185  
Db 5326 CTGACGCTTACCTCAAGCTCAAGCTCAAGCTCAAGCTTCTGGCGAACAAGCGGCG 5385

## RESULT 13

ADD32195  
ID ADD32195 standard; cDNA; 5822 BP.

AC ADD32195;

DT 15-JAN-2004 (first entry)

XX Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:5.

XX expression vector; Na v 1.9 sodium channel protein;

KW sodium channel protein; dorsal root ganglion neuron; mouse; gene; ss.

XX Mus musculus.

OS Key Location/Qualifiers

FT CDS 19..5316

FT /tag= a

FT /product= "Na v 1.9 sodium channel protein"

XX WO2003080570-A2.

XX 02-OCT-2003.

XX 20-MAR-2003; 2003WO-US008611.

XX 20-MAR-2002; 2002US-0365550P.

XX (TRAN-) TRANSMOLECULAR INC.

XX Conda MA, Greenwood JD;

XX WPI; 2003-876895/81.

XX P-PSDB; ADD32196.

XX Expression vector useful for stable cloning and expression of Nav1.9  
XX sodium channel at the mRNA and protein levels comprises a nucleic acid  
XX sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
XX fragment.

XX Disclosure; SEQ ID NO 5; 125pp; English.

XX The present invention describes an expression vector comprising a nucleic  
XX acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
XX its fragment, and producing a sodium current when transfected in a cell.  
XX Also described: (1) a recombinant cell comprising the plasmid selected  
XX from pNaN, pCMV-rNaN-GFP, pLG338XN-rNaN and the plasmid described above;

CC (2) a method of making a cell or cell line that produces a Na v 1.9  
CC sodium channel-dependent sodium current by: (a) providing a cell that has  
CC been transfected with the expression vector; and (b) culturing the cell  
CC under conditions that allow expression of Na v 1.9 sodium channel protein  
CC to produce a sodium current into the transfected cell; (3) a method of  
CC screening for an agent that modulates sodium current in a cell by: (a)  
CC exposing the cell or cell line produced by the method to the agent; and  
CC (b) measuring sodium current following exposure to the agent, where an  
CC alteration in the level of sodium current is indicative of an agent.  
CC capable of modulating sodium current in a cell; and (4) a recombinant  
CC cell comprising the expression vector. The expression vectors are useful  
CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a mouse Na v 1.9 sodium channel protein, which  
CC is used in the exemplification of the present invention.

Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;

Query Match 38.7%; Score 86.4; DB 9; Length 5822;  
Best Local Similarity 71.1%; Pred. No. 8.4e-18;  
Matches 128; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

7 AGGTGACCAAAATGACTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTGCAT 66  
Db AAGATGATCAAGCTGACCTGAAGGCAAGCTCAAGTTCATGCTCCAGGTGTTGCAAT 5265  
5206 GGAGACTTGTCTAGCTTGAATGTGCCCCAAGATCAAGTTGATGATGAAACCCCCAC 5325  
Qy 67 GGAAGCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTCACTGTGACTG-AGCCCTCAC 125  
Db GGAGACTTGTCTAGCTTGAATGTGCCCCAAGATCAAGTTGATGATGAAACCCCCAC 5325  
5266 GGAGACTTGTCTAGCTTGAATGTGCCCCAAGATCAAGTTGATGATGAAACCCCCAC 5325  
Qy 126 CTCACGCTTACCTCATATGCTTCAAGCTTGCCTTCAGCTTCAGGCTCCAGGGTCCAG 185  
Db 5326 CTGACGCTTACCTCAAGCTCAAGCTCAAGCTCAAGCTTCTGGCGAACAAGCGGCG 5385

## RESULT 14

AAK60244  
ID AAK60244 standard; cDNA; 5334 BP.

AC AAK60244;

DT 11-AUG-1999 (first entry)

XX Stabilised cDNA encoding type 5 sodium channel protein designated PNS.

XX Type 5 sodium channel; PNS; nervous system; plexiform;

KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;

KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;

KW neuropathic pain; migraine; headache; ss.

XX Synthetic.

OS Rattus sp.

XX FR2771103-A1.

XX 21-MAY-1999.

XX 19-NOV-1998; 98FR-00014551.

XX 20-NOV-1997; 97US-0066225P.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Diétrich PS, Fish LM, Knare R, Rabert DK, Sangameswaran L;

XX WPI; 1999-315739/27.

XX Isolated DNA encoding sodium channel of the nervous system.

XX Example 7; Fig 5A-E; 90pp; French.

XX The present sequence encodes a type 5 sodium channel protein designated

CC PMS. The protein is a sodium ion channel of the nervous system, and is  
CC highly expressed in plexiform and dorsal root ganglia. The protein can be  
CC used to identify inhibitors of sodium channel proteins that are resistant  
CC to tetrodotoxin (TTX). The inhibitors are potentially useful for treating  
CC epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related  
CC neuropathy, and especially neuropathic pain, e.g. migraine and headache  
XX  
SQ Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1362 T; 0 U; 0 Other:  
Query Match 29.1%; Score 65; DB 2; Length 5334;  
Best Local Similarity 73.5%; Pred. No. 9.2e-11;  
Matches 83; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 15 CAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTTTGGCAATGAGACTT 74  
DB 5219 CAAACTGAGGCTGAAAGGACAGGTCAAGTTCATGCGACAGTGTTCATGAGAGACTT 5278  
75 GTCTAGCTTTGGGGTGCCCAAGGCAAGTTCACACTGTGACTGAGCCCTCACT 127  
DB 5279 GTCCAGCTTGGATGTGGCCCAAGGTCAAGTTCACATGACTGAACCTCATCT 5331  
RESULT 15  
ADD32209 standard; cDNA; 5298 BP.  
XX  
AC ADD32209;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Rat Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:19.  
XX  
KM expression vector; Na v 1.9 sodium channel protein;  
XX sodium channel protein; dorsal root ganglion neuron; rat; gene; ss.  
XX  
OS Rattus norvegicus.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..5298  
FT /\*tag= a  
FT /product= "Na v 1.9 sodium channel protein"  
XX  
PN MO2003080570-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 20-MAR-2003; 2003WO-US008611.  
XX  
PR 20-MAR-2002; 2002US-0365550P.  
XX  
PA (TRAN-) TRANSMOLECULAR INC.  
XX  
PI Gonda MA, Greenwood JD;  
XX  
PI WPI; 2003-876895/81.  
XX  
DR P-PSDB; ADD32210.  
XX  
PT Expression vector useful for stable cloning and expression of Nav1.9  
PT sodium channel at the mRNA and protein levels comprises a nucleic acid  
PT sequence that encodes a mammalian Nav1.9 sodium channel protein or its  
PT fragment.  
XX  
PS Claim 13; SEQ ID NO 19; 125pp; English.  
XX  
CC The present invention describes an expression vector comprising a nucleic  
CC acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or  
CC its fragment, and producing a sodium current when transfected in a cell.  
CC Also described: (1) a recombinant cell comprising the plasmid selected  
CC from pRiN, pCMV-rNan-GFP, pUG338M-rNan and the plasmid described above;  
CC (2) a method of making a cell or cell line that produces a Na v 1.9  
CC sodium channel-dependent sodium current by: (a) providing a cell that has  
CC been transfected with the expression vector; and (b) culturing the cell  
CC under conditions that allow expression of Na v 1.9 sodium channel protein

CC to produce a sodium current into the transfected cell; (3) a method of  
CC screening for an agent that modulates sodium current in a cell by: (a)  
CC exposing the cell or cell line produced by the method to the agent; and  
CC (b) measuring sodium current following exposure to the agent, where an  
CC alteration in the level of sodium current is indicative of an agent  
CC capable of modulating sodium current in a cell; and (4) a recombinant  
CC cell comprising the expression vector. The expression vectors are useful  
CC for the stable cloning and expression of the Na v 1.9 sodium channel at  
CC the mRNA and protein levels, and for producing sodium channel currents  
CC characteristic of native currents in dorsal root ganglion neurons. The  
CC present sequence encodes a rat Na v 1.9 sodium channel protein, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other:  
Query Match 26.1%; Score 58.2; DB 9; Length 5298;  
Best Local Similarity 72.8%; Pred. No. 1.6e-08;  
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 15 CAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTTTGGCAATGAGACTT 74  
DB 5196 CAAACTGAGGCTGAAAGGACAGGTCAAGTTCATGCGACAGTGTTCATGAGAGACTT 5255  
75 GTCTAGCTTTGGGGTGCCCAAGGCAAGTTCACACTGTGACTGA 117  
DB 5256 GTCCAGCTTGGATGTGGCCCAAGGTCAAGTTCACATGACTGA 5298  
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Job time : 165.414 secs

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OM nucleic - nucleic search, using SW model

Run on: March 22, 2004, 19:33:04 ; Search time 136.581 Seconds  
(without alignments)  
6039.709 Million cell updates/sec

Title: US-09-646-224A-17

Perfect score: 223

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/us07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	200.6	90.0	5860	US-10-388-470-41 Sequence 41, Appl
2	100.6	45.1	5875	US-10-388-470-1 Sequence 1, Appl
3	86.4	38.7	5822	US-10-388-470-4 Sequence 4, Appl
4	33.8	15.2	639	US-10-027-632-26965 Sequence 26965, A
5	32.8	14.7	1214	US-09-885-478-3 Sequence 3, Appl
6	32.8	14.7	1214	US-09-899-732-3 Sequence 3, Appl
7	32.8	14.7	1214	US-10-341-751-3 Sequence 3, Appl
8	32.8	14.7	1214	US-10-029-314-3 Sequence 3, Appl
9	31	13.9	807	US-10-027-632-135714 Sequence 135714, A
10	31	13.9	807	US-10-027-632-135715 Sequence 135715, A
11	30.6	13.7	732	US-10-027-632-26966 Sequence 26966, A
12	30.6	13.7	14536	US-09-970-944-3 Sequence 3, Appl
13	30.6	13.7	14536	US-10-160-758-6 Sequence 6, Appl
14	30.6	13.7	14536	US-10-160-758-7 Sequence 7, Appl
15	30.4	13.6	174424	US-09-967-768A-314 Sequence 314, App

C	16	30.4	13.6	174424	10	US-09-960-706-969	Sequence 969, App
C	17	30	13.5	1208	9	US-09-962-055-16	Sequence 16, Appl
C	18	30	13.5	1208	9	US-09-976-740-16	Sequence 16, Appl
C	19	30	13.5	1208	12	US-10-671-242-16	Sequence 16, Appl
C	20	30	13.5	1208	13	US-10-023-529-16	Sequence 16, Appl
C	21	30	13.5	1208	13	US-10-023-529-16	Sequence 16, Appl
C	22	30	13.5	1208	15	US-10-616-187-16	Sequence 16, Appl
C	23	30	13.5	1208	14	US-10-102-806-247	Sequence 247, App
C	24	30	13.5	1445	10	US-09-945-527-6	Sequence 6, Appl
C	25	30	13.5	12425	9	US-09-976-740-50	Sequence 50, Appl
C	26	30	13.5	12425	12	US-10-671-242-50	Sequence 50, Appl
C	27	30	13.5	12425	13	US-10-023-529-50	Sequence 50, Appl
C	28	30	13.5	12425	13	US-10-023-529-50	Sequence 50, Appl
C	29	30	13.5	12425	15	US-10-616-187-50	Sequence 50, Appl
C	30	29.8	13.4	935	15	US-10-027-632-311467	Sequence 311467, A
C	31	29.8	13.4	2459	14	US-10-146-473-36	Sequence 36, Appl
C	32	29.8	13.4	19929	10	US-09-764-891-9967	Sequence 9967, Ap
C	33	29.8	13.4	20907	10	US-09-764-891-9966	Sequence 9966, Ap
C	34	29.6	13.3	434	15	US-10-027-632-311467	Sequence 311467, A
C	35	29.6	13.3	434	15	US-10-027-632-311468	Sequence 311468, A
C	36	29.6	13.3	591	15	US-10-027-632-292362	Sequence 292362, A
C	37	29.6	13.3	613	15	US-10-027-632-4315	Sequence 4315, Ap
C	38	29.6	13.3	613	15	US-10-027-632-4316	Sequence 4316, Ap
C	39	29.4	13.2	594	12	US-10-142-426-10	Sequence 10, Appl
C	40	29.4	13.2	594	14	US-10-123-155-10	Sequence 10, Appl
C	41	29.4	13.2	594	14	US-10-146-721-10	Sequence 10, Appl
C	42	29.4	13.2	594	14	US-10-140-472-10	Sequence 10, Appl
C	43	29.4	13.2	594	14	US-10-141-761-10	Sequence 10, Appl
C	44	29.4	13.2	594	14	US-10-142-885-10	Sequence 10, Appl
C	45	29.4	13.2	594	14	US-10-158-790-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-10-388-470-41  
Sequence 41, Application US/10388470  
GENERAL INFORMATION:  
Publication No. US20030228662A1  
APPLICANT: Ddb-Hajj, Sulayman  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US/09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: Full length cDNA sequence for human NAN  
US-10-388-470-41

Query Match 90.0%; Score 200.6; DB 15; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 1e-57;  
Matches 214; Conservative 0%; Mismatches 4; Indels 1; Gaps 1;  
Db 5295 CCAAGTGCACCAAAATGACTT-GGAAACGGCGCTCATTCCACACTCCAGACTCTTTCGA 64  
5 CAAAGTGCACCAAAATGACTTGCAGAAAGCGGCTCATTCCACACTCCAGACTCTTTCGA 64

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Qy 65 ATGAGACTTGTCTAGCTTTGGGGGNGGCCAAGGGGCAAGCTCCACTGTGAGCCCTCA 124
Db 5354 ATGAGACTTGTCTAGCTTTGGGGGNGGCCAAGGGGCAAGCTCCACTGTGAGCCCTCA 5413
Qy 125 CCTCCAGCCCTACCTCATAGCTTCAACAGCCTTGGCTTCAAGCTCTGAGCTCCAGGGTCA 184
Db 5414 CCTCCAGCCCTACCTCATAGCTTCAACAGCCTTGGCTTCAAGCTCTGAGCTCCAGGGTCA 5473
Qy 185 GCAGCTTAGTGTATCAACAGGAGCTGGATTCCACCAATT 223
Db 5474 GCAGCTTAGTGTATCAACAGGAGCTGGATTCCACCAATT 5512

RESULT 2
US-10-388-470-1
; Sequence 1, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Maxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT FILING DATE: 2003-03-17
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5875
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(5335)
; OTHER INFORMATION: cDNA sequence for rat Nan
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1996)..(4042)
; OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
; OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
; OTHER INFORMATION: or Lys.
US-10-388-470-1

Query Match 45.1%; Score 100.6; DB 15; Length 5875;
Best Local Similarity 74.3%; Pred. No. 9,4e-24;
Matches 127; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 15 CAAATGACTTGGGAAAGGGCCCTCATCTCACTCCAGACTCTTTGCAATGAGACTT 74
Db 5236 CAAATGAGGCTGAAGGAGAGGTCAAGTTCATCGACCAAGGTGTTTCAATGAGACTT 5295
Qy 75 GTTAGCTTTGGGGGTGGCCAAAGGCAAGTCCACTGTGAGCTTCACTCCAGCC 134
Db 5236 GTTCAAGCTTGGATGTGGCCAAAGTTCAGAGTTTCAATGATGAACTCATCTCCAGCC 5355
Qy 135 TACCTCATAGCTTCAACAGCCTTGCCTTAGCCTCTGAGCTCCAGGGGTGAG 185
Db 5356 TACCTCATAGCTTCAACAGCCTTGCCTTAGCCTCTGAGCAGAGCGGCGAG 5406

RESULT 3
US-10-388-470-4
; Sequence 4, Application US/10388470
; Publication No. US20030228662A1
; GENERAL INFORMATION:
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; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Maxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT FILING DATE: 2003-03-17
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US/09/354,147C
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(5313)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse Nan, n = a or c or g or t
US-10-388-470-4

Query Match 38.7%; Score 86.4; DB 15; Length 5822;
Best Local Similarity 71.1%; Pred. No. 6,2e-19;
Matches 128; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

Qy 7 AGTGAACCAAAAGACTTGGGAAAGGGCCCTATTCCACTCCAGACTCTTTGCAT 66
Db 5206 AAGATGATCAAGCTGAAGCTGAAGGCAAGCTCATCTCCAGGTGTTTGCAT 5265
Qy 67 GGAGACTTGTCTAGCTTTGGGGTGCCCAAGGGCAAGTCCACTGTGACTG-AGCCCTCAG 125
Db 5266 GGAGACTTGTCTAGCTTTGGGGTGCCCAAGTCCAGGTTCATTGTGACTGAAACCCCTCAG 5325
Qy 126 CTCACGCTTACCTCATAGCTTCAACAGCCTTGCCTTCAAGCTCTGAGCTCCAGGGGTGAG 185
Db 5326 CTCACGCTTACCTCATAGCTTCAACAGCCTTGCCTTCAAGCTCTGAGCTCCAGGGGTGAG 5385

RESULT 4
US-10-027-632-26965/c
; Sequence 26965, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT FILING DATE: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 26965  
LENGTH: 639  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-26965

Query Match  
Best Local Similarity 51.0%; Score 33.8; DB 15; Length 639;  
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 31 AACGGGCTTATTCACCACTTCAGACTCTTTGCAATGAGACTTGTCTAGCTTTGGGCTG 90  
DB 521 AAGGCTTCTTCTACATATCTGAGTGGGCTGGCTGGCTGGATCTCGTGGCTG 462  
QY 91 GCCAAGGCAAGGCTCCACTGTGACTGAGCCCTCACTTCCAGCCTTCAATAGCTTCAAC 150  
DB 461 GGGTGGGAACGCTCCACGTGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 402  
QY 151 AGCCTTGCCTTCAAGCCTCTGAGCTCCAGGGGTGACA 187  
DB 401 GGGCGGGCTCTGAGCATGAGATGCTCCTTGAGCAGCA 365

## RESULT 5

US-09-885-478-3/C  
Sequence 3, Application US/09885478  
Patent No. US20020111306A1  
GENERAL INFORMATION:

APPLICANT: SALON, JOHN A.  
APPLICANT: LAZ, THOMAS M.  
APPLICANT: MAGORNY, RAISA  
APPLICANT: WILSON, AMY E.  
TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1)  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: 1795/57453-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/885,478  
CURRENT FILING DATE: 2001-09-24  
PRIOR APPLICATION NUMBER: PCT/US99/31169  
PRIOR FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 1214  
TYPE: DNA  
ORGANISM: RATTUS NORVEGICUS  
US-09-885-478-3

Query Match  
Best Local Similarity 52.1%; Score 32.8; DB 9; Length 1214;  
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTCTTTCAGATGAGACTTGTCTAGCTTTGGGCTGGCCAAAGGCAAGT 104  
DB 1138 ATCTCTCCCAAGGCTTTGATGGGGTGGCTGACTTGGAGCGACTGGGAATTGTACAGT 1079  
QY 105 CCACTGTGACTGAGCCCTCACTTCCAGCCTTCACTTCAAGCTTGCCTTCAAG 164  
DB 1078 GCGTTTGTCTTGTCT 1019  
QY 165 CCTGTGAGCTCCAGGGGTCA 184  
DB 1018 CCCCTGGGCTGACAGGCTTCA 999

## RESULT 6

US-09-899-732-3/C  
Sequence 3, Application US/09899732  
Patent No. US20030082623A1  
GENERAL INFORMATION:

APPLICANT: SALON et al, John A.  
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof  
FILE REFERENCE: 1795/57453-C/JPM

CURRENT APPLICATION NUMBER: US/09/899,732  
CURRENT FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 09/610,635  
PRIOR FILING DATE: 2000-07-05  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1214  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-899-732-3

Query Match  
Best Local Similarity 52.1%; Score 32.8; DB 10; Length 1214;  
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTCTTTCAGATGAGACTTGTCTAGCTTTGGGCTGGCCAAAGGCAAGT 104  
DB 1138 ATCTCTCCCAAGGCTTTGATGGGGTGGCTGACTTGGAGCGACTGGGAATTGTACAGT 1079  
QY 105 CCACTGTGACTGAGCCCTCACTTCCAGCCTTCACTTCAAGCTTGCCTTCAAG 164  
DB 1078 GCGTTTGTCTTGTCT 1019  
QY 165 CCTGTGAGCTCCAGGGGTCA 184  
DB 1018 CCCCTGGGCTGACAGGCTTCA 999

## RESULT 7

US-10-341-751-3/C  
Sequence 3, Application US/10341751  
Patent No. US2004003855A1  
GENERAL INFORMATION:

APPLICANT: SALON et al, John A.  
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof  
FILE REFERENCE: 1795/57453-C/JPM  
CURRENT APPLICATION NUMBER: US/10/341,751  
CURRENT FILING DATE: 2003-01-14  
PRIOR APPLICATION NUMBER: 09/610,635  
PRIOR FILING DATE: 2000-07-05  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1214  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-341-751-3

Query Match  
Best Local Similarity 52.1%; Score 32.8; DB 12; Length 1214;  
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 45 ACCACTCCAGACTCTTTCAGATGAGACTTGTCTAGCTTTGGGCTGGCCAAAGGCAAGT 104  
DB 1138 ATCTCTCCCAAGGCTTTGATGGGGTGGCTGACTTGGAGCGACTGGGAATTGTACAGT 1079  
QY 105 CCACTGTGACTGAGCCCTCACTTCCAGCCTTCACTTCAAGCTTGCCTTCAAG 164  
DB 1078 GCGTTTGTCTTGTCT 1019  
QY 165 CCTGTGAGCTCCAGGGGTCA 184  
DB 1018 CCCCTGGGCTGACAGGCTTCA 999

## RESULT 8

US-10-029-314-3/C  
Sequence 3, Application US/10029314  
Patent No. US2003007701A1  
GENERAL INFORMATION:

APPLICANT: SALON et al, John A.

```

? TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
? TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
? FILE REFERENCE: 1795/57453-C/JPM
? CURRENT APPLICATION NUMBER: US/10/029,314
? CURRENT FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 09/899,732
? PRIOR FILING DATE: 2001-07-05
? PRIOR APPLICATION NUMBER: 09/610,635
? PRIOR FILING DATE: 2000-07-05
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 1214
? TYPE: DNA
? ORGANISM: Rattus norvegicus
? IS-10-029-314-3

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	Query Match	Similarity	14.7%	Pred. 33.8%	DB 14	Length 1214
	Best Local	Similarity	52.1%	Pred. No. 0.69		
	Matches	73	Conservative	0	Mismatches	67
			Indels	0	Gaps	0
QY	45	ACCACTCAGACTCTTTGCAATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGT	104			
Db	1138	ATCTCTCCCAAGGTTTATGGGGTGAGCTGACTTTGAGGGGACCTGGGGAATTGTACAGT	1072			
QY	105	CCACTGTAGTGAAGCCCTCACTCCAGGCTTACTCATAGCTTCAAGGCTTGCCTTCAAG	164			
Db	1078	GCTTTTGCTTTCTGTGCTCTCTCATCAGCTGTCTGACCGTTGCTGACCGTGGAGCTG	1012			
QY	165	CCTTGAAGCTCCAGGGGTCA	184			
Db	1018	CCCTGGGCTGACAGGCTTCA	999			

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RESULT 9
US-10-027-632-135714/c
: Sequence 135714, Application us/10027632
: Publication NO. US20030204075A9
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218, 006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198, 676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193, 483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185, 218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167, 363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156, 358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146, 002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 135714
: LENGTH: 807
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-135714

```

[illegible]

Db 13 CTTCCTGGTGAAGCACTGAGAGCTTCACCTTGTGAAGAGAGCTGCCTGGCTGTGTCTACTCC 72

Dy 141 ATAGCTTCAAGAGCTTGTGCTTTCAGGCTCTGAGTCTC 175

Dd 71 CTGCAATCCAAACCTGCTCTTCAAGCTCTGAGAGCC 37

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RESULT 10
US-10-027-632-135715/c
; Sequence 135715, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ. ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135715
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-135715

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Query Match	13.9%;	Score 31;	DB 15;	Length 807;
Best Local Similarity	57.9%;	Pred. No. 2.6;		
Matches	55;	Conservative	0;	Mismatches 40; Indels 0; Gaps

  

QY	81	CTTGGGCTGAGCCAAAGGCAAGGTCACTGTGATCAGAGCCCTTACCTCAGCGCTTACCTC	14
DB	131	CTTCTTGTGAGGCACATGACAGCTTCATCTTTGAAGAGATGCCCTGTGTCTACTCC	72
QY	141	ATAGCTTCAAGCCTTGCTTCAGCCTTGAAGCTC	175
DB	71	CTGGCATTCGAACCCCTGTGCTTCAGCCTTGAAGCC	37

RESULT 11  
 US-10-027-632-26966  
 ; Sequence 26966, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 26966  
LENGTH: 732  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-26966

Query Match 13.7%; Score 30.6; DB 15; Length 732;  
Best Local Similarity 49.1%; Pred. No. 3.4;  
Matches 78; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 31 AAGGGGCTGATTCACCACTCCAGACTCTTGGCAATGAGACTGTCTAGCTTTGGGGTG 90  
DB 456 AAGGCTTCTTCATCATATCTGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515  
QY 91 GCCAAGGCAAGGTCCACTGTGACTGAGCCCTGACCTCCAGGCTTACCTGATGCTTAC 150  
DB 516 GGGTGGGAAGGCTCCACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575  
QY 151 AGCCTTGCTTCAAGCTCTGAGCTCCAGGGGTACGA 187  
DB 576 GGCGGGGCTCTGAGCATGAGATTCCCTGAGCAGCA 612

## RESULT 12

US-09-970-944-3/c  
Sequence 3, Application US/09970944  
Publication No. US20030204052A1  
GENERAL INFORMATION:  
APPLICANT: Heriman, John L  
APPLICANT: Rastelli, Luca  
APPLICANT: Shimkets, Richard A  
TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding Same and  
TITLE OF INVENTION: Antibodies Directed Against these Proteins  
FILE REFERENCE: 21402-138  
CURRENT APPLICATION NUMBER: US/09/970,944  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: 60/237,862  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 3  
LENGTH: 14536  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-970-944-3

Query Match 13.7%; Score 30.6; DB 11; Length 14536;  
Best Local Similarity 49.1%; Pred. No. 6.8;  
Matches 81; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 44 CACCACTCCAGACTCTTGGCAATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAG 103  
DB 14244 CACCACTCCAGACTCTTGGCAATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAG 14185  
QY 104 TCCACTGTGACTGAGCCCTGACCTCCAGGCTTACCTGATGAGCTTCCAGGCTTGCTTCA 163  
DB 14184 ACATGTGTAGACATGTGCCACATTCACCTCCATGATGAGGCTTGAAGTGGCTGACAGTA 14125  
QY 164 GCCTGTGAGCTCCAGGGGTCCAGGCTTATGTATCAACGGGAG 208  
DB 14124 ATACTGTATGAGGAGGCGCTGTCAGTGGAGAGGAGGCAATGGCAG 14080

RESULT 13  
US-10-160-758-6/c  
Sequence 6, Application US/10160758

Publication No. US20030036076A1  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
TITLE OF INVENTION: CADS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
FILE REFERENCE: EX02-089C  
CURRENT APPLICATION NUMBER: US/10/160,758  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/357,253  
PRIOR FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 6  
LENGTH: 14536  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-160-758-6

Query Match 13.7%; Score 30.6; DB 14; Length 14536;  
Best Local Similarity 49.1%; Pred. No. 6.8;  
Matches 81; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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DB 14244 CACCACTCCAGACTCTTGGCAATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAG 14185  
QY 104 TCCACTGTGACTGAGCCCTGACCTCCAGGCTTACCTGATGAGCTTCCAGGCTTGCTTCA 163  
DB 14184 ACATGTGTAGACATGTGCCACATTCACCTCCATGATGAGGCTTGAAGTGGCTGACAGTA 14125  
QY 164 GCCTGTGAGCTCCAGGGGTCCAGGCTTATGTATCAACGGGAG 208  
DB 14124 ATACTGTATGAGGAGGCGCTGTCAGTGGAGAGGAGCAATGGCAG 14080

## RESULT 14

US-10-160-758-7/c  
Sequence 7, Application US/10160758  
Publication No. US20030036076A1  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
TITLE OF INVENTION: CADS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
FILE REFERENCE: EX02-089C  
CURRENT APPLICATION NUMBER: US/10/160,758  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/357,253  
PRIOR FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 7  
LENGTH: 14536  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-160-758-7

Query Match 13.7%; Score 30.6; DB 14; Length 14536;  
Best Local Similarity 49.1%; Pred. No. 6.8;  
Matches 81; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 44 CACCACTCCAGACTCTTGGCAATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAG 103  
DB 14244 CACCACTCCAGACTCTTGGCAATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAG 14185  
QY 104 TCCACTGTGACTGAGCCCTGACCTCCAGGCTTACCTGATGAGCTTCCAGGCTTGCTTCA 163  
DB 14184 ACATGTGTAGACATGTGCCACATTCACCTCCATGATGAGGCTTGAAGTGGCTGACAGTA 14125

QY 164 GCCCTGAGCTCCAGGGGTGAGAGCTTAGTATCAACAGGAG 208  
DB 14124 ATACTGATGGCGCTCTGAGTGAGAGGCAATGCGAG 14080

## RESULT 15

US-09-967-768A-314/C  
; Sequence 314, Application US/09967768A  
; Patent No. US2002015087A1  
; GENERAL INFORMATION:  
; APPLICANT: Augustus, Meena  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-72  
; CURRENT APPLICATION NUMBER: US/09/967,768A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,109  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,034  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,111  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 314  
; LENGTH: 174424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-967-768A-314

Query March 13.6% Score 30.4; DB 9; Length 174424;

Best Local Similarity 59.1%; Pred. No. 14; Mismatches 36; Indels 0; Gaps 0;

Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 85 GGGGTGCGCAAGGCGAGGTCACATGTCAGAGCCCTCACCGCCTTACCTCATAG 144

DB 39522 GGGCGCGTCGAGGGCGAGCGGCTAAGGAGCATCCCTTCCGAGACTCCTCT 39463

QY 145 CTTACAGCCTTGCTTCTGAGCTTGAG 172

DB 39462 CTCACCGCGCGGCCCGAGGCTTGAG 39435

Search completed: March 23, 2004, 05:15:23  
Job time : 156.581 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: March 22, 2004, 15:45:54 ; Search time 1680.4 Seconds  
(without alignments)  
4669.435 Million cell updates/sec

Title: US-09-646-224A-17

Sequence: 1 Tgaccaaggtgcgacccaat.....ggagatgcattaccaaat 223

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	200.6	90.0	532	US-09-821-837-6884	Sequence 6884, Ap
3	200.6	90.0	555	US-09-397-022-5398	Sequence 5398, Ap
4	200.6	90.0	555	US-09-808-383-5398	Sequence 5398, Ap
5	200.6	90.0	588	US-60-160-190-1098	Sequence 1098, Ap
6	200.6	90.0	588	US-60-160-190-775	Sequence 775, Ap
7	200.6	90.0	589	US-60-169-841-628	Sequence 628, Ap
8	200.6	90.0	589	US-60-169-841-1341	Sequence 1341, Ap
9	200.6	90.0	589	US-60-213-846-155	Sequence 155, Ap
10	200.6	90.0	586	PCT-US00-19342-41	Sequence 41, Appl
11	200.6	90.0	586	PCT-US00-09611-3	Sequence 3, Appl
12	200.6	90.0	586	US-10-388-470-41	Sequence 41, Appl
13	200.6	90.0	586	US-60-365-550-3	Sequence 3, Appl
14	200.6	90.0	623	US-60-516-609-317	Sequence 317, App
15	200.6	90.0	649	US-09-770-175-8399	Sequence 8399, Ap
16	200.2	89.8	115159	US-60-466-412-84151	Sequence 84151, A
17	199.6	89.5	517	US-09-821-837-6819	Sequence 6819, Ap
18	199	89.2	6528	US-10-296-130-1	Sequence 1, Appl
19	199	89.2	6528	US-60-485-101-251	Sequence 251, App
20	186.6	83.7	452	US-09-277-463B-111	Sequence 111, App
21	186.6	83.7	452	US-09-397-022-3054	Sequence 3054, Ap
22	186.6	83.7	452	US-09-605-784A-787	Sequence 787, App
23	186.6	83.7	452	US-09-808-383-3054	Sequence 3054, Ap
24	186.6	83.7	452	US-09-977-564-111	Sequence 111, App
25	177.6	79.6	539	US-09-821-710-7644	Sequence 7644, Ap
26	152.2	68.3	201	US-60-466-412-152304	Sequence 152304, A
27	144.6	64.8	370	US-60-213-846-1233	Sequence 1233, Ap
28	100.6	45.1	479	US-09-821-837-7613	Sequence 7613, Ap
29	100.6	45.1	896	US-09-652-917-2955	Sequence 2955, Ap
30	100.6	45.1	5875	PCT-US00-19342-1	Sequence 1, Appl
31	100.6	45.1	5875	PCT-US99-02008-1	Sequence 1, Appl
32	100.6	45.1	5875	US-10-388-470-1	Sequence 1, Appl
33	100.6	45.1	5897	US-09-646-224A-1	Sequence 1, Appl
34	100.6	45.1	5905	PCT-US03-03482-3471	Sequence 3471, Ap
35	100.6	45.1	5905	PCT-US03-08611-1	Sequence 1, Appl
36	100.6	45.1	5905	US-10-219-051B-908	Sequence 908, App
37	100.6	45.1	5905	US-10-357-507-3471	Sequence 3471, Ap
38	100.6	45.1	5905	US-10-357-139-12	Sequence 12, Appl
39	100.6	45.1	5905	US-60-365-550-1	Sequence 1, Appl
40	100.6	45.1	5905	US-60-485-101-488	Sequence 488, App
41	100.6	45.1	5906	US-60-485-101-5	Sequence 5, Appl
42	100.6	45.1	5908	US-09-195-851-1	Sequence 1, Appl
43	99.6	44.7	561	US-60-126-221-97	Sequence 97, Appl
44	94.6	42.4	5080	US-10-170-235-13985	Sequence 13985, A
45	94.2	42.2	143	US-60-453-050-33594	Sequence 33594, A

## ALIGNMENTS

RESULT 1  
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Sequence 17, Application US/09646224A  
GENERAL INFORMATION:  
APPLICANT: Glaxo Wellcome PLC  
APPLICANT: Tate, Simon N  
APPLICANT: Grose, David T  
APPLICANT: Hicks, Caroline A  
TITLE OF INVENTION: Ion Channels  
FILE REFERENCE: PG3432  
CURRENT APPLICATION NUMBER: US/09/646,224A  
CURRENT FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: GB 9805793.8  
PRIOR FILING DATE: 1998-03-18  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 223  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-646-224A-17  
Query Match 100.0%; Score 223; DB 27; Length 223;  
Best Local Similarity 100.0%; Pred. No. 2,3e-57;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 121 CTCACCTCCAGCTTACTATAGCTTACAGCTTCCCTTCAGCTTCAGCTTCAGGG 180  
QY 181 GTCACGACTTATGTATCAACAGGAGTGAGATTACCAATT 223  
DB 181 GTCACGACTTATGTATCAACAGGAGTGAGATTACCAATT 223  
RESULT 2  
US-09-821-837-6884  
Sequence 6884, Application US/09821837  
GENERAL INFORMATION:  
APPLICANT: Geating, David P.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
FILE REFERENCE: 1600,2076-001  
CURRENT APPLICATION NUMBER: US/09/821,837  
CURRENT FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: US 60/193,481  
PRIOR FILING DATE: 2000-03-29  
NUMBER OF SEQ ID NOS: 9928  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6884  
LENGTH: 532  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-821-837-6884  
Query Match 90.0%; Score 200.6; DB 33; Length 532;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 5 CAAGGTGACCAAAATGATCTGGGAAACGGGCTCATTCACCACTGACACTCTTTGCA 64  
DB 266 CCAGGTGACCAAAATGATCTGGGAAACGGGCTCATTCACCACTGACACTCTTTGCA 324  
QY 65 ATGAGACTTGTCTAGCTTTGGGTGGCCAAAGGCAAGGTGCACTGTGAGACCTCTCA 124  
DB 325 ATGAGACTTGTCTAGCTTTGGGTGGCCAAAGGCAAGGTGCACTGTGAGACCTCTCA 384  
QY 125 CTTCCAGCTTACTTCAATGCTTACAGCTTGGCTTCAAGCTTGTAGCTTCAGGGGTCA 184  
DB 385 CTTCCAGCTTACTTCAATGCTTACAGCTTGGCTTCAAGCTTGTAGCTTCAGGGGTCA 444  
QY 185 GCAGCTTAGTATCAACAGGAGTGATTCACCAATT 223  
DB 445 GCAGCTTAGTATCAACAGGAGTGATTCACCAATT 483  
RESULT 3  
US-09-397-022-5398  
Sequence 5398, Application US/09397022  
GENERAL INFORMATION:  
APPLICANT: Geating, David P.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

FILE OF INVENTION: HUMAN FETAL SKIN LIBRARY  
FILE REFERENCE: MLN98-46PM  
CURRENT APPLICATION NUMBER: US/09/397,022  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,465  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/106,443  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/107,257  
PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: 60/126,906  
PRIOR FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: 60/132,099  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 5775  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 5398  
LENGTH: 555  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-397-022-5398

Query Match 90.0%; Score 200.6; DB 19; Length 555;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 5 CAAGTGACCAAAATGACTTGGGAAACGGGCTTCACTCCAGACTCTTTGCA 64  
DB 271 CCAAGGTGACCAAAATGACTT-GGAAACGGGCTTCACTCCAGACTCTTTGCA 329  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 124  
DB 330 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 389  
QY 125 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 184  
DB 390 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 449  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 223  
DB 450 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 488

RESULT 4  
US-09-808-383-5398  
Sequence 5398, Application US/09808383  
GENERAL INFORMATION:  
APPLICANT: Geating, David P.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
FILE REFERENCE: 1600.1046-002  
CURRENT APPLICATION NUMBER: US/09/808,383  
CURRENT FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: US 09/397,022  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: US 60/100,465  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: US 60/106,443  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: US 60/107,257  
PRIOR FILING DATE: 1998-11-15  
PRIOR APPLICATION NUMBER: US 60/126,906  
PRIOR FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: US 60/132,099  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 5775  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 5398  
LENGTH: 555  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-808-383-5398

Query Match 90.0%; Score 200.6; DB 33; Length 555;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 5 CAAGTGACCAAAATGACTTGGGAAACGGGCTTCACTCCAGACTCTTTGCA 64  
DB 271 CCAAGGTGACCAAAATGACTT-GGAAACGGGCTTCACTCCAGACTCTTTGCA 329  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 124  
DB 330 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 389  
QY 125 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 184  
DB 390 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 449  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 223  
DB 450 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 488

RESULT 5  
US-60-160-190-1098  
Sequence 1098, Application US/60160190  
GENERAL INFORMATION:  
APPLICANT: BONAZZI, VIVIEN  
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
FILE REFERENCE: CL000115  
CURRENT APPLICATION NUMBER: US/60/160,190  
CURRENT FILING DATE: 1998-10-19  
NUMBER OF SEQ ID NOS: 2384  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1098  
LENGTH: 588  
TYPE: DNA  
ORGANISM: HUMAN  
US-60-160-190-1098

Query Match 90.0%; Score 200.6; DB 72; Length 588;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 5 CAAGTGACCAAAATGACTTGGGAAACGGGCTTCACTCCAGACTCTTTGCA 64  
DB 275 CCAAGGGGACCAAAATGACTT-GGAAACGGGCTTCACTCCAGACTCTTTGCA 333  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 124  
DB 334 ATGAGACTTGTCTAGCTTTGGGGTGGCCCAAGGCAAGGTCCACTGTGACTGAGCCCTCA 393  
QY 125 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 184  
DB 394 CCTCCAGGCTTCACTTATGCTTCAAGGCTTGCCTTCAAGCTTCAAGGCTTCA 453  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 223  
DB 454 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAATT 492

RESULT 6  
US-60-160-190-775  
Sequence 775, Application US/60160190  
GENERAL INFORMATION:  
APPLICANT: BONAZZI, VIVIEN  
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
FILE REFERENCE: CL000115  
CURRENT APPLICATION NUMBER: US/60/160,190  
CURRENT FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 2384  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 775  
; LENGTH: 589  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-160-190-775

Query Match 90.0%; Score 200.6; DB 72; Length 589;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACTCAGACTCTTTGCA 64  
DB 276 CCAAGGGGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACTCAGACTCTTTGCA 334  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 124  
DB 335 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 394  
QY 125 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 184  
DB 395 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 454  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 223  
DB 455 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 493

RESULT 7  
US-60-169-841-628  
; Sequence 628; Application US/60169841  
; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
; FILE REFERENCE: CL000163  
; CURRENT APPLICATION NUMBER: US/60/169,841  
; CURRENT FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 2910  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 628  
; LENGTH: 589  
; TYPE: DNA  
; ORGANISM: Human  
US-60-169-841-628

Query Match 90.0%; Score 200.6; DB 72; Length 589;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACTCAGACTCTTTGCA 64  
DB 276 CCAAGGGGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACTCAGACTCTTTGCA 334  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 124  
DB 335 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 394  
QY 125 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 184  
DB 395 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 454  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 223  
DB 455 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 493

RESULT 8  
US-60-169-841-1341  
; Sequence 1341; Application US/60169841  
; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS  
; FILE REFERENCE: CL000163  
; CURRENT APPLICATION NUMBER: US/60/169,841  
; CURRENT FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 2910  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1341  
; LENGTH: 589  
; TYPE: DNA  
; ORGANISM: Human  
US-60-169-841-1341

Query Match 90.0%; Score 200.6; DB 72; Length 589;  
Best Local Similarity 97.7%; Pred. No. 2.1e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACTCAGACTCTTTGCA 64  
DB 276 CCAAGGGGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACTCAGACTCTTTGCA 334  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 124  
DB 335 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 394  
QY 125 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 184  
DB 395 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 454  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 223  
DB 455 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 493

RESULT 9  
US-60-213-846-155/c  
; Sequence 155; Application US/60213846  
; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000703  
; CURRENT APPLICATION NUMBER: US/60/213,846  
; CURRENT FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 155  
; LENGTH: 972  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-213-846-155

Query Match 90.0%; Score 200.6; DB 77; Length 972;  
Best Local Similarity 97.7%; Pred. No. 2.4e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACTCAGACTCTTTGCA 64  
DB 554 CCAAGGTGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACTCAGACTCTTTGCA 496  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 124  
DB 495 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGGCAAGCTCAGCTGTGAGCTTCA 436  
QY 125 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 184  
DB 435 CCTCAGAGCTTACTTACAGAGCTTGGCTTCAAGCTCTGAGCTCAGAGGCTCA 376  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGTGATTCACCAATT 223



Db 375 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 337

RESULT 10  
PCT-US00-19342-41

Sequence 41, Application PC/TUS0019342  
GENERAL INFORMATION:

APPLICANT: Vale University  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-02-WO  
CURRENT APPLICATION NUMBER: PCT/US00/19342  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/354,147  
PRIOR FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: Full length cDNA sequence for human Nan  
PCT-US00-19342-41

Query Match 90.0%; Score 200.6; DB 1; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 3,9e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACCACTCCAGACTCTTTTGA 64  
DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACCACTCCAGACTCTTTGCA 5353  
QY 65 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 124  
DB 5354 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 5413  
QY 125 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 184  
DB 5414 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 5473  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512

RESULT 11  
PCT-US03-08611-3

Sequence 3, Application PC/TUS0308611  
GENERAL INFORMATION:  
APPLICANT: Transmolecular, Inc.  
APPLICANT: GONDA, Matthew A.  
APPLICANT: GREENWOOD, John D.  
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Chan  
FILE REFERENCE: 51530-5007-WO  
CURRENT APPLICATION NUMBER: PCT/US03/08611  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: US 60/365,550  
PRIOR FILING DATE: 2002-03-20  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION:  
PCT-US03-08611-3

Query Match 90.0%; Score 200.6; DB 1; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 3,9e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACCACTCCAGACTCTTTTGA 64  
DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACCACTCCAGACTCTTTGCA 5353  
QY 65 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 124  
DB 5354 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 5413  
QY 125 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 184  
DB 5414 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 5473  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512

RESULT 12

US-10-388-470-41  
Sequence 41, Application US/10388470  
GENERAL INFORMATION:  
APPLICANT: Dib-Hajj, Sulayman  
APPLICANT: Waxman, Stephen G.  
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
FILE REFERENCE: 44574-5004-01-US  
CURRENT APPLICATION NUMBER: US/10/388,470  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US 09/354,147C  
PRIOR FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US 60/072,990  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: US 60/109,402  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: PCT/US99/02008  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 5860  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31)..(5403)  
OTHER INFORMATION: Full length cDNA sequence for human Nan  
US-10-388-470-41

Query Match 90.0%; Score 200.6; DB 50; Length 5860;  
Best Local Similarity 97.7%; Pred. No. 3,9e-50;  
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCTATTCACCACTCCAGACTCTTTTGA 64  
DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAAACGGGCTCTATTCACCACTCCAGACTCTTTGCA 5353  
QY 65 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 124  
DB 5354 ATGGAACCTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGTCCACTGTGAGTGAAGCCCTCA 5413  
QY 125 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 184  
DB 5414 CTTCCAGCCTTACTCTATAGCTTACAGAGCTTGCTTACAGCTCTGAGCTCCAGGGGTCA 5473  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223  
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512

```
RESULT 13
US-60-365-550-3
; Sequence 3, Application US/60365550
; GENERAL INFORMATION:
; APPLICANT: Transmolecular, Inc.
; APPLICANT: GONDA, Matthew A
; APPLICANT: GREENWOOD, John D
; APPLICANT: DIB-HAJI, Sulayman D
; APPLICANT: MAXMAN, Steven G
; TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Chan
; FILE REFERENCE: 51530-5007-PR
; CURRENT APPLICATION NUMBER: US/60/365,550
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 09/354,147
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: 60/109,402
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION:
US-60-365-550-3
```

```
Query Match      90.0%; Score 200.6; DB 93; Length 5860;
Best Local Similarity 97.7%; Pred. No. 3.9e-50;
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64
DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 5353

QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 124
DB 5354 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 5413

QY 125 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 184
DB 5414 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 5473

QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512
```

```
RESULT 14
US-60-516-609-317
; Sequence 317, Application US/60516609
; GENERAL INFORMATION:
; APPLICANT: Oncotech, Inc.
; APPLICANT: Fruehauf, John P.
; APPLICANT: Pecka, Michael
; TITLE OF INVENTION: Methods for Identifying and Classifying Tumor Samples of
; TITLE OF INVENTION: Uncertain Etiology
; FILE REFERENCE: MHB 03-341
; CURRENT APPLICATION NUMBER: US/60/516,609
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 1065
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317
; LENGTH: 6237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

```
; NAME/KEY: misc_feature
; OTHER INFORMATION: gb:AF188679.1; Homo sapiens voltage-gated sodium channel type XI
; OTHER INFORMATION: alpha subunit (SCN11A).
US-60-516-609-317
```

```
Query Match      90.0%; Score 200.6; DB 108; Length 6237;
Best Local Similarity 97.7%; Pred. No. 4e-50;
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64
DB 5295 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 5353

QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 124
DB 5354 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 5413

QY 125 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 184
DB 5414 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 5473

QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223
DB 5474 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5512
```

```
RESULT 15
US-09-770-175-8399
; Sequence 8399, Application US/09770175
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600,2058-001
; CURRENT APPLICATION NUMBER: US/09/770,175
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,874
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 8967
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8399
; LENGTH: 6499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-770-175-8399
```

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Query Match      90.0%; Score 200.6; DB 32; Length 6499;
Best Local Similarity 97.7%; Pred. No. 4e-50;
Matches 214; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY 5 CAAGGTGACCAAAATGACTTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64
DB 5461 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 5519

QY 65 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 124
DB 5520 ATGAGACTTGTCTAGCTTTGGGGTGGCCAAAGGCAAGCTGCTGACTGAGCCCTCA 5579

QY 125 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 184
DB 5580 CTTCCAGCCTTACTCTATGAGCTTTCACAGCCTTGCTTGAAGCTTCAGAGGGGTCA 5639

QY 185 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 223
DB 5640 GCAGCTTAGTGTATCAACAGGAGTGATTCACCAAAATT 5678
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Search completed: March 23, 2004, 04:00:48
Job time : 1689.54 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: March 22, 2004, 16:13:34 ; Search time 282.599 Seconds  
(without alignments)  
414.412 Million cell updates/sec

Title: US-09-646-224A-17

Perfect score: 223  
Sequence: 1 Tgaccagaagtgaccacaat.....ggagatgattcacaat 223

Scoring table: IDENTITY NUC  
Gapco 10.0 , Gapext 1.0

Searched: 1155024 seqs, 262583689 residues

Total number of hits satisfying chosen parameters: 2310048

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents NA New:\*  
1: /cgn2\_6/prodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/prodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	89.2	1400	US-60-545-213-2723	Sequence 2723, Ap
2	199	89.2	1400	US-60-545-213-2724	Sequence 2724, Ap
3	199	89.2	1400	US-60-545-213-6995	Sequence 6995, Ap
4	199	89.2	1400	US-60-545-213-6996	Sequence 6996, Ap
5	31	13.9	1057	US-10-767-701-6910	Sequence 6910, Ap
6	30.2	13.5	128811	US-10-796-280-12234	Sequence 12234, A
7	29.4	13.0	21142	US-60-548-091-5682	Sequence 5682, Ap
8	29	13.0	25930	US-10-796-280-12414	Sequence 12414, A
9	29	13.0	252907	US-10-417-375A-66	Sequence 66, Appl
10	28.8	12.9	600	US-60-545-213-8364	Sequence 4092, Ap
11	28.8	12.9	600	US-10-100-683-1370	Sequence 8364, Ap
12	28.8	12.9	1471	US-10-100-683-1370	Sequence 370, Ap
13	28.8	12.9	1514	US-10-100-683-5456	Sequence 5456, Ap
14	28.8	12.9	4628	US-10-100-683-13346	Sequence 13346, A
15	28.6	12.8	4132	US-10-775-920-271	Sequence 271, Appl
16	28.6	12.8	4204	US-10-775-920-270	Sequence 270, Appl
17	28.6	12.8	4204	US-10-775-920-273	Sequence 273, Appl
18	28.6	12.8	4231	US-10-280-752-97	Sequence 97, Appl
19	28.6	12.8	4252	US-10-775-920-272	Sequence 272, Appl
20	28.6	12.8	123593	US-10-796-280-12388	Sequence 12388, A
21	28.4	12.7	201	US-10-767-471-10851	Sequence 28959, A
22	28.4	12.7	209320	US-10-767-471-10861	Sequence 10861, A
23	28.4	12.7	495635	US-10-765-790-12	Sequence 12, Appl
24	28.4	12.7	705636	US-10-765-790-10	Sequence 30, Appl
25	28.2	12.6	30826	US-10-100-683-12760	Sequence 12760, A
26	28.2	12.6	86081	US-60-548-091-5624	Sequence 5624, Ap

C 27	28	12.6	2271	6	US-10-100-683-3366	Sequence 3366, Ap
C 28	28	12.6	27407	6	US-10-021-698A-927	Sequence 927, Appl
C 29	28	12.6	64669	7	US-10-767-471-10845	Sequence 10845, A
C 30	27.8	12.5	66686	7	US-60-548-091-5680	Sequence 5680, Ap
C 31	27.8	12.5	105314	7	US-60-548-091-5600	Sequence 5600, Ap
C 32	27.8	12.5	519599	6	US-10-765-790-73	Sequence 73, Appl
C 33	27.6	12.4	623	6	US-10-773-236-124	Sequence 124, Appl
C 34	27.6	12.4	1656	6	US-10-767-701-14214	Sequence 14214, A
C 35	27.6	12.4	2244	6	US-10-773-236-24	Sequence 24, Appl
C 36	27.4	12.3	35867	6	US-10-767-471-10843	Sequence 10843, A
C 37	27.4	12.3	643250	6	US-10-796-280-12230	Sequence 12230, A
C 38	27.2	12.2	533	6	US-10-767-701-21553	Sequence 21553, A
C 39	27.2	12.2	655	6	US-10-767-701-6332	Sequence 6332, Ap
C 40	27.2	12.2	1481	5	US-09-830-915D-30	Sequence 30, Appl
C 41	27.2	12.2	2096	6	US-10-100-683-3836	Sequence 3836, Appl
C 42	27.2	12.2	14749	6	US-10-767-471-10851	Sequence 10851, A
C 43	27.2	12.2	157953	6	US-10-796-280-12293	Sequence 12393, A
C 44	27.2	12.2	780759	6	US-10-767-471-10626	Sequence 10626, A
C 45	27	12.1	201	7	US-60-548-091-7470	Sequence 7470, Ap

#### ALIGNMENTS

RESULT 1  
US-60-545-213-2723  
Sequence 2723, Application US/60545213  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042099)  
CURRENT APPLICATION NUMBER: US/60/545, 213  
CURRENT FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2723  
LENGTH: 1400  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-545-213-2723

Query Match 89.2%; Score 199; DB 7; Length 1400;  
Best Local Similarity 97.3%; Pred. No. 3.3e-59;  
Matches 213; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	5	CAAGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTGCA	64
DB	336	CAAGTGACCAAAATGACTT-GGAAACGGGCTCATTCACCACTCCAGACTCTTGCA	394
QY	65	ATGAGACTTGTCTAGCTTGGGGTGGCCAAAGGCAAGTCTGACTGAGCCCTCA	124
DB	395	ATGAGACTTGTCTAGCTTGGGGTGGCCAAAGGCAAGTCTGACTGAGCCCTCA	454
QY	125	CTTCCAGCCTTACCTCATAGCTTCAAGCCTTGCTTCACTTGAAGCTTCAGGGGTCA	184
DB	455	CTTCCAGCCTTACCTCATAGCTTCAAGCCTTGCTTCACTTGAAGCTTCAGGGGTCA	514
QY	185	GCAGCTTAGTGTATCAACAGGGAGTGGATTACCAAAATT	223
DB	515	GCAGCTTAGTGTATCAACAGGGAGTGGATTACCAAAATT	553

RESULT 2  
US-60-545-213-2724  
Sequence 2724, Application US/60545213  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042099)

;; CURRENT APPLICATION NUMBER: US/60/545,213  
;; CURRENT FILING DATE: 2004-02-18  
;; NUMBER OF SEQ ID NOS: 303284  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO: 2724  
;; LENGTH: 1400  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-60-545-213-2724

Query Match 89.2%; Score 199; DB 7; Length 1400;  
Best Local Similarity 97.3%; Pred. No. 3.3e-59;  
Matches 213; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64  
DB 336 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 394  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 124  
DB 395 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 454  
QY 125 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 184  
DB 455 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 514  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 223  
DB 515 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 553

RESULT 3  
US-60-545-213-6995  
; Sequence 6995, Application US/60545213  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mount, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042099)  
; CURRENT APPLICATION NUMBER: US/60/545,213  
; CURRENT FILING DATE: 2004-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 6995  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-545-213-6995

Query Match 89.2%; Score 199; DB 7; Length 1400;  
Best Local Similarity 97.3%; Pred. No. 3.3e-59;  
Matches 213; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64  
DB 336 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 394  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 124  
DB 395 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 454  
QY 125 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 184  
DB 455 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 514  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 223  
DB 515 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 553

RESULT 4  
US-60-545-213-6996

;; Sequence 6996, Application US/60545213  
;; GENERAL INFORMATION:  
;; APPLICANT: Wyeth  
;; APPLICANT: Mount, William Martin  
;; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
;; TITLE OF INVENTION: Target Genes  
;; FILE REFERENCE: AM101083 (031896-042099)  
;; CURRENT APPLICATION NUMBER: US/60/545,213  
;; CURRENT FILING DATE: 2004-02-18  
;; NUMBER OF SEQ ID NOS: 303284  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO: 6996  
;; LENGTH: 1400  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-60-545-213-6996

Query Match 89.2%; Score 199; DB 7; Length 1400;  
Best Local Similarity 97.3%; Pred. No. 3.3e-59;  
Matches 213; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 5 CAAGGTGACCAAAATGACTTGGGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 64  
DB 336 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCTCATTCACCACTCCAGACTCTTTGCA 394  
QY 65 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 124  
DB 395 ATGAGACTTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCA 454  
QY 125 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 184  
DB 455 CCTCAGCGCTACTCATAGCTTTCACAGCCTTGCCTTCAAGCTTGAAGCTCCAGGGGTCA 514  
QY 185 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 223  
DB 515 GCAGCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 553

RESULT 5  
US-10-767-701-6910  
; Sequence 6910, Application US/10767701  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO: 6910  
; LENGTH: 1057  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1057)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: clone ID: SORBI-28MAV03-CLUS59646\_1  
US-10-767-701-6910

Query Match 13.9%; Score 31; DB 6; Length 1057;  
Best Local Similarity 53.8%; Pred. No. 0.52;  
Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 72 CTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCAAGCTTCAAC 131  
DB 190 CTGTCTAGCTTTGGGGTGCCCAAGGCAAGTCCACTGTGACTGAGCCCTCAAGCTTCAAC 249  
QY 132 GCCTACCTTAGTGTATCAACAGGAGTGGATTCCACCAAAATT 190

Db 250 GCGCAGCGCGCGCTCCGTAACGGGCTCCGAGCCGATAGCCCGCTGCTGCTGCT 308

RESULT 6  
US-10-796-280-12234

; Sequence 12234, Application US/10796280

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CI001510

; CURRENT APPLICATION NUMBER: US/10/796,280

; CURRENT FILING DATE: 2004-03-10

; NUMBER OF SEQ ID NOS: 68533

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12234

; LENGTH: 128811

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-796-280-12234

Query Match 13.5%; Score 30.2; DB 6; Length 128811;

Best Local Similarity 62.7%; Pred. No. 7.1;

Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 104 TCACCTGTGACTGAGCCTTCACTCCAGCCTTACCTATAGCTTGCAGAGCTTGCCTTCA 163

98951 TGGCTGTCTCTCTGAGGAGCTTCTCAGGTTCCCATGACTTGTGAAATGCT 99010

164 GCCTGTGAGCTCCAG 178

99011 GATTTCGCCCCCAG 99025

RESULT 7

US-60-548-091-5682/c

; Sequence 5682, Application US/60548091

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CI001506

; CURRENT APPLICATION NUMBER: US/60/548,091

; CURRENT FILING DATE: 2004-02-27

; NUMBER OF SEQ ID NOS: 24433

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5682

; LENGTH: 21142

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-548-091-5682

Query Match 13.2%; Score 29.4; DB 7; Length 21142;

Best Local Similarity 56.8%; Pred. No. 6.4;

Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 108 CTGTGACTGAGCCTTCACTCCAGCCTTACCTATAGCTTGCAGAGCTTGCCTTCA 167

5373 CCGTGGGGGAGGCCCTCTCTTACTTCTGGGGCCGGGCTCCCATTCCTCCCTCAGGCC 5314

168 CTGAGCTTCAGGGGCTCAGAGCTTATGTATCAAC 202

5313 CTCAGCAGCCAGAGCCTAGCATAGTTCCCCAC 5279

RESULT 8

US-10-796-280-12414

; Sequence 12414, Application US/10796280

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CI001510

; CURRENT APPLICATION NUMBER: US/10/796,280

; CURRENT FILING DATE: 2004-03-10

; NUMBER OF SEQ ID NOS: 68533

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12414

; LENGTH: 25930

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-796-280-12414

Query Match 13.0%; Score 29; DB 6; Length 25930;

Best Local Similarity 53.0%; Pred. No. 9.6;

Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Db 24 TTGGGAAAGCGGCTTATTCACCTCCAGACTCTTTGAAATGAGACTTGTCTAGCTT 83

11234 TTGGGAAAGCTTACCTCTGATCAGAGGATCATATTAATCGAGTTGTCTGAGGCTTTGAGT 11293

84 TGGGGTGGCCAGGAGGAGGTCACCTGTGACTGAGCCTTCACTCCAGCCTTCACTC 140

11294 TGGGGTGGCCAGGAGGATCACCACCTTCAATTGAAATTCCTCCCTCCAGGCTGAATC 11350

RESULT 9

US-10-417-375A-66/c

; Sequence 66, Application US/10417375A

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer

; FILE REFERENCE: 529452001600

; CURRENT APPLICATION NUMBER: US/10/417,375A

; CURRENT FILING DATE: 2003-04-15

; NUMBER OF SEQ ID NOS: 176

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 66

; LENGTH: 252907

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-417-375A-66

Query Match 13.0%; Score 29; DB 6; Length 252907;

Best Local Similarity 58.8%; Pred. No. 24;

Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 99 CAAGTTCACCTGAGCTGAGCCTTCACTCCAGCCTTACCTATAGCTTGCAGAGCTTGC 158

52747 CCAGCACTTCCGTGTGAGCCTGCAAGGCTGCTCCCATCTGCTGCCAGACTGCT 52688

159 CTTGAGCCTTGTGAGCTTCAGGGGTC 183

52687 CTCAAACTCTGTGGCTCAAGGGGTC 52663

RESULT 10

US-60-545-213-4092

; Sequence 4092, Application US/60545213

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; FILE REFERENCE: AM101083 (031896-042099)

; CURRENT APPLICATION NUMBER: US/60/545,213

; CURRENT FILING DATE: 2004-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4092

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-545-213-4092

FRONT AFFILIATION NUMBER: US 80/038,892

[illegible]

RESULT 14  
US-10-100-683-13346/c  
Sequence 13346, Application US/10100683  
GENERAL INFORMATION:  
APPLICANT: Rosen, et al.  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: P8900  
CURRENT APPLICATION NUMBER: US/10/100,683  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US 60/040,162  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: US 60/043,576  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: US 60/047,601  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: US 60/056,845  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/043,580  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: US 60/047,599  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: US 60/056,664  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/043,314  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: US 60/047,632  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: US 60/056,892  
PRIOR FILING DATE: 1997-08-22  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1346  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 13346  
LENGTH: 4628  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-100-683-13346

Query Match 12.9%; Score 28.8; DB 6; Length 4628;  
Best Local Similarity 56.2%; Pred. No. 5.5;  
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 85 GGGGTGGCCAAAGGCGCAAGTCTGACTGAGCCTTCACTCCAGCCTTACTAG 144  
DB 546 GGTATTGCCAAGGTCAAGGCGCAAGTCTGAGCCTTACTAGTGGCGCCACTTACTAG 487  
QY 145 CTTACAGCCTTGGCTTCAAGCCTTCTGAGCTCCAGG 180  
DB 486 CTTACAGCCTTGGCTTCAAGCCTTCTGAGCTCCAGG 451

RESULT 15  
US-10-775-920-271  
Sequence 1271, Application US/10775920  
GENERAL INFORMATION:  
APPLICANT: Mergen Ltd  
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES  
TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED  
TITLE OF INVENTION: IN CERTAIN CANCERS  
FILE REFERENCE: Mergen - 0010B  
CURRENT APPLICATION NUMBER: US/10/775,920  
CURRENT FILING DATE: 2004-02-10  
PRIOR APPLICATION NUMBER: US 60/447,900  
PRIOR FILING DATE: 2003-02-13  
NUMBER OF SEQ ID NOS: 385  
SOFTWARE: Patent Ver. 3.2  
SEQ ID NO: 271  
LENGTH: 4132  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-775-920-271

Query Match 12.8%; Score 28.6; DB 6; Length 4132;  
Best Local Similarity 53.0%; Pred. No. 6.2;  
Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 81 CTTTGGGTGGCCCAAGGCGCAAGTCTGACTGAGCCTTCACTCCAGCCTTACTAG 140  
DB 1389 CTTTGGGTGGCCCAAGGCGCAAGTCTGACTGAGCCTTCACTCCAGCCTTACTAG 1448  
QY 141 ATAGCTTACAGCCTTGGCTTCAAGCCTTCTGAGCTCCAGGGGTACAGCCTTACTAG 195  
DB 1449 CTTACCATCTTCCCGCATGTTCAACCCAGAGGAGCGGAGCTGACGCTTACTAG 1503

Search completed: March 23, 2004, 04:51:24  
Job time: 321.599 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 15:35:59 ; Search time 1308.4 Seconds  
(without alignments)  
5089.629 Million cell updates/sec

Title: US-09-646-224A-17

Perfect score: 223  
Sequence: 1 tgcacgaagtgcacccaat.....ggagctgattccacccaatt 223

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estcom:\*  
16: em\_esthum:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_pig:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.6	42.4	4614	29	AY404475 Homo sapi
2	59.8	29	4556	29	AY404477 Mus muscu
3	35.8	16.1	995	9	AL571390 AL571390
4	34.6	15.3	723	13	BX673737 BX673737

5	34.4	15.4	521	28	AQ848329 LMAUFV1.1
6	34.2	15.3	576	28	CE037831 Cigr-gss-
7	34.2	15.2	775	28	BH899137 CE000204
8	33.8	15.2	564	9	AV565889 AV565889
9	33.8	15.2	571	9	AV561225 AV561225
10	33.8	15.2	632	14	CF948308 UI-D-GC1-
11	33.4	15.0	796	29	CC517185 CH240_363
12	33.4	15.0	923	29	CNS0610R T3 end of
13	33.4	15.0	994	29	CNS06CV0 T3 end of
14	33.4	15.0	1001	29	CNS007C8 AL066993 Drosophila
15	33.4	15.0	1001	29	CNS007C8 B1417342 LjNEST38a
16	33.2	14.9	587	13	BU048840 PE LBA003
17	33.2	14.9	610	13	BU785965 in48d05_Y
18	33	14.8	666	10	B6638780 CB376456 AMGNNUC:N
19	32.8	14.7	782	29	CG317804 BFP80892 AU238205
20	32.6	14.6	629	28	BH874175 BZ211062 CH230-426
21	32.6	14.6	643	12	B1771086 B1915983 603177095
22	32.6	14.6	909	28	CC422910 AK086309 Mus muscu
23	32.6	14.6	931	28	CC422914 BH196236 B196236
24	32.4	14.5	522	10	BE230112 BB05876 BB05876
25	32.4	14.5	547	28	BZ902586 A0830694 HS 5563_A
26	32.4	14.5	675	13	BU265240 A1632307 tE22d06.X
27	32.2	14.4	462	14	CB736496 B0816339 N063D12_P
28	32.2	14.4	632	9	AU238205 BMS44658 AGENCOURT
29	32.2	14.4	831	10	BP980892 A1198288 q161d04.x
30	32.2	14.4	860	28	BZ211062 A1498877 tme8h04.x
31	32.2	14.4	893	12	B1915983 BH911957 PST1174-1
32	32.2	14.4	3016	11	AK086309 A0458786 HS 5060_B
33	32	14.3	315	10	BH196236 A0460354 RFC1-11-2
34	32	14.3	315	10	BB05876 BB541268 BB541268
35	32	14.3	478	28	A0830694 HS 5563_A
36	32	14.3	528	9	A1632307 tE22d06.X
37	32	14.3	653	13	B0816339 BMS44658 AGENCOURT
38	31.8	14.3	994	12	BM544658 A1198288 q161d04.x
39	31.6	14.2	454	9	A1498877 tme8h04.x
40	31.6	14.2	454	9	A1498877 tme8h04.x
41	31.6	14.2	460	28	BH911957 PST1174-1
42	31.6	14.2	512	28	A0458786 HS 5060_B
43	31.6	14.2	528	28	A0460354 RFC1-11-2
44	31.4	14.1	250	10	BB541268 BB541268
45	31.4	14.1	494	12	B1681465 460866 MA

## ALIGNMENTS

RESULT 1	AY404475	4614 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY404475				
DEFINITION	Homo sapiens SCN11A gene, VIRUTAL TRANSCRIPT, partial sequence.				
ACCESSION	AY404475				
VERSION	AY404475.1	GI:39760452			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,				
AUTHORS	Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,				
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 4614)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,				
	Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,				
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source  
1..4614  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/gene="SCN11A"  
/locus\_tag="HCM1903"

ORIGIN

Query Match 42.4%; Score 94.6; DB 29; Length 4614;  
Best Local Similarity 95.6%; Pred. No. 2.6e-16;  
Matches 108; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 5 CAAGGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTCTTTTGA 64  
Db 4503 CCAAGGTACCAAAATGACTT-GGAAACGGGCTCATTCACCACTCCAGACTCTTTTGA 4561  
Qy 65 ATGAGACTTGTCTGCTTTGGGGTGGCCAAAGGCGCAAGTCCACTGTGACTGA 117  
Db 4562 ATGAGACTTGTCTGCTTTGGGGTGGCCAAAGGCGCAAGTCCACTGTGACTGA 4614

RESULT 2  
AY040477 4556 bp DNA linear GSS 16-DEC-2003  
LOCUS Mus musculus SCN11A gene, VIRtual TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY040477 GI:39760454  
VERSION AY040477.1 GI:39760454  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS 1 (bases 1 to 4556)  
Clarke, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tenenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene clusters  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
2 (bases 1 to 4556)  
Clarke, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tenenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
source  
1..4556  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/gene="SCN11A"  
/locus\_tag="HCM1903"

ORIGIN

Query Match 26.8%; Score 59.8; DB 29; Length 4556;  
Best Local Similarity 71.2%; Pred. No. 3.9e-06;  
Matches 79; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 7 AGGTGACCAAAATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTTTTGAAT 66

Db 4446 AAGATGATCAAGCTGAGAGTGAAGGAGGTCAGAGTTCATGCTCCAGAGTGTTCGAT 4505

Qy 67 GGAGACTTGTCTACTTTGGGGTGGCCAAAGGCGCAAGTCCACTGTGACTGA 117  
Db 4506 GGAGACTTGTCTACTTTGGGGTGGCCAAAGGCGCAAGTCCACTGTGACTGA 4556

RESULT 3  
AL571390 995 bp mRNA linear EST 31-MAY-2003  
LOCUS AL571390 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
DEFINITION clone CSOD1023YC04 3-PRIME, mRNA sequence.  
ACCESSION AL571390  
VERSION AL571390.2 GI:1292790  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 995)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 16, 2001 this sequence version replaced gi:12928639.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10873.f. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSOD1023B02NP1&cluster=10873.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSOD1023B02NP1.

FEATURES  
source  
1..995  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1023YC04"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (CT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 16.1%; Score 35.8; DB 9; Length 995;  
Best Local Similarity 39.6%; Pred. No. 18;  
Matches 57; Conservative 27; Mismatches 60; Indels 0; Gaps 0;

Qy 33 CGGGCTCATTCACCACTCCAGACTCTTGCATGAGACTTGTCTAGCTTTGGGGTGC 92  
Db 850 CGGNSCGMHTTCCSAGGCTGACTTSCSTGGGAMMSCTTGTCTTGGSGKGG 909

Qy 93 CAAGGCGAAGTTCACCTGTGACTGAGCCCTTCACCTCCAGCTTCACTTACAG 152  
Db 910 GDTMGSCGCGAGGCTGTCVYMAAYTTGTGCTSCBGGCTCCCTTSGACTATWAT 969

Qy 153 CTTGCTTCAAGCTCTGAGCTCC 176  
Db 970 AMCTCHKTTTGGCWC CGGSGCTCY 993

RESULT 4  
BX673737/c 723 bp mRNA linear EST 28-OCT-2003  
LOCUS BX673737 Sus Scrofa library (scac) Sus scrofa CDNA clone  
DEFINITION scac00401.a.14 5prim, mRNA sequence.

ACCESSION BX673737.1 GI:38007633  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX673737  
EST.  
Sus scrofa (pig)  
Sus scrofa  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
1 (bases 1 to 723)  
Bonnat, A., Tosser-Klopp, G., Benne, F., Cabu, C., Villegier, S.,  
Soares, M., Bernaldo, F. and Harey, F.  
A Pig Normalised Multi-Tissue cDNA Library  
Unpublished (2003)  
Contact: Tosser-Klopp G  
Genetique Animale  
Institut National de la Recherche Agronomique  
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan  
cedex, FRANCE  
Tel: 33 (0) 5.61.28.51.14  
Fax: 33 (0) 5.61.28.53.08  
Email: tosser@clouuse.inra.fr  
Clone distribution: AGENAS Resource centre, Francois PUMI,  
Francois.Pumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du  
genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,  
FRANCE. +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73  
Sequence cleaned of vector, adaptor and repetitions. Contact us  
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this  
sequence.  
Plate: 0040, row: a column: 14.  
Location/Qualifiers  
1..723  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="scac00401.a.14"  
/issue\_type="mixed"  
/clone\_lib="Sus Scrofa library (scac)"  
/note="Vector: pT73D-pac vector; tissues: adipose tissue,  
brain, kidney, liver, muscle, ovary, testis, heart,  
hypothalamus, pancreas, skin, spleen, thymus, placenta,  
pituitary gland, seminal vesicle, small intestine,  
uterus, adrenals, bulbo urethral gland, cerebral trunk,  
epididymis, female gonad, gall-bladder, hippocampus,  
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN  
Query Match 15.5%; Score 34.6; DB 13; Length 723;  
Best Local Similarity 58.1%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ATGACTTGGGAAACGGGCTCATTCACCACTCCAGACTTTGGCAATGAGACTGTCT 78  
DB 362 ATACCGGGGGGTACGGGTTCCTCCCGCAGCCAGGGTCTAGCAAGGGGAGATGCT 303  
QY 79 AGCTTTGGGGTGGCAAGGCAAGTCCACTGTGACGTGAGCCCTC 123  
DB 302 GCCCAGGAGGTGGGCGGGCAGACGCCGCTGTACTGAGGACTC 258

RESULT 5  
LOCUS A0848329 521 bp DNA linear GSS 25-MAY-2001  
DEFINITION LMAJFV1\_1m60d08.x1 Leishmania major FV1 random genomic library  
Leishmania major genomic clone LMAJFV1\_1m60d08.3, genomic survey  
sequence.  
ACCESSION A0848329  
VERSION A0848329.1 GI:6052977  
KEYWORDS GSS.  
SOURCE Leishmania major  
ORGANISM Leishmania major  
Bukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Leishmania.  
REFERENCE 1 (bases 1 to 521)  
Akopyants, N.S., Clifton, S.W., Martin, J., Page, D., Wylie, T., Li, L.,

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Kissinger, J.C., Roos, D.S. and Beverley, S.M.  
A survey of the Leishmania major Friedlin strain V1 genome by  
shotgun sequencing: a resource for DNA microarrays and expression  
profiling  
Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)  
21192569  
11295190  
Contact: Akopyants, NS / Beverley, SM  
Washu Leishmania Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
Library construction: Natalia S. Akopyants, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
If using this information please cite:  
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major  
Friedlin strain V1 genome by shotgun sequencing' and the Washington  
University Genome Sequencing Center for information on obtaining  
clone material please contact: Natalia S. Akopyants Ph.D.  
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.  
(beverley@borcim.wustl.edu)  
Seq primer: -40UP from G1bco  
Class: shotgun  
High quality sequence stop: 420.  
Location/Qualifiers  
1..521  
/organism="Leishmania major"  
/mol\_type="genomic DNA"  
/strain="Friedlin strain V1"  
/db\_xref="taxon:5654"  
/clone="LMAJFV1\_1m60d08"  
/lab\_host="TOP10 (Invitrogen)"  
/clone\_lib="Leishmania major FV1 random genomic library"  
/note="Vector: pZero-2 (Invitrogen); Site 1: BcoRV;  
Genomic DNA was isolated from stationary phase cells. For  
this library, DNA was sheared to give a tight size  
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA  
polymerase, dephosphorylated with Shrimp Alkaline  
Phosphatase and ligated into pZero-2 vector's EcoRV site."

ORIGIN  
Query Match 15.4%; Score 34.4; DB 28; Length 521;  
Best Local Similarity 48.5%; Pred. No. 32;  
Matches 95; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 28 GAAAGGGGCTCATTCACCACTCCAGACTCTTGCAGTGAAGACTGTAGCTTGGG 87  
DB 40 GATTAAGGGAAGCACTCCACTTGTGTGCAATGACAGCTCTGTGCGCGTCTCCG 99  
QY 88 GTGGCCAAAGGCAAGGTGCACTGTGACTGAGCCCTCAGAGCTTACTTACTTACTT 147  
DB 100 GTGTCCGGCGGCAATGCTGCTCCGTTTCAATCTGTGCTCCGCGGAGCGAGAGCT 159  
QY 148 CACAGCTTGTGCTTCAAGCTCTGAGCTCCAGGGGTGACAGCTTATGATCAACAGGGA 207  
DB 160 TACAGCCAAAGTCTTCAACCAAGAGAGGTGTGTCTCAATGCACTTATGACAGCTGTGCGT 219  
QY 208 GTGGATTCACCAACT 223  
DB 220 GTGGCAATCCCAACT 235

RESULT 6  
LOCUS CE037831 576 bp DNA linear GSS 24-SEP-2003  
DEFINITION tigr-gss-dog-17000349541289 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE037831  
VERSION CE037831.1 GI:35066898  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)

ORGANISM *Canis familiaris*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 576)  
Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M., and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
JOURNAL MEDLINE 2875432  
PubMed 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.  
FEATURES  
source location/Qualifiers  
1..576  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

Query Match 15.3%; Score 34.2; DB 29; Length 576;  
Best Local Similarity 55.5%; Pred. No. 39;  
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 52 CAGACTTTTGCATGAGACTGTCTAGCTTGGGGTGGCCAGGAGGCTCAGCTGT 111  
DB 2 CCGACTCTGGTTTGGCTGCTGCTGATTTGGGGTATGAGATCAAGCTCAGCTTG 61  
QY 112 GACGTAGGCTTCACCTCCACGCTACCTCATTGCTTCAAGCTTGCCTTCAAGCTTGC 170  
DB 62 GCTTCACACTCAGATGAGATGCTGCTGAGATCTCTGCTTCCCTCAGCTTCTG 120

RESULT 7  
BH899137/c 775 bp DNA linear GSS 30-AUG-2002  
LOCUS Ots00204 Ostreococcus tauri genomic shotgun library Ostreococcus  
DEFINITION tauri genomic clone ota21e06.b 5', genomic survey sequence.  
ACCESSION BH899137  
VERSION BH899137.1 GI:22550632  
KEYWORDS GSS.  
SOURCE Ostreococcus tauri  
ORGANISM Ostreococcus tauri  
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales;  
Mamiellaceae; Ostreococcus.  
REFERENCE 1 (bases 1 to 775)  
Derelle, E., Ferraz, C., Lagoda, P., Eychenne, S., Cooke, R., Regad, F.,  
Sabau, X., Courtles, C., Delserny, M., Demallie, J., Picard, A. and  
Moreau, H.  
DNA libraries for sequencing the genome of Ostreococcus tauri  
(Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic  
cell  
J. Phycol. 38 (6), 1150-1156 (2002)  
COMMENT Contact: Moreau H  
Laboratoire Arago  
CNRS UMR 7628  
BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France  
Tel: (33)468887309  
Fax: (33)468887398  
Email: h.moreau@obs-banyuls.fr  
Seq primer: forward  
Class: shotgun.  
FEATURES  
Location/Qualifiers

source 1..775  
/organism="Ostreococcus tauri"  
/mol\_type="genomic DNA"  
/strain="OTH0595"  
/db\_xref="taxon:70448"  
/clone\_lib="ota21e06.b"  
/note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;  
Shotgun library prepared after sonication of the genomic  
DNA. Blunt ligation in EcoRV site of Bluescript. Size  
selection of the inserts after agarose electrophoresis  
between 1 and 3 Kb."

Query Match 15.2%; Score 34; DB 28; Length 775;  
Best Local Similarity 55.5%; Pred. No. 52;  
Matches 91; Conservative 0; Mismatches 65; Indels 8; Gaps 1;  
QY 38 CTCATTCACCACTCCAGACTTTTGCATGAGAGACTTGTCTAGCTTGGGGTGCCAGG 97  
DB 173 CTGGTGCGCTCCAGGCGCATCGCGTCCACACCTCTGCGCTTCCGTTGCCATTC 114  
QY 98 GCAGATCCACTGTGACTGAGCCCTTCACTTCCAGCCTTCACTTCACTTCAAGCTTG 157  
DB 113 GC-----CTCCGCTCCGCGCCCTCCGCGCTCTCAATGCAAGTTCACGCGCG 62  
QY 158 CTTTACGCTCTGAGCTCCAGGCGGCTCAGAGCTTAGTATCAA 201  
DB 61 TGTGATATCCCGGATCACCCAGAGGCTTACAGCTGTTCATGAA 18

RESULT 8  
AV565889 564 bp mRNA linear EST 07-SEP-2000  
LOCUS AV565889 Arabidopsis thaliana green siliques Columbia Arabidopsis  
DEFINITION thaliana cDNA clone SQ232e07F 3', mRNA sequence.  
ACCESSION AV565889  
VERSION AV565889.1 GI:8737339  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 564)  
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)  
JOURNAL MEDLINE 20363093  
PubMed 10907847  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
FEATURES  
source Location/Qualifiers  
1..564  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="SQ232e07F"  
/issue\_type="green siliques"  
/clone\_lib="Arabidopsis thaliana green siliques Columbia"  
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:  
XhoI"

Query Match 15.2%; Score 33.8; DB 9; Length 564;  
Best Local Similarity 48.9%; Pred. No. 50;  
Matches 89; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 24 TTGGGAAAAGGGCTTCATTACCACTCCAGACTCTTTGCAATGAGACTGTGTAGCTT 83  
 DB 346 TCGGGAAACAAACCCGTTTCTCTCCACCGCTGCGCCGATGTAACAAATTCCTCAACTC 405  
 QY 84 TGGGGTGGCCAGGAGGCAAGTCCACTGTGACTAGAGCCCTCACCCTCCAGCGCTACTCATTA 143  
 DB 406 TGACTTCTTGGAGGCAATTTCTTGTGAGATCTTCCCATTAACATATCCATTTCTCTCT 465  
 QY 144 GCTTACAGCCTTGCTTCCCTTGAGCTCCAGGAGGCTCAGAGCTTACTGATGATCAACA 203  
 DB 466 TCTTTGCGAGTCACCAAGCACTTCTCATCTCCACGATGACAGAAAGCTTCTCTGATCA 525  
 QY 204 GG 205  
 DB 526 TG 527

RESULT 9  
 AV561225 571 bp mRNA linear EST 07-SEP-2000  
 LOCUS AV561225 Arabidopsis thaliana green siliques Columbia Arabidopsis  
 DEFINITION thaliana cDNA clone SQ147g09p 3', mRNA sequence.  
 ACCESSION AV561225  
 VERSION AV561225.1 GI:8732651  
 KEYWORDS EST.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 571)  
 Aamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
 of 12,028 non-redundant expressed sequence tags from normalized and  
 size-selected cDNA libraries  
 DNA Res. 7 (3), 175-180 (2000)  
 20363093  
 JOURNAL MEDLINE  
 PUBMED 10907847  
 COMMENT Contact: Erika Aamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yena 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: aamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
 Location/Qualifiers  
 1. 571  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="Columbia"  
 /db\_xref="taxon:3702"  
 /clone="SQ147g09p"  
 /tissue\_type="green siliques"  
 /clone\_1lb="Arabidopsis thaliana green siliques Columbia"  
 /note="Vector: pBluescriptII SK-, Site\_1: EcoRI, Site\_2:  
 XhoI"

ORIGIN  
 Query Match 15.2%; Score 33.8; DB 9; Length 571;  
 Best Local Similarity 48.9%; Pred. No. 50;  
 Matches 89; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 204 GG 205  
 DB 526 TG 527

RESULT 10  
 CF948308/c 632 bp mRNA linear EST 19-NOV-2003  
 LOCUS CF948308/c UI-D-GCI-aag-0-07-0-UI.61 UI-D-GCI Alexandrium tamarense cDNA clone  
 DEFINITION UI-D-GCI-aag-0-07-0-UI 3', mRNA sequence.  
 ACCESSION CF948308  
 VERSION CF948308.1 GI:38453126  
 KEYWORDS EST.  
 SOURCE Alexandrium tamarense  
 ORGANISM Alexandrium tamarense  
 Eukaryote; Alveolata; Dinophyceae; Gonyaulacales; Gonyaulacaceae;  
 Alexandrium.  
 1 (bases 1 to 632)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 JOURNAL MEDLINE  
 PUBMED 97044477  
 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@iowa.edu  
 Tissue Procurement: Provasoli-Guillard National Center for Culture  
 of Marine Phytoplankton (CCMP)  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 DNA Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/dinoflagellate.html  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 Location/Qualifiers  
 1. 632  
 /organism="Alexandrium tamarense"  
 /mol\_type="mRNA"  
 /strain="CCMP 1598"  
 /db\_xref="taxon:2926"  
 /clone="UI-D-GCI-aag-0-07-0-UI"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1lb="UI-D-GCI"  
 /note="Vector: pT73-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-D-GCI is a  
 normalized library derived from UI-D-GCI. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 TACCTCGACA. Tissue was obtained from the  
 Provasoli-Guillard National Center for Culture of Marine  
 Phytoplankton (CCMP).  
 TAG TISSUE=Alexandrium tamarense  
 TAG LIB=UI-D-GCI  
 TAG\_SEQ=TACCTCGACA"

ORIGIN  
 Query Match 15.2%; Score 33.8; DB 14; Length 632;  
 Best Local Similarity 53.4%; Pred. No. 53;  
 Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 84 TGGGTGGCCAGGCGAAGTTCACCTGTGACTGAGCCCTTCACCTTCACGCTTACTATTA 143  
 DB 256 TGGCAAGGCTGCACAGCTGCTGCACAGGAGCCAGTGCCTTCAAGTGCCTGCACAGCTTG 197  
 QY 144 GCTTCAACGCTTGCCTTCAAGCTTCAAGCTTCAGGGGTGCAGCATTATGATCAACA 203  
 DB 196 GCTGCAGGCGCCCGCTTCAATCTCGCGGTGCAGCGCGGCGACCTTCACTGTTCACCA 137  
 QY 204 GGGAGTGGATTCA 216  
 DB 136 GGAGGTGTGCGCA 124

RESULT 11  
 CCS17185/c  
 LOCUS  
 DEFINITION CCS17185 796 bp DNA linear GSS 17-JUN-2003  
 CH240\_363120.T7 CHORI-240 Bos taurus genomic clone CH240\_363120,  
 genomic survey sequence.

ACCESSION  
 VERSION CCS17185  
 KEYWORDS CCS17185.1 GI:31835473  
 GSS.

SOURCE  
 ORGANISM Bos taurus (cow)  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 796)

REFERENCE  
 AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smallue,D., Prabhu,A.-L.,  
 Teal,M., Cloutier,A., Lee,D., Gilm,N., Olson,T., Mayo,M.,  
 Buterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,  
 Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,  
 Schein,J., Marra,M., Masson,P., McWilliam,S., Barris,W.,  
 Dairymple,B.P. and Tellam,R.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
 Unpublished (2003)  
 OTHER\_GSSs: CH240\_363120.TARBA13P2  
 COMMENT Contact: Rob Holt

TITLE  
 JOURNAL The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6  
 TEL: 604-877-6085  
 FAX: 604-877-6276  
 Email: rhoit@cgsc.ca  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library  
 availability, please contact Pieter de Jong ([pdj@ongmail.cho.org](mailto:pdj@ongmail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/orderinginformation.htm>). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBMC) by CSIRO Livestock Industries, Australia and the  
 British Columbia Genome Sciences Centre, Canada.  
 Plate: 363 Row: I Column: 20  
 Seg primer: T7  
 Class: BAC ends.

FEATURES  
 source

1..796  
 Location/Qualifiers  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_363120"  
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 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: pTARBA1.3, Site\_1: MboI, Site\_2: MboI,  
 Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 15.0%; Score 33.4; DB 29; Length 796;  
 Best Local Similarity 58.6%; Pred. No. 79;  
 Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 7 AGGTGACCAAAATGACTTGGAGAAAAGGCGCTTCATTACCACTCCAGACTCTTTGCAAT 66  
 DB 590 AGAAGAACCAAGAACGATTAAGAGAAATTTGGCTGAGAAATTCATTCATGCTTTCAAC 531  
 QY 67 GGAGACTTGTCTACTTGGGTGGCCAGGCGCAAGTTC 105  
 DB 530 GAGGCTTGTGTGGGTGAGCATTTGATGAGCAAGAGAC 492

RESULT 12  
 CNS0610R  
 LOCUS  
 DEFINITION T3 end of clone AS00A016H06 of library AS00A from strain CLB 533  
 of Saccharomyces bayanus, genomic survey sequence.

ACCESSION  
 VERSION AL399697  
 KEYWORDS AL399697.1 GI:12154534  
 GSS.

SOURCE  
 ORGANISM Saccharomyces bayanus  
 Saccharomyces bayanus  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 1 (bases 1 to 923)

REFERENCE  
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,  
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,  
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,  
 Malpertuy,A., Neveglisse,C., Ozier-Kalogeropoulos,O., Potier,S.,  
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,  
 Wincker,P. and Weissenbach,J.  
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
 yeast species for molecular evolution studies  
 FEMS Lett. 487 (1), 3-12 (2000)

REFERENCE  
 PUBMED 11152876  
 TITLE  
 JOURNAL 2 (bases 1 to 923)  
 MEDLINE Bon,E., Neveglisse,C., Casaregola,S., Artiguenave,F., Wincker,P.,  
 Aigle,M. and Durrens,P.  
 Genomic exploration of the hemiascomycetous yeasts: 5.  
 Saccharomyces bayanus var. uvarum  
 FEMS Lett. 487 (1), 37-41 (2000)

REFERENCE  
 PUBMED 11152880  
 TITLE  
 JOURNAL 3 (bases 1 to 923)  
 MEDLINE Direct Submission  
 Submitted (07-SEP-2000) Genoscope - Centre National de Sequenage,  
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
 seqref@genoscope.cns.fr - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
 This GSS is part of a random genomic sequencing program of thirteen  
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,  
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia  
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
 5 kb were prepared and both extremities were sequenced. See  
 keywords for description of this sequence and for the sequence of  
 the other extremity of this insert.

FEATURES  
 source

1..923  
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 /organism="Saccharomyces bayanus"  
 /mol\_type="genomic DNA"  
 /strain="CLB 533"  
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 /db\_xref="taxon:4931"  
 /clone="AS00A016H06"  
 /clone\_id="AS00A"  
 /note="end : T3"  
 complement(<12..>923)  
 /note="similar to Saccharomyces cerevisiae ORF YPR160w [  
 GPI, glycogen phosphorylase ]"  
 /evidence="not\_experimental"

ORIGIN

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Best Local Similarity	52.5%	Pred. No. 86		
Matches	73	Conservative 0	Mismatches 66	Indels 0
				Gaps 0
QY	15	CAAAATGACTTGGGAAAACGGGCGCTCATATTCACCACTCCAGACTCTTTTGCAATGAGACTT	74	
Db	683	CCAGATGCTCTGGGCAACAAATAGCGCAATAGGCCCAAGGGCGCATTTTTCGAAGGCTTTT	742	
QY	75	GCTTAGCTTTGGGGTGGCCCAAGGGCAAGTGCATCTGTACTGAGCCTTCACTTCCAGCC	134	
Db	743	GCAATACGGTGTGGTGTGTAGCAAAAGGCTTGGTGTGACATGTCACAACTTCGTGCC	802	
QY	135	TACCTCATAGCTTCACAGC	153	
Db	803	AATCTAATTTCTCCAAATC	821	
RESULT 13				
LOCUS	CNS06GV0	994 bp	DNA	linear
DEFINITION	T3 end of clone AS0A007F03 of library AS0A from strain CLIB 533			
ACCESSION	AL398194			
VERSION	AL398194.1			
KEYWORDS	GI:12151485			
SOURCE	GSS.			
ORGANISM	Saccharomyces bayanus			
REFERENCE	Saccharomyces bayanus			
AUTHORS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
	1 (bases 1 to 994)			
	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bototin-Pukhara,M., Bon,E., Broctier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durren,P., Lepingle,A., Lorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nicche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.			
	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies			
	FEBS Lett. 487 (1), 3-12 (2000)			
TITLE	2 (bases 1 to 994)			
	Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P., Aigle,M. and Durren,P.			
JOURNAL	Genomic exploration of the hemiascomycetous yeasts: 5.			
MEDLINE	Saccharomyces bayanus var. uvarum			
PUBMED	FEBS Lett. 487 (1), 37-41 (2000)			
REFERENCE	20584715			
AUTHORS	3 (bases 1 to 994)			
TITLE	11152880			
JOURNAL	Genoscope.			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage.			
PUBMED	Direct Submissions			
REFERENCE	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : beate@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
AUTHORS	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces fragilis var. fragilis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.			
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Source	/mol_type="genomic DNA"			
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	/varietal="uvarum"			
	/db_xref="taxon:4931"			
	/clone="AS0A007F03"			

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/clone="Tend : T3"
<5. .981
/note="similar to Saccharomyces cerevisiae ORF YPR160w [
GPH1 :glycogen phosphorylase ]
1 putative frameshift(6)"
/evidence=not_experimental

ORIGIN
Query Match 15.0%; Score 33.4; DB 29; Length 994;
Best Local Similarity 52.5%; Pred. No. 89;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OY 15 CAAATACCTTGGAAACGGGCTCATTTACCACTCCAGCTTTGGCAATGAGACTT 74
DB 377 CCAAGATCTTGGGCGACAAATGCGCGAATAGCCAAAGGGCCATTTTCCAAAGCTTCTT 318
OY 75 GTTCAGCTTTGGGGTGCGCCAAAGGCGAAGTGCATCTGATGAGCCCTCACTCCAGGCC 134
DB 317 GCATTAACGCTGTGTGTTGTGTAAACAAAGTCTTGTGATCAATGTCCAAAGCTTGTGCC 258
OY 135 TACCTCATAGCTTCACAGC 153
DB 257 AATCTAATTTCTCCAAATC 239

RESULT 14
CNS007C8 1001 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TERT end of BAC #
DEFINITION BACR15M24 of RPCT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL066983
AL066983.1 GI:4945547
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1001)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osogawa and
Aaron Mammoler in Pieter de Jong's laboratory in the department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCT-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
Location/Qualifiers
1. 1001
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_11b="RPCT-98"
/note="end : TERT"

ORIGIN
Query Match 15.0%; Score 33.4; DB 29; Length 1001;
Best Local Similarity 37.8%; Pred. No. 89;

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Search completed: March 22, 2004, 23:13:39  
Job time : 1324.4 secs

	Matches	51,	Conservative	28,	Mismatches	56,	Indels	0,	Gaps	0,
QY	6	AAAGTGCACCAAAATGACTTTGGGAAAACGGGCTATTCCACCCTCCAGACTCTTTGC	65							
Dδ	950	AAAGRGKAAAAAMTWTTTTTTGGAAAAAATRGAAAGSVGTTMAAAAAAMWAGRTTTTGGMA	891							
QY	66	TGGAGACTGTCTAGCTTTGGGGTGGCCAAAGGACCACTGTGACTGAGCCCTCAC	125							
Dδ	890	GRTGAAACMGTTTGGATYTGAGAGRGCCCTGTGTMAMMGAGVMTGMMSGMMGMGTAM	831							
QY	126	CTCCACGCGCTACTCTC	140							
Dδ	830	MTTTGGCGCCTTWTTC	816							

RESULT 15  
PT4177407

LOCUS	BI417342	459 bp	mRNA	linear	EST 15-ANG-2001
DEFINITION	LJN85318a3r Lotus japonicus nodu library 5 and 7 week-old Lotus				
	corniculatus var. japonicus cDNA 5', mRNA sequence.				
ACCESSION	BI417342				
VERSION	BI417342.1	GI:15188365			
KEYWORDS	EST.				
SOURCE	Lotus corniculatus var. japonicus (Lotus japonicus)				
ORGANISM	Lotus corniculatus var. japonicus				

## FEATURES

```

source
1. .459
/organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/cultivar="Gifu (B-129) "
/db_xref="taxon:34305"
/dev_stage="5 and 7 week-old plants"
/clone_lib="Lotus japonicus nodule library 5 and 7
week-old"
/note="Organ: Nodule; Vector: pSPORT1; Site 1: SalI;
Site 2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."

```

## ORIGIN

	Query Match	14.9%	Score 33.2	DB 12	Length 459
	Best Local Similarity	54.0%	Pred. No. 67		
	Matches	68	Conservative	0	Mismatches 58
				Indels	0
				Gaps	0
QY	43 TCACCACTCCAGACTCTTTCAGATGAGACATGTTCTAGCTTTGGGATGGCCAAAGGCAAG	102			
Db	186 TCACCACTCCCTTTCTTTCTTTCTTTATCTTTCTTTCTTTCTTTGGTGGGACCAATCCACAG	127			
QY	103 GTCCACTGTGACTAGAGCCTCACTCCACGCGCTTACTATAGCTTCACAGCCTTGTGCTTC	162			
Db	126 TTCGCGTTTGTCTTCTCCGATCAGTACGACCAACAGACTCTTTGCGTTCATCGTCCCTTC	67			
QY	163 AGCCTC 168				
Db	66 ACCGTC 61				



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